High-Resolution Profiling of Histone Methylations in th

Cell 129, 823-837 DOI: 10.1016/j.cell.2007.05.009

Citation Report

#	Article	IF	CITATIONS
1	Events at DNA replication origins and genome stability. , 0, , 35-55.		0
4	Incommensurable Goods, Alternative Possibilities, and the Self-Refutation of the Self-Refutation of Determinism. American Journal of Jurisprudence, 2005, 50, 165-171.	0.4	0
5	Reuniting the contrasting functions of H2A.ZThis paper is one of a selection of papers published in this Special Issue, entitled 27th International West Coast Chromatin and Chromosome Conference, and has undergone the Journal's usual peer review process Biochemistry and Cell Biology, 2006, 84, 528-535.	0.9	90
6	Thioredoxinâ€ASK1 complex levels regulate ROSâ€mediated p38 MAPK pathway activity in livers of aged and longâ€lived Snell dwarf mice. FASEB Journal, 2006, 20, 259-268.	0.2	180
7	Mammalian ASH1L Is a Histone Methyltransferase That Occupies the Transcribed Region of Active Genes. Molecular and Cellular Biology, 2007, 27, 8466-8479.	1.1	182
8	Domain-wide regulation of gene expression in the human genome. Genome Research, 2007, 17, 1286-1295.	2.4	127
9	p18 ^{Hamlet} Mediates Different p53-Dependent Responses to DNA Damage Inducing Agents. Cell Cycle, 2007, 6, 2319-2322.	1.3	20
10	Identification of DNA Methylation in 3' Genomic Regions that are Associated with Upregulation of Gene Expression in Colorectal Cancer. Epigenetics, 2007, 2, 161-172.	1.3	35
11	An antisense transcript spanning the CGG repeat region of FMR1 is upregulated in premutation carriers but silenced in full mutation individuals. Human Molecular Genetics, 2007, 16, 3174-3187.	1.4	241
12	PRMT6-mediated methylation of R2 in histone H3 antagonizes H3 K4 trimethylation. Genes and Development, 2007, 21, 3369-3380.	2.7	238
13	A new role for histone tail modifications in transcription elongation. Genes and Development, 2007, 21, 3209-3213.	2.7	21
14	CTCFBSDB: a CTCF-binding site database for characterization of vertebrate genomic insulators. Nucleic Acids Research, 2007, 36, D83-D87.	6.5	98
15	USF1 Recruits Histone Modification Complexes and Is Critical for Maintenance of a Chromatin Barrier. Molecular and Cellular Biology, 2007, 27, 7991-8002.	1.1	116
16	3'-O-modified nucleotides as reversible terminators for pyrosequencing. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 16462-16467.	3.3	42
17	MethyCancer: the database of human DNA methylation and cancer. Nucleic Acids Research, 2007, 36, D836-D841.	6.5	127
18	Acetylated Histone H3 and H4 Mark the Upregulated LMP2A Promoter of Epstein-Barr Virus in Lymphoid Cells. Journal of Virology, 2007, 81, 13242-13247.	1.5	27
19	Zellen mit zurückgedrehter Uhr. Nachrichten Aus Der Chemie, 2007, 55, 995-996.	0.0	1
20	Methods of DNA methylation analysis. Current Opinion in Clinical Nutrition and Metabolic Care, 2007, 10, 576-581.	1.3	109

TION RE

		EPORT	
#	Article	IF	CITATIONS
21	Whole-Genome Mapping of Histone H3 Lys4 and 27 Trimethylations Reveals Distinct Genomic Compartments in Human Embryonic Stem Cells. Cell Stem Cell, 2007, 1, 286-298.	5.2	536
22	Human ES Cell Profiling Broadens the Reach of Bivalent Domains. Cell Stem Cell, 2007, 1, 237-238.	5.2	37
23	RNA Polymerase II: Just Stopping By. Cell, 2007, 130, 16-18.	13.5	12
24	A Ubiquitin-like Protein Involved in Membrane Fusion. Cell, 2007, 130, 18-20.	13.5	14
25	H3K27 Demethylases, at Long Last. Cell, 2007, 131, 29-32.	13.5	278
26	ChIP-Seq Data Reveal Nucleosome Architecture of Human Promoters. Cell, 2007, 131, 831-832.	13.5	77
27	Response: Mapping Nucleosome Positions Using ChIP-Seq Data. Cell, 2007, 131, 832-833.	13.5	32
28	We gather together: insulators and genome organization. Current Opinion in Genetics and Development, 2007, 17, 400-407.	1.5	367
29	MSL Complex Is Attracted to Genes Marked by H3K36 Trimethylation Using a Sequence-Independent Mechanism. Molecular Cell, 2007, 28, 121-133.	4.5	195
30	Demethylation of H3K27 Regulates Polycomb Recruitment and H2A Ubiquitination. Science, 2007, 318, 447-450.	6.0	678
31	Genetics and Epigenetics of the Multifunctional Protein CTCF. Current Topics in Developmental Biology, 2007, 80, 337-360.	1.0	151
32	Dynamics and interplay of nuclear architecture, genome organization, and gene expression. Genes and Development, 2007, 21, 3027-3043.	2.7	358
33	Genome-wide analysis of DNA methylation patterns. Development (Cambridge), 2007, 134, 3959-3965.	1.2	224
34	Concise Review: Roles of Polycomb Group Proteins in Development and Disease: A Stem Cell Perspective. Stem Cells, 2007, 25, 2498-2510.	1.4	183
35	Cancer genome analysis: a landscape seen from many angles. Drug Discovery Today Disease Mechanisms, 2007, 4, 269-276.	0.8	0
36	Putative Zinc Finger Protein Binding Sites Are Over-Represented in the Boundaries of Methylation-Resistant CpG Islands in the Human Genome. PLoS ONE, 2007, 2, e1184.	1.1	16
37	Genome-scale ChIP-chip analysis using 10,000 human cells. BioTechniques, 2007, 43, 791-797.	0.8	87
38	Loss of the glycine N-methyltransferase gene leads to steatosis and hepatocellular carcinoma in mice. Hepatology, 2008, 47, 1191-1199.	3.6	262

#	Article	IF	CITATIONS
39	The role of chromatinâ€remodeling factor PKL in balancing osmotic stress responses during Arabidopsis seed germination. Plant Journal, 2007, 52, 927-936.	2.8	138
40	Faster still and faster. Nature, 2007, 448, 10-11.	13.7	3
41	The epigenomic era opens. Nature, 2007, 448, 548-549.	13.7	39
42	The personal side of genomics. Nature, 2007, 449, 627-628.	13.7	26
44	Genome-wide in situ exon capture for selective resequencing. Nature Genetics, 2007, 39, 1522-1527.	9.4	635
45	ENCODE and our very busy genome. Nature Genetics, 2007, 39, 817-818.	9.4	16
46	Clinical variability in ciliary disorders. Nature Genetics, 2007, 39, 818-819.	9.4	10
47	Stalled polymerases and transcriptional regulation. Nature Genetics, 2007, 39, 1421-1422.	9.4	5
48	ChIP-seq: welcome to the new frontier. Nature Methods, 2007, 4, 613-614.	9.0	215
49	Prion biology: the quest for the test. Nature Methods, 2007, 4, 614-616.	9.0	11
51	Multivalent engagement of chromatin modifications by linked binding modules. Nature Reviews Molecular Cell Biology, 2007, 8, 983-994.	16.1	914
52	Localized H3K36 methylation states define histone H4K16 acetylation during transcriptional elongation in Drosophila. EMBO Journal, 2007, 26, 4974-4984.	3.5	153
53	Primers on chromatin. Nature Structural and Molecular Biology, 2007, 14, 1110-1115.	3.6	34
54	Covalent modifications of histones during development and disease pathogenesis. Nature Structural and Molecular Biology, 2007, 14, 1008-1016.	3.6	574
55	How chromatin-binding modules interpret histone modifications: lessons from professional pocket pickers. Nature Structural and Molecular Biology, 2007, 14, 1025-1040.	3.6	1,288
56	Epigenetics for ecologists. Ecology Letters, 2008, 11, 106-115.	3.0	804
57	Developmental information but not promoter activity controls the methylation state of histone H3 lysine 4 on two photosynthetic genes in maize. Plant Journal, 2008, 53, 465-474.	2.8	30
58	Recruitment of coregulator complexes to the βâ€globin gene locus by TFIIâ€I and upstream stimulatory factor. FEBS Journal, 2007, 274, 6065-6073.	2.2	19

#	Article	IF	CITATIONS
59	Signaling and epigenetic regulation of pituitary development. Current Opinion in Cell Biology, 2007, 19, 605-611.	2.6	69
60	Mapping the genome landscape using tiling array technology. Current Opinion in Plant Biology, 2007, 10, 534-542.	3.5	61
61	Histone modifications and dynamic regulation of genome accessibility in plants. Current Opinion in Plant Biology, 2007, 10, 645-652.	3.5	256
63	Cellular Stress Response: A Novel Target for Chemoprevention and Nutritional Neuroprotection in Aging, Neurodegenerative Disorders and Longevity. Neurochemical Research, 2008, 33, 2444-2471.	1.6	259
64	The ploidy effects in plant gene expression: Progress, problems and prospects. Science in China Series C: Life Sciences, 2008, 51, 295-301.	1.3	13
65	An Overview of Epigenetic Assays. Molecular Biotechnology, 2008, 38, 179-183.	1.3	48
66	Sodium arsenite modulates histone acetylation, histone deacetylase activity and HMGN protein dynamics in human cells. Chromosoma, 2008, 117, 147-157.	1.0	90
67	DNA methylation in mouse embryonic stem cells and development. Cell and Tissue Research, 2008, 331, 31-55.	1.5	41
68	Characterization of the human DYRK1A promoter and its regulation by the transcription factor E2F1. BMC Molecular Biology, 2008, 9, 30.	3.0	25
69	Deregulation of histone lysine methyltransferases contributes to oncogenic transformation of human bronchoepithelial cells. Cancer Cell International, 2008, 8, 15.	1.8	129
70	Single-epitope recognition imaging of native chromatin. Epigenetics and Chromatin, 2008, 1, 10.	1.8	23
71	Singleâ€molecule analysis of chromatin: Changing the view of genomes one molecule at a time. Journal of Cellular Biochemistry, 2008, 105, 330-337.	1.2	18
72	Chromatin organization and virus gene expression. Journal of Cellular Physiology, 2008, 216, 295-302.	2.0	60
73	Molecular basis of oncostatin Mâ€induced SOCSâ€3 expression in astrocytes. Glia, 2008, 56, 1250-1262.	2.5	37
74	Epigenetic regulation of <i>Hox</i> gene activation: the waltz of methyls. BioEssays, 2008, 30, 199-202.	1.2	55
75	Long-range regulation of cytokine gene expression. Current Opinion in Immunology, 2008, 20, 272-280.	2.4	22
76	RNAi and chromatin in T cell development and function. Current Opinion in Immunology, 2008, 20, 131-138.	2.4	18
77	Array-Based DNA Diagnostics: Let the Revolution Begin. Annual Review of Medicine, 2008, 59, 113-129.	5.0	131

ARTICLE IF CITATIONS # Nascent RNA Sequencing Reveals Widespread Pausing and Divergent Initiation at Human Promoters. 78 6.0 1,758 Science, 2008, 322, 1845-1848. Cancer Epigenetics: Modifications, Screening, and Therapy. Annual Review of Medicine, 2008, 59, 79 5.0 241 267-280. Epigenetic Regulation of Vascular Endothelial Gene Expression. Circulation Research, 2008, 102, 80 2.0 194 873-887. Enhancer requirement for histone methylation linked with gene activation. FEBS Journal, 2008, 275, 5994-6001. Cohesins localize with CTCF at the KSHV latency control region and at cellular c-myc and H19/lgf2 82 3.5 326 insulators. EMBO Journal, 2008, 27, 654-666. A mono-allelic bivalent chromatin domain controls tissue-specific imprinting at Grb10. EMBO Journal, 3.5 2008, 27, 2523-2532. CTCF regulates cell cycle progression of $\hat{l}\pm\hat{l}^2$ T cells in the thymus. EMBO Journal, 2008, 27, 2839-2850. 84 3.5 155 Cohesin mediates transcriptional insulation by CCCTC-binding factor. Nature, 2008, 451, 796-801. 13.7 1,050 86 Nucleosome organization in the Drosophila genome. Nature, 2008, 453, 358-362. 13.7 636 Histone H2A.Z and DNA methylation are mutually antagonistic chromatin marks. Nature, 2008, 456, 13.7 125-129. Accurate whole human genome sequencing using reversible terminator chemistry. Nature, 2008, 456, 88 13.7 3,118 53-59. An integrated software system for analyzing ChIP-chip and ChIP-seq data. Nature Biotechnology, 2008, 89 9.4 26, 1293-1300. Design and analysis of ChIP-seq experiments for DNA-binding proteins. Nature Biotechnology, 2008, 26, 90 9.4 825 1351-1359. Moving AHEAD with an international human epigenome project. Nature, 2008, 454, 711-715. 13.7 177 Nonprocessive methylation by Dot1 leads to functional redundancy of histone H3K79 methylation 92 3.6 163 states. Nature Structural and Molecular Biology, 2008, 15, 550-557. The effect of H3K79 dimethylation and H4K20 trimethylation on nucleosome and chromatin structure. 210 Nature Structural and Molećular Biology, 2008, 15, 1122-1124. Histone H4 lysine 20 monomethylation promotes transcriptional repression by L3MBTL1. Oncogene, 94 2.6 137 2008, 27, 4293-4304. A Bayesian deconvolution strategy for immunoprecipitation-based DNA methylome analysis. Nature 9.4 Biotechnology, 2008, 26, 779-785.

	CHATION R	EPORI	
#	Article	IF	CITATIONS
96	What would you do if you could sequence everything?. Nature Biotechnology, 2008, 26, 1125-1133.	9.4	175
97	Combinatorial patterns of histone acetylations and methylations in the human genome. Nature Genetics, 2008, 40, 897-903.	9.4	2,034
98	The chromatin-remodeling enzyme BRG1 coordinates CIITA induction through many interdependent distal enhancers. Nature Immunology, 2008, 9, 785-793.	7.0	95
99	Priming for T helper type 2 differentiation by interleukin 2–mediated induction of interleukin 4 receptor α-chain expression. Nature Immunology, 2008, 9, 1288-1296.	7.0	234
101	BAC TransgeneOmics: a high-throughput method for exploration of protein function in mammals. Nature Methods, 2008, 5, 409-415.	9.0	568
102	Genome-wide analysis of transcription factor binding sites based on ChIP-Seq data. Nature Methods, 2008, 5, 829-834.	9.0	627
103	Sequence census methods for functional genomics. Nature Methods, 2008, 5, 19-21.	9.0	227
104	A rapid micro chromatin immunoprecipitation assay (ChIP). Nature Protocols, 2008, 3, 1032-1045.	5.5	259
105	Nucleosome destabilization in the epigenetic regulation of gene expression. Nature Reviews Genetics, 2008, 9, 15-26.	7.7	404
106	Genome-wide approaches to studying chromatin modifications. Nature Reviews Genetics, 2008, 9, 179-191.	7.7	343
107	Dynamic histone H3 methylation during gene induction: HYPB/Setd2 mediates all H3K36 trimethylation. EMBO Journal, 2008, 27, 406-420.	3.5	445
108	Applications of chromatin immunoprecipitation-based epigenomic tools in nutritional studies. Nutrition Reviews, 2008, 66, S49-S53.	2.6	0
109	Proper Gcn5 histone acetyltransferase expression is required for normal anteroposterior patterning of the mouse skeleton. Development Growth and Differentiation, 2008, 50, 321-330.	0.6	28
110	Light optical precision measurements of the active and inactive Prader–Willi syndrome imprinted regions in human cell nuclei. Differentiation, 2008, 76, 66-82.	1.0	45
111	THIS ARTICLE HAS BEEN RETRACTED â€ ⁻ Epigenetic regulator polycomb group protein complexes control cell fate and cancer. Cancer Science, 2008, 99, 1077-1084.	1.7	22
112	Control of cytokine gene transcription in Th1 and Th2 cells. Clinical and Experimental Allergy, 2008, 38, 1422-1431.	1.4	62
113	Genomics and the immune system. Immunology, 2008, 124, 23-32.	2.0	8
114	Control of <i>ILâ€4</i> expression in T helper 1 and 2 cells. Immunology, 2008, 124, 437-444.	2.0	40

#	Article	IF	CITATIONS
115	Epigenetic mechanisms regulate Mallory Denk body formation in the livers of drug-primed mice. Experimental and Molecular Pathology, 2008, 84, 113-121.	0.9	28
116	Using quality scores and longer reads improves accuracy of Solexa read mapping. BMC Bioinformatics, 2008, 9, 128.	1.2	261
117	Probabilistic base calling of Solexa sequencing data. BMC Bioinformatics, 2008, 9, 431.	1.2	82
118	Empirical methods for controlling false positives and estimating confidence in ChIP-Seq peaks. BMC Bioinformatics, 2008, 9, 523.	1.2	190
119	Prediction of regulatory elements in mammalian genomes using chromatin signatures. BMC Bioinformatics, 2008, 9, 547.	1.2	92
120	Genome-wide analysis of alternative promoters of human genes using a custom promoter tiling array. BMC Genomics, 2008, 9, 349.	1.2	50
121	Identifying Positioned Nucleosomes with Epigenetic Marks in Human from ChIP-Seq. BMC Genomics, 2008, 9, 537.	1.2	122
122	Conservation and implications of eukaryote transcriptional regulatory regions across multiple species. BMC Genomics, 2008, 9, 623.	1.2	7
123	All and only CpG containing sequences are enriched in promoters abundantly bound by RNA polymerase II in multiple tissues. BMC Genomics, 2008, 9, 67.	1.2	52
124	Diversity of core promoter elements comprising human bidirectional promoters. BMC Genomics, 2008, 9, S3.	1.2	59
125	Nuclear functions in space and time: Gene expression in a dynamic, constrained environment. FEBS Letters, 2008, 582, 1960-1970.	1.3	23
126	DACT3 Is an Epigenetic Regulator of Wnt/β-Catenin Signaling in Colorectal Cancer and Is a Therapeutic Target of Histone Modifications. Cancer Cell, 2008, 13, 529-541.	7.7	216
127	The RNA polymerase II core promoter — the gateway to transcription. Current Opinion in Cell Biology, 2008, 20, 253-259.	2.6	319
128	The first five years of the Wnt targetome. Cellular Signalling, 2008, 20, 795-802.	1.7	107
129	Emerging DNA sequencing technologies for human genomic medicine. Drug Discovery Today, 2008, 13, 569-577.	3.2	57
130	Human MHC architecture and evolution: implications for disease association studies. International Journal of Immunogenetics, 2008, 35, 179-192.	0.8	191
131	H2A.Z: View from the Top. Structure, 2008, 16, 166-179.	1.6	240
132	Structural Insight into the Recognition of the H3K4me3 Mark by the TFIID Subunit TAF3. Structure, 2008, 16, 1245-1256.	1.6	123

		CEPORI	
#	Article	IF	Citations
133	Genome-wide RNA polymerase II: not genes only!. Trends in Biochemical Sciences, 2008, 33, 265-273.	3.7	63
134	Bioinformatics challenges of new sequencing technology. Trends in Genetics, 2008, 24, 142-149.	2.9	438
135	The impact of next-generation sequencing technology on genetics. Trends in Genetics, 2008, 24, 133-141.	2.9	1,848
136	The methylome: approaches for global DNA methylation profiling. Trends in Genetics, 2008, 24, 231-237.	2.9	258
137	The chromosome glue gets a little stickier. Trends in Genetics, 2008, 24, 382-389.	2.9	17
138	Transcriptional and epigenetic regulations of embryonic stem cells. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2008, 647, 52-58.	0.4	20
139	Epigenomics and breast cancer. Pharmacogenomics, 2008, 9, 1879-1902.	0.6	153
140	Short read fragment assembly of bacterial genomes. Genome Research, 2008, 18, 324-330.	2.4	371
141	A Novel CpG Island Set Identifies Tissue-Specific Methylation at Developmental Gene Loci. PLoS Biology, 2008, 6, e22.	2.6	533
142	Developmental origins of disease and determinants of chromatin structure: maternal diet modifies the primate fetal epigenome. Journal of Molecular Endocrinology, 2008, 41, 91-102.	1.1	388
143	Human Telomere Structure and Biology. Annual Review of Genomics and Human Genetics, 2008, 9, 1-19.	2.5	109
144	Illumina Genome Analyzer II System. , 0, , 13-28.		2
145	Model-based Analysis of ChIP-Seq (MACS). Genome Biology, 2008, 9, R137.	13.9	13,517
146	Asymmetric histone modifications between the original and derived loci of human segmental duplications. Genome Biology, 2008, 9, R105.	13.9	21
147	Porin new light onto chromatin and nuclear organization. Genome Biology, 2008, 9, 222.	13.9	6
148	RNA polymerase II stalling: loading at the start prepares genes for a sprint. Genome Biology, 2008, 9, 220.	13.9	38
149	Histone deacetylase inhibition accelerates the early events of stem cell differentiation: transcriptomic and epigenetic analysis. Genome Biology, 2008, 9, R65.	13.9	86
150	Epigenetics in the Nervous System: Figure 1 Journal of Neuroscience, 2008, 28, 11753-11759.	1.7	200

#	Article	IF	CITATIONS
151	Stem Cell Research and Therapeutics. , 2008, , .		3
152	Mapping short DNA sequencing reads and calling variants using mapping quality scores. Genome Research, 2008, 18, 1851-1858.	2.4	2,275
153	CD4 T cells: fates, functions, and faults. Blood, 2008, 112, 1557-1569.	0.6	1,333
154	Divergent Transcription from Active Promoters. Science, 2008, 322, 1849-1851.	6.0	801
155	Genome-wide identification of <i>in vivo</i> protein-DNA binding sites from ChIP-Seq data. Nucleic Acids Research, 2008, 36, 5221-5231.	6.5	500
156	Transcription Termination and RNA Degradation Contribute to Silencing of RNA Polymerase II Transcription within Heterochromatin. Molecular Cell, 2008, 29, 313-323.	4.5	129
157	Interaction of the Glucocorticoid Receptor with the Chromatin Landscape. Molecular Cell, 2008, 29, 611-624.	4.5	285
158	Lineage-Specific Polycomb Targets and De Novo DNA Methylation Define Restriction and Potential of Neuronal Progenitors. Molecular Cell, 2008, 30, 755-766.	4.5	802
159	Chromatin Insulators: Regulatory Mechanisms and Epigenetic Inheritance. Molecular Cell, 2008, 32, 1-9.	4.5	178
160	EZH1 Mediates Methylation on Histone H3 Lysine 27 and Complements EZH2 in Maintaining Stem Cell Identity and Executing Pluripotency. Molecular Cell, 2008, 32, 491-502.	4.5	838
161	Developmental and epigenetic regulation of the human TLR3 gene. Molecular Immunology, 2008, 46, 27-36.	1.0	17
162	CD4-CD8 Lineage Commitment Is Regulated by a Silencer Element at the ThPOK Transcription-Factor Locus. Immunity, 2008, 28, 346-358.	6.6	127
163	Decoding the Epigenetic Language of Neuronal Plasticity. Neuron, 2008, 60, 961-974.	3.8	468
164	Epigenetic principles and mechanisms underlying nervous system functions in health and disease. Progress in Neurobiology, 2008, 86, 305-341.	2.8	252
165	Applications of next-generation sequencing technologies in functional genomics. Genomics, 2008, 92, 255-264.	1.3	1,013
166	Unraveling Epigenetic Regulation in Embryonic Stem Cells. Cell Stem Cell, 2008, 2, 123-134.	5.2	152
167	Drosophila HP1c isoform interacts with the zinc-finger proteins WOC and Relative-of-WOC to regulate gene expression. Genes and Development, 2008, 22, 3007-3023.	2.7	62
168	Histone methylation marks play important roles in predicting the methylation status of CpG islands. Biochemical and Biophysical Research Communications, 2008, 374, 559-564.	1.0	45

#	Article	IF	CITATIONS
169	A glimpse into the epigenetic landscape of gene regulation. Current Opinion in Genetics and Development, 2008, 18, 116-122.	1.5	62
170	Chromatin state maps: new technologies, new insights. Current Opinion in Genetics and Development, 2008, 18, 109-115.	1.5	77
171	High-Resolution Mapping andÂCharacterization of Open Chromatin across the Genome. Cell, 2008, 132, 311-322.	13.5	1,246
172	Cohesins Functionally Associate with CTCF on Mammalian Chromosome Arms. Cell, 2008, 132, 422-433.	13.5	800
173	FoxA1 Translates Epigenetic Signatures into Enhancer-Driven Lineage-Specific Transcription. Cell, 2008, 132, 958-970.	13.5	863
174	Dynamic Regulation of Nucleosome Positioning in the Human Genome. Cell, 2008, 132, 887-898.	13.5	1,211
175	Integration of External Signaling Pathways with the Core Transcriptional Network in Embryonic Stem Cells. Cell, 2008, 133, 1106-1117.	13.5	2,279
176	Connecting microRNA Genes to the Core Transcriptional Regulatory Circuitry of Embryonic Stem Cells. Cell, 2008, 134, 521-533.	13.5	1,332
177	H2AZ Is Enriched at Polycomb Complex Target Genes in ES Cells and Is Necessary for Lineage Commitment. Cell, 2008, 135, 649-661.	13.5	307
178	The PHD domain of the sea urchin RAG2 homolog, SpRAG2L, recognizes dimethylated lysine 4 in histone H3 tails. Developmental and Comparative Immunology, 2008, 32, 1221-1230.	1.0	19
179	Future impact of integrated high-throughput methylome analyses on human health and disease. Journal of Genetics and Genomics, 2008, 35, 391-401.	1.7	41
180	Tackling the epigenome in the pluripotent stem cells. Journal of Genetics and Genomics, 2008, 35, 403-412.	1.7	13
181	Epigenetic regulation of genes during development: A conserved theme from flies to mammals. Journal of Genetics and Genomics, 2008, 35, 413-429.	1.7	33
183	Programmed Cell Death in Plants: Orchestrating an Intrinsic Suicide Program Within Walls. Critical Reviews in Plant Sciences, 2008, 27, 413-423.	2.7	29
184	Association between active genes occurs at nuclear speckles and is modulated by chromatin environment. Journal of Cell Biology, 2008, 182, 1083-1097.	2.3	231
185	A Global View of Gene Activity and Alternative Splicing by Deep Sequencing of the Human Transcriptome. Science, 2008, 321, 956-960.	6.0	1,164
186	Similar active genes cluster in specialized transcription factories. Journal of Cell Biology, 2008, 181, 615-623.	2.3	131
187	CTCF physically links cohesin to chromatin. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 8309-8314.	3.3	449

ARTICLE IF CITATIONS # De novo fragment assembly with short mate-paired reads: Does the read length matter?. Genome 188 2.4 220 Research, 2009, 19, 336-346. Cell-type selective chromatin remodeling defines the active subset of FOXA1-bound enhancers. Genome 189 2.4 Research, 2009, 19, 372-380. How chromatin remodelling allows shuffling of immunoglobulin heavy chain genes. Molecular 190 2.9 4 BioSystems, 2008, 4, 790. X chromosome inactivation: heterogeneity of heterochromatin. Biochemistry and Cell Biology, 2008, 0.9 86, 370-379. Computational epigenetics. Bioinformatics, 2008, 24, 1-10. 192 180 1.8 H3K27me3 forms BLOCs over silent genes and intergenic regions and specifies a histone banding pattern on a mouse autosomal chromosome. Genome Research, 2009, 19, 221-233. 2.4 DOT1L/KMT4 Recruitment and H3K79 Methylation Are Ubiquitously Coupled with Gene Transcription in 194 1.1 441 Mammalian Cells. Molecular and Cellular Biology, 2008, 28, 2825-2839. Species-Specific Transcription in Mice Carrying Human Chromosome 21. Science, 2008, 322, 434-438. 6.0 260 E2F in vivo binding specificity: Comparison of consensus versus nonconsensus binding sites. Genome 196 2.4 121 Research, 2008, 18, 1763-1777. Transcription-Coupled Methylation of Histone H3 at Lysine 36 Regulates Dosage Compensation by Enhancing Recruitment of the MSL Complex in <i>Drosophila melanogaster</i>. Molecular and 1.1 64 Cellular Biology, 2008, 28, 3401-3409. Analysis of transcription factor interactions in osteoblasts using competitive chromatin 198 6.5 28 immunoprecipitation. Nucleic Acids Research, 2008, 36, 1723-1730. Global analysis of the insulator binding protein CTCF in chromatin barrier regions reveals 199 2.4 587 demarcation of active and repressive domains. Genome Research, 2009, 19, 24-32. Substantial biases in ultra-short read data sets from high-throughput DNA sequencing. Nucleic Acids 200 6.5 914 Research, 2008, 36, e105. Chromatin structure analyses identify miRNA promoters. Genes and Development, 2008, 22, 3172-3183. 2.7 541 Aberrant chromatin at genes encoding stem cell regulators in human mixed-lineage leukemia. Genes 202 2.7 237 and Development, 2008, 22, 3403-3408. Using ChIP-chip technology to reveal common principles of transcriptional repression in normal and 2.4 44 cancer cells. Genome Research, 2008, 18, 521-532. A genomic analysis of RNA polymerase II modification and chromatin architecture related to 3â€² end RNA 204 2.4 50 polyadenylation. Genome Research, 2008, 18, 1224-1237. Transcript Profiling by 3â€2-Untranslated Region Sequencing Resolves Expression of Gene Families. Plant 2.3 Physiology, 2008, 146, 32-44.

\sim			~
	ΙΤΑΤΙ	ON	Report
0	/		ILLI OKT

#	Article	IF	CITATIONS
206	Microplate-based chromatin immunoprecipitation method, Matrix ChIP: a platform to study signaling of complex genomic events. Nucleic Acids Research, 2008, 36, e17.	6.5	75
207	A systematic characterization of factors that regulate Drosophila segmentation via a bacterial one-hybrid system. Nucleic Acids Research, 2008, 36, 2547-2560.	6.5	152
209	Frequent switching of Polycomb repressive marks and DNA hypermethylation in the PC3 prostate cancer cell line. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 12979-12984.	3.3	325
210	Transient high glucose causes persistent epigenetic changes and altered gene expression during subsequent normoglycemia. Journal of Experimental Medicine, 2008, 205, 2409-2417.	4.2	931
211	Comparative analysis of human chromosome 7q21 and mouse proximal chromosome 6 reveals a placental-specific imprinted gene, <i>TFPI2</i> / <i>Tfpi2</i> , which requires EHMT2 and EED for allelic-silencing. Genome Research, 2008, 18, 1270-1281.	2.4	72
212	Scanning the human genome at kilobase resolution. Genome Research, 2008, 18, 751-762.	2.4	16
213	DNA methyltransferase 3B (DNMT3B) mutations in ICF syndrome lead to altered epigenetic modifications and aberrant expression of genes regulating development, neurogenesis and immune function. Human Molecular Genetics, 2008, 17, 690-709.	1.4	216
214	Defining a Chromatin Pattern that Characterizes DNA-Hypermethylated Genes in Colon Cancer Cells. Cancer Research, 2008, 68, 5753-5759.	0.4	109
215	Role of histone modifications in defining chromatin structure and function. Biological Chemistry, 2008, 389, 353-363.	1.2	105
216	Bivalent domains enforce transcriptional memory of DNA methylated genes in cancer cells. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 19809-19814.	3.3	99
217	Histone Methylation Patterns Are Cell-Type Specific in Human Monocytes and Lymphocytes and Well Maintained at Core Genes. Journal of Immunology, 2008, 180, 2264-2269.	0.4	41
218	Di-methyl H4 Lysine 20 Targets the Checkpoint Protein Crb2 to Sites of DNA Damage. Journal of Biological Chemistry, 2008, 283, 33168-33174.	1.6	58
219	High-Resolution Mapping of Epigenetic Modifications of the Rice Genome Uncovers Interplay between DNA Methylation, Histone Methylation, and Gene Expression. Plant Cell, 2008, 20, 259-276.	3.1	281
220	Identification of active transcriptional regulatory modules by the functional assay of DNA from nucleosome-free regions. Genome Research, 2008, 18, 930-938.	2.4	32
221	Enhancer Blocking Activity of the Insulator at <i>H19-ICR</i> Is Independent of Chromatin Barrier Establishment. Molecular and Cellular Biology, 2008, 28, 3767-3775.	1.1	15
222	A Genome-Wide Screen for β-Catenin Binding Sites Identifies a Downstream Enhancer Element That Controls c <i>-Myc</i> Gene Expression. Molecular and Cellular Biology, 2008, 28, 7368-7379.	1.1	110
223	CCCTC-Binding Factor Confines the Distal Action of Estrogen Receptor. Cancer Research, 2008, 68, 9041-9049.	0.4	36
224	The Histone-Like NF-Y Is a Bifunctional Transcription Factor. Molecular and Cellular Biology, 2008, 28, 2047-2058.	1.1	107

#	Article	IF	CITATIONS
225	The Transcriptional Status but Not the Imprinting Control Region Determines Allele-Specific Histone Modifications at the Imprinted <i>H19</i> Locus. Molecular and Cellular Biology, 2008, 28, 71-82.	1.1	42
226	Evolution of the mammalian transcription factor binding repertoire via transposable elements. Genome Research, 2008, 18, 1752-1762.	2.4	501
227	Global analysis of in vivo Foxa2-binding sites in mouse adult liver using massively parallel sequencing. Nucleic Acids Research, 2008, 36, 4549-4564.	6.5	137
228	Maternal depletion of CTCF reveals multiple functions during oocyte and preimplantation embryo development. Development (Cambridge), 2008, 135, 2729-2738.	1.2	112
229	Beyond histone methyl-lysine binding: How malignant brain tumor (MBT) protein L3MBTL1 impacts chromatin structure. Cell Cycle, 2008, 7, 578-585.	1.3	28
230	Will the transcription control elements in chromatin please stand up?. Epigenetics, 2008, 3, 179-180.	1.3	0
231	Clobal histone acetylation induces functional genomic reorganization at mammalian nuclear pore complexes. Genes and Development, 2008, 22, 627-639.	2.7	165
232	Gene duplication in the epigenomic era: Roles of chromatin modifications. Epigenetics, 2008, 3, 250-253.	1.3	3
233	Certain and Progressive Methylation of Histone H4 at Lysine 20 during the Cell Cycle. Molecular and Cellular Biology, 2008, 28, 468-486.	1.1	264
234	Preferential Dimethylation of Histone H4 Lysine 20 by Suv4-20. Journal of Biological Chemistry, 2008, 283, 12085-12092.	1.6	115
235	Epigenetic mechanisms of gene regulation during mammalian spermatogenesis. Epigenetics, 2008, 3, 21-27.	1.3	41
237	Epithelial Progeny of Estrogen-Exposed Breast Progenitor Cells Display a Cancer-like Methylome. Cancer Research, 2008, 68, 1786-1796.	0.4	127
238	Replication stress induces tumor-like microdeletions in <i>FHIT</i> /FRA3B. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 246-251.	3.3	107
239	Aire employs a histone-binding module to mediate immunological tolerance, linking chromatin regulation with organ-specific autoimmunity. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 15878-15883.	3.3	155
240	Catalytic Function of the PR-Set7 Histone H4 Lysine 20 Monomethyltransferase Is Essential for Mitotic Entry and Genomic Stability. Journal of Biological Chemistry, 2008, 283, 19478-19488.	1.6	137
241	Analysis of intergenic transcription and histone modification across the human immunoglobulin heavy-chain locus. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 15872-15877.	3.3	42
242	Cell Cycle– and Chaperone-Mediated Regulation of H3K56ac Incorporation in Yeast. PLoS Genetics, 2008, 4, e1000270.	1.5	133
243	ZOOM! Zillions of oligos mapped. Bioinformatics, 2008, 24, 2431-2437.	1.8	187

#	Article	IF	CITATIONS
244	Genomewide Analysis of PRC1 and PRC2 Occupancy Identifies Two Classes of Bivalent Domains. PLoS Genetics, 2008, 4, e1000242.	1.5	878
245	Transcription of laminin γ1 chain gene in rat mesangial cells: constitutive and inducible RNA polymerase II recruitment and chromatin states. American Journal of Physiology - Renal Physiology, 2008, 294, F525-F533.	1.3	12
246	The Insulator Binding Protein CTCF Positions 20 Nucleosomes around Its Binding Sites across the Human Genome. PLoS Genetics, 2008, 4, e1000138.	1.5	321
247	The Genomic Distribution and Function of Histone Variant HTZ-1 during C. elegans Embryogenesis. PLoS Genetics, 2008, 4, e1000187.	1.5	97
248	Regulation of p53 Target Gene Expression by Peptidylarginine Deiminase 4. Molecular and Cellular Biology, 2008, 28, 4745-4758.	1.1	200
249	Genomic Sequence Is Highly Predictive of Local Nucleosome Depletion. PLoS Computational Biology, 2008, 4, e13.	1.5	156
250	The Evolution of Epigenetic Regulators CTCF and BORIS/CTCFL in Amniotes. PLoS Genetics, 2008, 4, e1000169.	1.5	72
251	EagleView: A genome assembly viewer for next-generation sequencing technologies. Genome Research, 2008, 18, 1538-1543.	2.4	112
252	Profiling the HeLa S3 transcriptome using randomly primed cDNA and massively parallel short-read sequencing. BioTechniques, 2008, 45, 81-94.	0.8	355
253	CHD8 Is an ATP-Dependent Chromatin Remodeling Factor That Regulates β-Catenin Target Genes. Molecular and Cellular Biology, 2008, 28, 3894-3904.	1.1	187
254	High-resolution human core-promoter prediction with CoreBoost_HM. Genome Research, 2009, 19, 266-275.	2.4	96
255	DNA methylation profile of tissue-dependent and differentially methylated regions (T-DMRs) in mouse promoter regions demonstrating tissue-specific gene expression. Genome Research, 2008, 18, 1969-1978.	2.4	161
256	Two strategies for gene regulation by promoter nucleosomes. Genome Research, 2008, 18, 1084-1091.	2.4	351
257	A Novel High-Throughput Screening System Identifies a Small Molecule Repressive for Matrix Metalloproteinase-9 Expression. Molecular Pharmacology, 2008, 73, 919-929.	1.0	20
258	Ultra-high-throughput sequencing, microarray-based genomic selection and pharmacogenomics. Pharmacogenomics, 2008, 9, 5-9.	0.6	6
259	The histone H2B-specific ubiquitin ligase RNF20/hBRE1 acts as a putative tumor suppressor through selective regulation of gene expression. Genes and Development, 2008, 22, 2664-2676.	2.7	240
260	Developmental regulation of histone H3 methylation at lysine 4 in the porcine ovary. Reproduction, 2008, 135, 829-838.	1.1	29
261	The new paradigm of flow cell sequencing: Table 1 Genome Research, 2008, 18, 839-846.	2.4	185

#	Article	IF	Citations
262	Epigenetics meets next-generation sequencing. Epigenetics, 2008, 3, 318-321.	1.3	36
263	Characterization of Drosophila melanogaster JmjC+N histone demethylases. Nucleic Acids Research, 2008, 36, 2852-2863.	6.5	58
264	FindPeaks 3.1: a tool for identifying areas of enrichment from massively parallel short-read sequencing technology. Bioinformatics, 2008, 24, 1729-1730.	1.8	252
265	Fine Haplotype Structure of a Chromosome 17 Region in the Laboratory and Wild Mouse. Genetics, 2008, 178, 1777-1784.	1.2	22
266	Detection and characterization of silencers and enhancer-blockers in the greater <i>CFTR</i> locus. Genome Research, 2008, 18, 1238-1246.	2.4	45
267	<i>Drosophila</i> UTX Is a Histone H3 Lys27 Demethylase That Colocalizes with the Elongating Form of RNA Polymerase II. Molecular and Cellular Biology, 2008, 28, 1041-1046.	1.1	120
268	Polarization of Primary Human Monocytes by IFN-Î ³ Induces Chromatin Changes and Recruits RNA Pol II to the TNF-α Promoter. Journal of Immunology, 2008, 180, 5257-5266.	0.4	35
269	Genome-wide analysis reveals regulatory role of G4 DNA in gene transcription. Genome Research, 2008, 18, 233-241.	2.4	136
270	Four-color DNA sequencing with 3â€2- <i>O</i> -modified nucleotide reversible terminators and chemically cleavable fluorescent dideoxynucleotides. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 9145-9150.	3.3	138
271	Inferring causal relationships among different histone modifications and gene expression. Genome Research, 2008, 18, 1314-1324.	2.4	116
272	An HMM approach to genome-wide identification of differential histone modification sites from ChIP-seq data. Bioinformatics, 2008, 24, 2344-2349.	1.8	141
273	A transdimensional Bayesian model for pattern recognition in DNA sequences. Biostatistics, 2008, 9, 668-685.	0.9	5
274	Genome-wide profiling of salt fractions maps physical properties of chromatin. Genome Research, 2009, 19, 460-469.	2.4	204
275	Pharmacoepigenomics in colorectal cancer: a step forward in predicting prognosis and treatment response. Pharmacogenomics, 2008, 9, 1903-1916.	0.6	23
276	Overreplication of short DNA regions during S phase in human cells. Genes and Development, 2008, 22, 375-385.	2.7	30
277	Unique ERα Cistromes Control Cell Type-Specific Gene Regulation. Molecular Endocrinology, 2008, 22, 2393-2406.	3.7	119
278	Drosophila Kismet Regulates Histone H3 Lysine 27 Methylation and Early Elongation by RNA Polymerase II. PLoS Genetics, 2008, 4, e1000217.	1.5	115
280	Control of differentiation in a self-renewing mammalian tissue by the histone demethylase JMJD3. Genes and Development, 2008, 22, 1865-1870.	2.7	239

#	Article	IF	CITATIONS
281	A novel mode of enhancer evolution: The Tal1 stem cell enhancer recruited a MIR element to specifically boost its activity. Genome Research, 2008, 18, 1422-1432.	2.4	31
282	PR-Set7 Establishes a Repressive <i>trans</i> -Tail Histone Code That Regulates Differentiation. Molecular and Cellular Biology, 2008, 28, 4459-4468.	1.1	26
283	Histone Modifications and Expression of Light-Regulated Genes in Arabidopsis Are Cooperatively Influenced by Changing Light Conditions Â. Plant Physiology, 2008, 147, 2070-2083.	2.3	80
284	Emerging methods for analysis of the cancer methylome. Pharmacogenomics, 2008, 9, 1869-1878.	0.6	10
285	CTCF-dependent enhancer-blocking by alternative chromatin loop formation. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 20398-20403.	3.3	194
286	Genome-wide relationship between histone H3 lysine 4 mono- and tri-methylation and transcription factor binding. Genome Research, 2008, 18, 1906-1917.	2.4	163
287	An integrated resource for genome-wide identification and analysis of human tissue-specific differentially methylated regions (tDMRs). Genome Research, 2008, 18, 1518-1529.	2.4	350
288	H3 K79 dimethylation marks developmental activation of the β-globin gene but is reduced upon LCR-mediated high-level transcription. Blood, 2008, 112, 406-414.	0.6	15
289	Stem cell–specific epigenetic priming and B cell–specific transcriptional activation at the mouse Cd19 locus. Blood, 2008, 112, 1673-1682.	0.6	58
290	Next-generation sequencing: applications beyond genomes. Biochemical Society Transactions, 2008, 36, 1091-1096.	1.6	111
291	Long-Short-Long Games in mRNA Identification: The Length Matters. Current Pharmaceutical Biotechnology, 2008, 9, 362-367.	0.9	5
292	Mapping Key Features of Transcriptional Regulatory Circuitry in Embryonic Stem Cells. Cold Spring Harbor Symposia on Quantitative Biology, 2008, 73, 183-193.	2.0	34
293	Cancer Genomics. , 2008, , 267-282.		0
294	Methyl-DNA immunoprecipitation (MeDIP): Hunting down the DNA methylome. BioTechniques, 2008, 44, 35-43.	0.8	175
295	BEAF Regulates Cell-Cycle Genes through the Controlled Deposition of H3K9 Methylation Marks into Its Conserved Dual-Core Binding Sites. PLoS Biology, 2008, 6, e327.	2.6	60
296	ChromaSig: A Probabilistic Approach to Finding Common Chromatin Signatures in the Human Genome. PLoS Computational Biology, 2008, 4, e1000201.	1.5	135
297	NF-Y Dependent Epigenetic Modifications Discriminate between Proliferating and Postmitotic Tissue. PLoS ONE, 2008, 3, e2047.	1.1	53
298	An NF-Y-Dependent Switch of Positive and Negative Histone Methyl Marks on CCAAT Promoters. PLoS ONE, 2008, 3, e2066.	1.1	28

#	Article	IF	CITATIONS
299	ZNF198 Stabilizes the LSD1–CoREST–HDAC1 Complex on Chromatin through Its MYM-Type Zinc Fingers. PLoS ONE, 2008, 3, e3255.	1.1	72
300	Screening for PPAR Responsive Regulatory Modules in Cancer. PPAR Research, 2008, 2008, 1-8.	1.1	4
301	A Global View of Transcriptional Regulation by Nuclear Receptors: Gene Expression, Factor Localization, and DNA Sequence Analysis. Nuclear Receptor Signaling, 2008, 6, nrs.06005.	1.0	96
302	ChIP-Seq: Mapping of Protein–DNA Interactions. , 0, , 201-215.		1
303	The Organization of Histone H3 Modifications as Revealed by a Panel of Specific Monoclonal Antibodies. Cell Structure and Function, 2008, 33, 61-73.	0.5	273
304	Understanding the regulatory genome. International Journal of Developmental Biology, 2009, 53, 1367-1378.	0.3	19
305	Emerging molecular approaches in stem cell biology. BioTechniques, 2009, 46, 367-371.	0.8	1
306	Computational Identification of Protein Methylation Sites through Bi-Profile Bayes Feature Extraction. PLoS ONE, 2009, 4, e4920.	1.1	167
307	Targeted Deletion of Multiple CTCF-Binding Elements in the Human C-MYC Gene Reveals a Requirement for CTCF in C-MYC Expression. PLoS ONE, 2009, 4, e6109.	1.1	41
308	Epigenetic Silencing in Friedreich Ataxia Is Associated with Depletion of CTCF (CCCTC-Binding Factor) and Antisense Transcription. PLoS ONE, 2009, 4, e7914.	1.1	102
309	Applications and Case Studies of the Next-Generation Sequencing Technologies in Food, Nutrition and Agriculture. Recent Patents on Food, Nutrition & amp; Agriculture, 2009, 1, 75-79.	0.5	9
310	Role of polycomb proteins Ring1A and Ring1Bin the epigenetic regulation of gene expression. International Journal of Developmental Biology, 2009, 53, 355-370.	0.3	59
311	Targeted Recruitment of Histone Modifications in Humans Predicted by Genomic Sequences. Journal of Computational Biology, 2009, 16, 341-355.	0.8	16
312	TIGERA: A New Tool for Illumina Gene Expression Reads Analysis. , 2009, , .		0
313	Covalent modifications of histones during mitosis and meiosis. Cell Cycle, 2009, 8, 3688-3694.	1.3	86
314	RNA Pol II Accumulates at Promoters of Growth Genes During Developmental Arrest. Science, 2009, 324, 92-94.	6.0	156
315	Ensembl 2009. Nucleic Acids Research, 2009, 37, D690-D697.	6.5	721
316	Native Chromatin Preparation and Illumina/Solexa Library Construction. Cold Spring Harbor Protocols, 2009, 2009, pdb.prot5237.	0.2	26

		CITATION REPORT		
#	Article		IF	Citations
317	RazerS—fast read mapping with sensitivity control. Genome Research, 2009, 19, 164	1 6-1654.	2.4	125
318	Ndy1/KDM2B immortalizes mouse embryonic fibroblasts by repressing the <i>Ink4a</i> locus. Proceedings of the National Academy of Sciences of the United States of Ameri 2641-2646.	> / <i>Arf</i> ca, 2009, 106,	3.3	123
319	Monomethylation of Histone H4-Lysine 20 Is Involved in Chromosome Structure and S Essential for Mouse Development. Molecular and Cellular Biology, 2009, 29, 2278-229		1.1	271
320	Establishment of Histone Modifications after Chromatin Assembly. Nucleic Acids Rese 5032-5040.	arch, 2009, 37,	6.5	94
321	IL-1 family members and STAT activators induce cytokine production by Th2, Th17, and Proceedings of the National Academy of Sciences of the United States of America, 200 13463-13468.		3.3	362
322	The H4 Tail Domain Participates in Intra- and Internucleosome Interactions with Protei during Folding and Oligomerization of Nucleosome Arrays. Molecular and Cellular Biol 538-546.		1.1	147
323	Vernalization-induced flowering in cereals is associated with changes in histone methy <i>VERNALIZATION1</i> gene. Proceedings of the National Academy of Sciences of th America, 2009, 106, 8386-8391.		3.3	208
324	Developmental roles of the histone lysine demethylases. Development (Cambridge), 2	009, 136, 879-889.	1.2	195
325	Lineage-specific DNA methylation in T cells correlates with histone methylation and en Genome Research, 2009, 19, 1165-1174.	hancer activity.	2.4	206
326	Combining Chromatin Immunoprecipitation and Oligonucleotide Tiling Arrays (ChIP-Cl Functional Genomic Studies. Methods in Molecular Biology, 2009, 556, 155-164.	nip) for	0.4	3
327	CEAS: <i>cis</i> -regulatory element annotation system. Bioinformatics, 2009, 25, 260)5-2606.	1.8	415
328	Chromatin Immunoprecipitation (ChIP). Cold Spring Harbor Protocols, 2009, 2009, pd	b.prot5279.	0.2	203
329	Epigenetic inactivation of the Sotos overgrowth syndrome gene histone methyltransfe human neuroblastoma and glioma. Proceedings of the National Academy of Sciences of States of America, 2009, 106, 21830-21835.	erase NSD1 in of the United	3.3	190
330	Integration target site selection by a resurrected human endogenous retrovirus. Genes Development, 2009, 23, 633-642.	s and	2.7	95
331	The CTCF Insulator Protein Is Posttranslationally Modified by SUMO. Molecular and Ce 2009, 29, 714-725.	llular Biology,	1.1	109
332	A wave of nascent transcription on activated human genes. Proceedings of the Nation Sciences of the United States of America, 2009, 106, 18357-18361.	al Academy of	3.3	145
333	The human insulin gene is part of a large open chromatin domain specific for human is Proceedings of the National Academy of Sciences of the United States of America, 200 17419-17424.		3.3	49
334	Induction of Myelin Protein Zero by Early Growth Response 2 through Upstream and Ir Elements. Journal of Biological Chemistry, 2009, 284, 20111-20120.	ntragenic	1.6	42

#	Article	IF	CITATIONS
335	Critical Role for the Transcription Regulator CCCTC-Binding Factor in the Control of Th2 Cytokine Expression. Journal of Immunology, 2009, 182, 999-1010.	0.4	56
336	Analysis of Histones in Xenopus laevis. Journal of Biological Chemistry, 2009, 284, 1075-1085.	1.6	43
337	Identification of EMS-Induced Mutations in <i>Drosophila melanogaster</i> by Whole-Genome Sequencing. Genetics, 2009, 182, 25-32.	1.2	123
338	Identification of Isn1 and Sdt1 as Glucose- and Vitamin-regulated Nicotinamide Mononucleotide and Nicotinic Acid Mononucleotide 5â€2-Nucleotidases Responsible for Production of Nicotinamide Riboside and Nicotinic Acid Riboside. Journal of Biological Chemistry, 2009, 284, 34861-34869.	1.6	51
339	Systems Biology: Understanding Function from Genes to Networks. Current Proteomics, 2009, 6, 93-103.	0.1	1
340	The Beauty of Being a Variant: H2A.Z and the SWR1 Complex in Plants. Molecular Plant, 2009, 2, 565-577.	3.9	130
341	A Multifactorial Signature of DNA Sequence and Polycomb Binding Predicts Aberrant CpG Island Methylation. Cancer Research, 2009, 69, 282-291.	0.4	71
342	Subcellular partitioning-dependent functional switching of Arabidopsis photoreceptor phytochrome B in response to brassinosteroids. Interdisciplinary Bio Central, 2009, 1, 1-5.	0.1	0
343	Paternal deletion of Meg1/Grb10 DMR causes maternalization of the Meg1/Grb10 cluster in mouse proximal Chromosome 11 leading to severe pre- and postnatal growth retardation. Human Molecular Genetics, 2009, 18, 1424-1438.	1.4	64
344	Four histone variants mark the boundaries of polycistronic transcription units in <i>Trypanosoma brucei</i> . Genes and Development, 2009, 23, 1063-1076.	2.7	312
345	Eset partners with Oct4 to restrict extraembryonic trophoblast lineage potential in embryonic stem cells. Genes and Development, 2009, 23, 2507-2520.	2.7	218
346	The presence of RNA polymerase II, active or stalled, predicts epigenetic fate of promoter CpG islands. Genome Research, 2009, 19, 1974-1982.	2.4	121
347	Identification of candidate regulatory SNPs by combination of transcription-factor-binding site prediction, SNP genotyping and haploChIP. Nucleic Acids Research, 2009, 37, e85-e85.	6.5	34
348	Molecular interactions between HNF4a, FOXA2 and GABP identified at regulatory DNA elements through ChIP-sequencing. Nucleic Acids Research, 2009, 37, 7498-7508.	6.5	63
349	S region sequence, RNA polymerase II, and histone modifications create chromatin accessibility during class switch recombination. Journal of Experimental Medicine, 2009, 206, 1817-1830.	4.2	132
350	MotifMap: a human genome-wide map of candidate regulatory motif sites. Bioinformatics, 2009, 25, 167-174.	1.8	118
351	Structure and functional characterization of the atypical human kinase haspin. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 20198-20203.	3.3	144
352	Novel Roles of GATA1 in Regulation of Angiogenic Factor AGGF1 and Endothelial Cell Function. Journal of Biological Chemistry, 2009, 284, 23331-23343.	1.6	57

#	Article	IF	CITATIONS
353	N Terminus of Swr1 Binds to Histone H2AZ and Provides a Platform for Subunit Assembly in the Chromatin Remodeling Complex. Journal of Biological Chemistry, 2009, 284, 6200-6207.	1.6	99
354	Analysis of Lentiviral Vector Integration in HIV+ Study Subjects Receiving Autologous Infusions of Gene Modified CD4+ T Cells. Molecular Therapy, 2009, 17, 844-850.	3.7	136
355	Relating periodicity of nucleosome organization and gene regulation. Bioinformatics, 2009, 25, 1782-1788.	1.8	13
356	Comparative analysis of H2A.Z nucleosome organization in the human and yeast genomes. Genome Research, 2009, 19, 967-977.	2.4	88
357	High-throughput chromatin information enables accurate tissue-specific prediction of transcription factor binding sites. Nucleic Acids Research, 2009, 37, 14-25.	6.5	57
358	Analysis of a Promoter Polymorphism in the SMDF Neuregulin 1 Isoform in Schizophrenia. Neuropsychobiology, 2009, 59, 205-212.	0.9	6
359	Transcription Factor CTF1 Acts as a Chromatin Domain Boundary That Shields Human Telomeric Genes from Silencing. Molecular and Cellular Biology, 2009, 29, 2409-2418.	1.1	15
360	Dynamic Histone Variant Exchange Accompanies Gene Induction in T Cells. Molecular and Cellular Biology, 2009, 29, 1972-1986.	1.1	67
361	The Peroxisome Proliferator-Activated Receptor γ/Retinoid X Receptor α Heterodimer Targets the Histone Modification Enzyme PR-Set7/Setd8 Gene and Regulates Adipogenesis through a Positive Feedback Loop. Molecular and Cellular Biology, 2009, 29, 3544-3555.	1.1	175
362	Genomic actions of estrogen receptor α: what are the targets and how are they regulated?. Endocrine-Related Cancer, 2009, 16, 1073-1089.	1.6	128
363	Animal Models of Epigenetic Inheritance. Seminars in Reproductive Medicine, 2009, 27, 369-379.	0.5	26
364	Kinetic Complexity of the Global Response to Glucocorticoid Receptor Action. Endocrinology, 2009, 150, 1766-1774.	1.4	91
365	Targeting of EZH2 to a defined genomic site is sufficient for recruitment of Dnmt3a but not de novo DNA methylation. Epigenetics, 2009, 4, 404-414.	1.3	74
366	Degrees make all the difference: The multifunctionality of histone H4 lysine 20 methylation. Epigenetics, 2009, 4, 273-276.	1.3	36
367	ChIP-seq Data Plays an Important Role in a Cytosine-Based DNA Methylation Prediction Model. , 2009, , .		0
368	Epigenetic inheritance through self-recruitment of the polycomb repressive complex 2. Epigenetics, 2009, 4, 133-138.	1.3	33
369	Next-generation sequencing reveals complex relationships between the epigenome and transcriptome in maize. Plant Signaling and Behavior, 2009, 4, 760-762.	1.2	12
370	Histone H3 lysine 27 trimethylation in adult differentiated colon associated to cancer DNA hypermethylation. Epigenetics, 2009, 4, 107-113.	1.3	25

		CITATION REPORT		
#	Article		IF	CITATIONS
371	Epigenetic regulation of developmental timing in floral stem cells. Epigenetics, 2009, 4,	564-567.	1.3	10
372	Investigating repetitively matching short sequencing reads: The enigmatic nature of H3 Epigenetics, 2009, 4, 476-486.	K9me3.	1.3	11
373	The regulation of intestinal mucin MUC2 expression by short-chain fatty acids: implicat epithelial protection. Biochemical Journal, 2009, 420, 211-219.	ions for	1.7	445
374	Modular Organization in a Cell: Concepts and Applications. Current Bioinformatics, 200	09, 4, 207-217.	0.7	0
375	Environmental Influences on Epigenetic Profiles. Seminars in Reproductive Medicine, 20)09, 27, 380-390.	0.5	61
376	Research Highlights. Epigenomics, 2009, 1, 21-23.		1.0	2
377	Efficient frequency-based de novo short-read clustering for error trimming in next-gene sequencing. Genome Research, 2009, 19, 1309-1315.	ration	2.4	53
378	Extralarge XLαs (XXLαs), a Variant of Stimulatory G Protein α-Subunit (Gsα), Is a Disti Membrane-Anchored GNAS Product that Can Mimic Gsα. Endocrinology, 2009, 150, 35		1.4	32
379	Restricting Dosage Compensation Complex Binding to the X Chromosomes by H2A.Z/H Genetics, 2009, 5, e1000699.	ITZ-1. PLoS	1.5	29
380	Discovery and Annotation of Functional Chromatin Signatures in the Human Genome. I Computational Biology, 2009, 5, e1000566.	PLoS	1.5	143
381	Differential epigenetic modifications of histones at the myosin heavy chain genes in fas skeletal muscle fibers and in response to muscle unloading. American Journal of Physiol Physiology, 2009, 297, C6-C16.	t and slow ogy - Cell	2.1	69
382	Transcriptional Dysregulation in NIPBL and Cohesin Mutant Human Cells. PLoS Biology, e1000119.	2009, 7,	2.6	199
383	The Euchromatic and Heterochromatic Landscapes Are Shaped by Antagonizing Effects Transcription on H2A.Z Deposition. PLoS Genetics, 2009, 5, e1000687.	of	1.5	117
384	Exhaustive Search for Over-represented DNA Sequence Motifs with CisFinder. DNA Res 261-273.	earch, 2009, 16,	1.5	113
385	How eukaryotic genes are transcribed. Critical Reviews in Biochemistry and Molecular B 44, 117-141.	iology, 2009,	2.3	129
386	DNA Specificity Determinants Associate with Distinct Transcription Factor Functions. P 2009, 5, e1000778.	LoS Genetics,	1.5	161
387	Genome-Wide uH2A Localization Analysis Highlights Bmi1-Dependent Deposition of the Repressed Genes. PLoS Genetics, 2009, 5, e1000506.	e Mark at	1.5	58
388	Nucleosomes are preferentially positioned at exons in somatic and sperm cells. Cell Cyc 3420-3424.	le, 2009, 8,	1.3	95

#	Article	IF	CITATIONS
389	Open chromatin encoded in DNA sequence is the signature of â€~master' replication origins in human cells. Nucleic Acids Research, 2009, 37, 6064-6075.	6.5	52
390	Epigenetics of human T cells during the G ₀ →G ₁ transition. Genome Research, 2009, 19, 1325-1337.	2.4	19
391	Corepressive Action of CBP on Androgen Receptor Transactivation in Pericentric Heterochromatin in a <i>Drosophila</i> Experimental Model System. Molecular and Cellular Biology, 2009, 29, 1017-1034.	1.1	29
392	Recruitment of Polycomb group complexes and their role in the dynamic regulation of cell fate choice. Development (Cambridge), 2009, 136, 3531-3542.	1.2	370
393	Misguided Transcriptional Elongation Causes Mixed Lineage Leukemia. PLoS Biology, 2009, 7, e1000249.	2.6	173
394	Regulatory patterns of histone modifications to control the DNA methylation status at CpG islands. Interdisciplinary Bio Central, 2009, 1, 15-21.	0.1	4
395	Transcription Initiation Activity Sets Replication Origin Efficiency in Mammalian Cells. PLoS Genetics, 2009, 5, e1000446.	1.5	216
396	W-ChIPMotifs: a web application tool for <i>de novo</i> motif discovery from ChIP-based high-throughput data. Bioinformatics, 2009, 25, 3191-3193.	1.8	42
397	Evolutionary Conserved Motif Finder (ECMFinder) for genome-wide identification of clustered YY1- and CTCF-binding sites. Nucleic Acids Research, 2009, 37, 2003-2013.	6.5	18
398	Visualization of genomic data with the Hilbert curve. Bioinformatics, 2009, 25, 1231-1235.	1.8	61
399	Massive transcriptional start site analysis of human genes in hypoxia cells. Nucleic Acids Research, 2009, 37, 2249-2263.	6.5	103
400	Cutting Edge: Developmental Stage-Specific Recruitment of Cohesin to CTCF Sites throughout Immunoglobulin Loci during B Lymphocyte Development. Journal of Immunology, 2009, 182, 44-48.	0.4	169
401	CTCF and its protein partners: divide and rule?. Journal of Cell Science, 2009, 122, 1275-1284.	1.2	135
402	Histone H2A.Z is essential for estrogen receptor signaling. Genes and Development, 2009, 23, 1522-1533.	2.7	133
403	Chromatin Structure Is Implicated in "Late―Elongation Checkpoints on the U2 snRNA and β-Actin Genes. Molecular and Cellular Biology, 2009, 29, 4002-4013.	1.1	38
404	DNasel hypersensitivity at gene-poor, FSH dystrophy-linked 4q35.2. Nucleic Acids Research, 2009, 37, 7381-7393.	6.5	15
405	Using reads to annotate the genome: influence of length, background distribution, and sequence errors on prediction capacity. Nucleic Acids Research, 2009, 37, e104-e104.	6.5	21
406	Heritable Imprinting Defect Caused by Epigenetic Abnormalities in Mouse Spermatogonial Stem Cells1. Biology of Reproduction, 2009, 80, 518-527.	1.2	41

			2
#	ARTICLE	IF	CITATIONS
407	A histone demethylase is necessary for regeneration in zebrafish. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 19889-19894.	3.3	110
408	Hear Today, Gone Tomorrow: An Assessment of Portable Entertainment Player Use and Hearing Acuity in a Community Sample. Journal of the American Board of Family Medicine, 2009, 22, 17-23.	0.8	36
409	Hierarchical hidden Markov model with application to joint analysis of ChIP-chip and ChIP-seq data. Bioinformatics, 2009, 25, 1715-1721.	1.8	33
410	Transcriptional competence in pluripotency: Figure 1 Genes and Development, 2009, 23, 2793-2798.	2.7	30
411	Genomic distribution of CHD7 on chromatin tracks H3K4 methylation patterns. Genome Research, 2009, 19, 590-601.	2.4	210
412	Coactivator Function Defines the Active Estrogen Receptor Alpha Cistrome. Molecular and Cellular Biology, 2009, 29, 3413-3423.	1.1	68
413	Common fragile sites are characterized by histone hypoacetylation. Human Molecular Genetics, 2009, 18, 4501-4512.	1.4	48
414	Inactive X chromosome-specific reduction in placental DNA methylation. Human Molecular Genetics, 2009, 18, 3544-3552.	1.4	66
415	Inactive X chromosome-specific histone H3 modifications and CpG hypomethylation flank a chromatin boundary between an X-inactivated and an escape gene. Nucleic Acids Research, 2009, 37, 7416-7428.	6.5	48
416	Methylation of <i>TFPI2</i> in Stool DNA: A Potential Novel Biomarker for the Detection of Colorectal Cancer. Cancer Research, 2009, 69, 4691-4699.	0.4	204
417	Predictive chromatin signatures in the mammalian genome. Human Molecular Genetics, 2009, 18, R195-R201.	1.4	196
418	The Target of the NSD Family of Histone Lysine Methyltransferases Depends on the Nature of the Substrate. Journal of Biological Chemistry, 2009, 284, 34283-34295.	1.6	257
419	Analysis of Histones in Xenopus laevis. Journal of Biological Chemistry, 2009, 284, 1064-1074.	1.6	66
420	Epigenetic analysis of the critical region I for premature ovarian failure: demonstration of a highly heterochromatic domain on the long arm of the mammalian X chromosome. Journal of Medical Genetics, 2009, 46, 585-592.	1.5	33
421	Human Immunodeficiency Virus Integration Efficiency and Site Selection in Quiescent CD4 ⁺ T Cells. Journal of Virology, 2009, 83, 6222-6233.	1.5	48
422	Postrecruitment Regulation of RNA Polymerase II Directs Rapid Signaling Responses at the Promoters of Estrogen Target Genes. Molecular and Cellular Biology, 2009, 29, 1123-1133.	1.1	77
423	BRG1 Increases Transcription of Proinflammatory Genes in Renal Ischemia. Journal of the American Society of Nephrology: JASN, 2009, 20, 1787-1796.	3.0	65
424	Nucleosome eviction from MHC class II promoters controls positioning of the transcription start site. Nucleic Acids Research, 2009, 37, 2514-2528.	6.5	11

#	Article	IF	CITATIONS
425	A T9G Mutation in the Prototype TATA-Box TCACTATATATAG Determines Nucleosome Formation and Synergy with Upstream Activator Sequences in Plant Promoters. Plant Physiology, 2009, 151, 2174-2186.	2.3	11
426	Genome-Wide and Organ-Specific Landscapes of Epigenetic Modifications and Their Relationships to mRNA and Small RNA Transcriptomes in Maize. Plant Cell, 2009, 21, 1053-1069.	3.1	291
427	Down-regulation of Gfi-1 expression by TGF-Î ² is important for differentiation of Th17 and CD103+ inducible regulatory T cells. Journal of Experimental Medicine, 2009, 206, 329-341.	4.2	124
428	Chromatin analysis of occluded genes. Human Molecular Genetics, 2009, 18, 2567-2574.	1.4	8
429	Epigenetic Modulation of Gene Expression from Quiescent Herpes Simplex Virus Genomes. Journal of Virology, 2009, 83, 8514-8524.	1.5	39
430	Chromatin poises miRNA- and protein-coding genes for expression. Genome Research, 2009, 19, 1742-1751.	2.4	135
431	Genome-wide colonization of gene regulatory elements by G4 DNA motifs. Nucleic Acids Research, 2009, 37, 6784-6798.	6.5	76
432	Native chromatin immunoprecipitation (N-ChIP) and ChIP-Seq of Schistosoma mansoni: Critical experimental parameters. Molecular and Biochemical Parasitology, 2009, 166, 70-76.	0.5	35
433	Next is now: new technologies for sequencing of genomes, transcriptomes, and beyond. Current Opinion in Plant Biology, 2009, 12, 107-118.	3.5	261
434	Epigenetic regulation of stress responses in plants. Current Opinion in Plant Biology, 2009, 12, 133-139.	3.5	984
435	Histone deacetylase inhibitors and candidate gene expression: An in vivo and in vitro approach to studying chromatin remodeling in a clinical population. Journal of Psychiatric Research, 2009, 43, 870-876.	1.5	75
436	Regeneration, repair and remembering identity: the three Rs of Hox gene expression. Trends in Cell Biology, 2009, 19, 268-275.	3.6	116
437	H2A.Z and DNA methylation: irreconcilable differences. Trends in Biochemical Sciences, 2009, 34, 158-161.	3.7	16
438	Next-generation sequencing technologies and their implications for crop genetics and breeding. Trends in Biotechnology, 2009, 27, 522-530.	4.9	805
439	Genetics and epigenetics: stability and plasticity during cellular differentiation. Trends in Genetics, 2009, 25, 129-136.	2.9	271
440	Improved ChIP-chip analysis by a mixture model approach. BMC Bioinformatics, 2009, 10, 173.	1.2	5
441	Gene set-based module discovery in the breast cancer transcriptome. BMC Bioinformatics, 2009, 10, 71.	1.2	28
442	Transcriptional interaction-assisted identification of dynamic nucleosome positioning. BMC Bioinformatics, 2009, 10, S31.	1.2	3

# 443	ARTICLE The evolutionary differentiation of two histone H2A.Z variants in chordates (H2A.Z-1 and H2A.Z-2) is mediated by a stepwise mutation process that affects three amino acid residues. BMC Evolutionary Biology, 2009, 9, 31.	IF 3.2	CITATIONS
444	Determination of enriched histone modifications in non-genic portions of the human genome. BMC Genomics, 2009, 10, 143.	1.2	182
445	An improved method for genome wide DNA methylation profiling correlated to transcription and genomic instability in two breast cancer cell lines. BMC Genomics, 2009, 10, 223.	1.2	31
446	Definition, conservation and epigenetics of housekeeping and tissue-enriched genes. BMC Genomics, 2009, 10, 269.	1.2	134
447	Efficient yeast ChIP-Seq using multiplex short-read DNA sequencing. BMC Genomics, 2009, 10, 37.	1.2	137
448	Histone modifications are specifically relocated during gene activation and nuclear differentiation. BMC Genomics, 2009, 10, 554.	1.2	8
449	Deciphering the transcriptional circuitry of microRNA genes expressed during human monocytic differentiation. BMC Genomics, 2009, 10, 595.	1.2	65
450	Characterizing nucleosome dynamics from genomic and epigenetic information using rule induction learning. BMC Genomics, 2009, 10, S27.	1.2	6
451	Mass spectrometry analysis of the variants of histone H3 and H4 of soybean and their post-translational modifications. BMC Plant Biology, 2009, 9, 98.	1.6	39
452	Impact of genome assembly status on ChIP-Seq and ChIP-PET data mapping. BMC Research Notes, 2009, 2, 257.	0.6	5
453	Histone acetylation characterizes chromatin presetting by NF1 and Oct1 and enhances glucocorticoid receptor binding to the MMTV promoter. Experimental Cell Research, 2009, 315, 2604-2615.	1.2	24
454	DLEU2, frequently deleted in malignancy, functions as a critical host gene of the cell cycle inhibitory microRNAs miR-15a and miR-16-1. Experimental Cell Research, 2009, 315, 2941-2952.	1.2	153
455	Nextâ€generation sequencing approaches in genetic rodent model systems to study functional effects of human genetic variation. FEBS Letters, 2009, 583, 1668-1673.	1.3	16
456	Metabolic defects provide a spark for the epigenetic switch in cancer. Free Radical Biology and Medicine, 2009, 47, 115-127.	1.3	75
457	Transcriptional memory at the nuclear periphery. Current Opinion in Cell Biology, 2009, 21, 127-133.	2.6	63
459	Epitopeâ€ŧagging Math5 and Pou4f2: New tools to study retinal ganglion cell development in the mouse. Developmental Dynamics, 2009, 238, 2309-2317.	0.8	26
460	Characterization of the expression pattern of the PRC2 core subunit <i>Suz12</i> during embryonic development of <i>Xenopus laevis</i> . Developmental Dynamics, 2009, 238, 3185-3192.	0.8	13
461	Analysis of epigenetic alterations to chromatin during development. Genesis, 2009, 47, 559-572.	0.8	42

#	Article	IF	CITATIONS
462	From sextant to GPS: Twentyâ€five years of mapping the genome with ChIP. Journal of Cellular Biochemistry, 2009, 107, 6-10.	1.2	7
463	Genomic location analysis by ChIP‣eq. Journal of Cellular Biochemistry, 2009, 107, 11-18.	1.2	153
464	ChIPâ€based methods for the identification of longâ€range chromatin interactions. Journal of Cellular Biochemistry, 2009, 107, 30-39.	1.2	246
465	Histone marks and chromatin remodelers on the regulation of <i>neurogenin1</i> gene in RA induced neuronal differentiation of P19 cells. Journal of Cellular Biochemistry, 2009, 107, 264-271.	1.2	28
466	Location, location, (ChIPâ€)location! Mapping chromatin landscapes one immunoprecipitation at a time. Journal of Cellular Biochemistry, 2009, 107, 1-5.	1.2	0
467	Stability of histone modifications across mammalian genomes: Implications for â€~epigenetic' marking. Journal of Cellular Biochemistry, 2009, 108, 22-34.	1.2	72
468	DNA methylation and histone modification regulate silencing of OPG during tumor progression. Journal of Cellular Biochemistry, 2009, 108, 315-325.	1.2	47
469	CCCTCâ€binding factor meets poly(ADPâ€ribose) polymeraseâ€1. Journal of Cellular Physiology, 2009, 219, 265-270.	2.0	32
470	Thioredoxin interacting protein (TXNIP) induces inflammation through chromatin modification in retinal capillary endothelial cells under diabetic conditions. Journal of Cellular Physiology, 2009, 221, 262-272.	2.0	214
471	Histone modifications associated with drought tolerance in the desert plant Zygophyllum dumosum Boiss. Planta, 2009, 231, 27-34.	1.6	35
472	Genome-wide analysis of histone H3 lysine 27 trimethylation by ChIP-chip in gastric cancer patients. Journal of Gastroenterology, 2009, 44, 305-312.	2.3	40
473	Changes in chromatin structure correlate with transcriptional activity of nucleolar rDNA in polytene chromosomes. Chromosoma, 2009, 118, 303-322.	1.0	10
474	The Current STATus of lymphocyte signaling: new roles for old players. Current Opinion in Immunology, 2009, 21, 161-166.	2.4	101
475	X chromosomal regulation in flies: when less is more. Chromosome Research, 2009, 17, 603-19.	1.0	19
476	Epigenetic regulation: methylation of histone and non-histone proteins. Science in China Series C: Life Sciences, 2009, 52, 311-322.	1.3	97
477	Foreword for inaugural issue of Journal of Neurodevelopmental Disorders. Journal of Neurodevelopmental Disorders, 2009, 1, 2-3.	1.5	2
478	Dynamic protein methylation in chromatin biology. Cellular and Molecular Life Sciences, 2009, 66, 407-22.	2.4	185
479	Antisense transcription: A critical look in both directions. Cellular and Molecular Life Sciences, 2009, 66, 94-112.	2.4	104

		CITATION REPORT		
#	Article		IF	CITATIONS
480	CCCTC-binding factor: to loop or to bridge. Cellular and Molecular Life Sciences, 2009,	66, 1647-1660.	2.4	52
481	Epigenetics: deciphering how environmental factors may modify autoimmune type 1 d Mammalian Genome, 2009, 20, 624-632.	iabetes.	1.0	71
482	KMT1E Mediated H3K9 Methylation Is Required for the Maintenance of Embryonic Ster Repressing Trophectoderm Differentiation. Stem Cells, 2010, 28, 201-212.	n Cells by	1.4	81
483	Networks and pathways in pigmentation, health, and disease. Wiley Interdisciplinary Re Biology and Medicine, 2009, 1, 359-371.	eviews: Systems	6.6	23
484	Sequence-dependent DNA helical rise and nucleosome stability. BMC Molecular Biolog	y, 2009, 10, 105.	3.0	6
485	Discriminating nucleosomes containing histone H2A.Z or H2A based on genetic and ep information. BMC Molecular Biology, 2009, 10, 18.	igenetic	3.0	9
486	DNA methylation-histone modification relationships across the desmin locus in human BMC Molecular Biology, 2009, 10, 51.	primary cells.	3.0	18
487	Multiple histone modifications in euchromatin promote heterochromatin formation by mechanisms in Saccharomyces cerevisiae. BMC Molecular Biology, 2009, 10, 76.	redundant	3.0	25
488	Characterization of the histone H2A.Z-1 and H2A.Z-2 isoforms in vertebrates. BMC Bio	logy, 2009, 7, 86.	1.7	89
489	Arabidopsis ING and Alfin1â€like protein families localize to the nucleus and bind to H3 homeodomain fingers. Plant Journal, 2009, 58, 511-524.	K4me3/2 via plant	2.8	122
490	Clobal analysis of mutual interaction surfaces of nucleosomes with comprehensive poi Genes To Cells, 2009, 14, 1271-1330.	nt mutants.	0.5	23
491	Epigenetics and T helper 1 differentiation. Immunology, 2009, 126, 299-305.		2.0	68
492	Histone H3 lysine 4 trimethylation marks meiotic recombination initiation sites. EMBO 28, 99-111.	Journal, 2009,	3.5	329
493	Distinct histone modifications define initiation and repair of meiotic recombination in t EMBO Journal, 2009, 28, 2616-2624.	he mouse.	3.5	195
494	Histone H1 binding is inhibited by histone variant H3.3. EMBO Journal, 2009, 28, 3635	-3645.	3.5	97
495	Active promoters and insulators are marked by the centrosomal protein 190. EMBO Joi 877-888.	urnal, 2009, 28,	3.5	145
496	Architectural roles of multiple chromatin insulators at the human apolipoprotein gene EMBO Journal, 2009, 28, 1234-1245.	cluster.	3.5	185
497	Genomic tools for dissecting oncogenic transcriptional networks in human leukemia. L 23, 1236-1242.	eukemia, 2009,	3.3	8

#	Article	IF	CITATIONS
498	Chromatin maps, histone modifications and leukemia. Leukemia, 2009, 23, 1243-1251.	3.3	54
499	Histone modifications at human enhancers reflect global cell-type-specific gene expression. Nature, 2009, 459, 108-112.	13.7	2,225
500	Cohesins form chromosomal cis-interactions at the developmentally regulated IFNG locus. Nature, 2009, 460, 410-413.	13.7	472
501	A histone H3 lysine 36 trimethyltransferase links Nkx2-5 to Wolf–Hirschhorn syndrome. Nature, 2009, 460, 287-291.	13.7	336
502	The logic of chromatin architecture and remodelling at promoters. Nature, 2009, 461, 193-198.	13.7	399
503	Genomic views of distant-acting enhancers. Nature, 2009, 461, 199-205.	13.7	549
504	An oestrogen-receptor-α-bound human chromatin interactome. Nature, 2009, 462, 58-64.	13.7	1,537
505	Targeted and genome-scale strategies reveal gene-body methylation signatures in human cells. Nature Biotechnology, 2009, 27, 361-368.	9.4	985
506	Histone H3 methylation links DNA damage detection to activation of the tumour suppressor Tip60. Nature Cell Biology, 2009, 11, 1376-1382.	4.6	387
507	Differential chromatin marking of introns and expressed exons by H3K36me3. Nature Genetics, 2009, 41, 376-381.	9.4	592
508	H3.3/H2A.Z double variant–containing nucleosomes mark 'nucleosome-free regions' of active promoters and other regulatory regions. Nature Genetics, 2009, 41, 941-945.	9.4	679
509	Computation for ChIP-seq and RNA-seq studies. Nature Methods, 2009, 6, S22-S32.	9.0	489
510	Nucleosome positioning and gene regulation: advances through genomics. Nature Reviews Genetics, 2009, 10, 161-172.	7.7	915
511	Linking DNA methylation and histone modification: patterns and paradigms. Nature Reviews Genetics, 2009, 10, 295-304.	7.7	1,944
512	ChIP–seq: advantages and challenges of a maturing technology. Nature Reviews Genetics, 2009, 10, 669-680.	7.7	1,728
513	The complex eukaryotic transcriptome: unexpected pervasive transcription and novel small RNAs. Nature Reviews Genetics, 2009, 10, 833-844.	7.7	394
514	Epigenetic control of T-helper-cell differentiation. Nature Reviews Immunology, 2009, 9, 91-105.	10.6	600
515	Application of 'next-generation' sequencing technologies to microbial genetics. Nature Reviews Microbiology, 2009, 7, 96-97.	13.6	269

#	Article	IF	CITATIONS
516	In the News. Nature Reviews Microbiology, 2009, 7, 260-261.	13.6	158
517	Nucleosome positioning as a determinant of exon recognition. Nature Structural and Molecular Biology, 2009, 16, 996-1001.	3.6	406
518	Chromatin organization marks exon-intron structure. Nature Structural and Molecular Biology, 2009, 16, 990-995.	3.6	569
519	Systems biology of innate immunity. Immunological Reviews, 2009, 227, 264-282.	2.8	139
520	Repressive but not activating epigenetic modifications are aberrant on the inactive X chromosome in live cloned cattle. Development Growth and Differentiation, 2009, 51, 585-594.	0.6	2
521	The Year in Human and Medical Genetics. Annals of the New York Academy of Sciences, 2009, 1151, 1-21.	1.8	8
522	Epigenetic Regulation of Mammalian Genomes by Transposable Elements. Annals of the New York Academy of Sciences, 2009, 1178, 276-284.	1.8	36
523	Methyltransferases in myelodysplastic syndromes: Guilty or not guilty?. Leukemia Research, 2009, 33, 601-602.	0.4	2
524	Retroviral integration sites (RIS) mark cis-regulatory elements. Critical Reviews in Oncology/Hematology, 2009, 71, 1-11.	2.0	1
525	Global Mapping of H3K4me3 and H3K27me3 Reveals Specificity and Plasticity in Lineage Fate Determination of Differentiating CD4+ T Cells. Immunity, 2009, 30, 155-167.	6.6	1,005
526	Genome-wide Analysis of Histone Methylation Reveals Chromatin State-Based Regulation of Gene Transcription and Function of Memory CD8+ T Cells. Immunity, 2009, 30, 912-925.	6.6	256
527	How cohesin and CTCF cooperate in regulating gene expression. Chromosome Research, 2009, 17, 201-214.	1.0	104
528	Survey of Schizophrenia and Bipolar Disorder Candidate Genes using Chromatin Immunoprecipitation and Tiled Microarrays (ChIP-chip). Journal of Neurogenetics, 2009, 23, 341-352.	0.6	14
529	Genomic imprinting: employing and avoiding epigenetic processes. Genes and Development, 2009, 23, 2124-2133.	2.7	220
530	Long-Term Evolution of Histone Families: Old Notions and New Insights into Their Mechanisms of Diversification Across Eukaryotes. , 2009, , 139-162.		35
531	ChIPing away at the genome: the new frontier travel guide. Molecular BioSystems, 2009, 5, 1421.	2.9	16
532	Genome-wide identification of DNA–protein interactions using chromatin immunoprecipitation coupled with flow cell sequencing. Journal of Endocrinology, 2009, 201, 1-13.	1.2	37
533	Histones: Annotating Chromatin. Annual Review of Genetics, 2009, 43, 559-599.	3.2	737

#	Article	IF	CITATIONS
534	Dual role for the methyltransferase G9a in the maintenance of β-globin gene transcription in adult erythroid cells. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 18303-18308.	3.3	80
535	Genome-Wide Views of Chromatin Structure. Annual Review of Biochemistry, 2009, 78, 245-271.	5.0	292
536	Massively Parallel Sequencing: The Next Big Thing in Genetic Medicine. American Journal of Human Genetics, 2009, 85, 142-154.	2.6	308
537	Commercial high-throughput sequencing and its applications in DNA analysis. Biologia (Poland), 2009, 64, 20-26.	0.8	4
538	Epigenetic Control of the Invasion-promoting MT1-MMP/MMP-2/TIMP-2 Axis in Cancer Cells. Journal of Biological Chemistry, 2009, 284, 12727-12734.	1.6	95
539	Mapping accessible chromatin regions using Sono-Seq. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 14926-14931.	3.3	186
540	CBP-mediated acetylation of histone H3 lysine 27 antagonizes <i>Drosophila</i> Polycomb silencing. Development (Cambridge), 2009, 136, 3131-3141.	1.2	468
541	A clustering approach for identification of enriched domains from histone modification ChIP-Seq data. Bioinformatics, 2009, 25, 1952-1958.	1.8	936
542	Deducing Causal Relationships among Different Histone Modifications, DNA Methylation and Gene Expression. , 2009, , .		0
543	Importance of Charge Independent Effects in Readout of the Trimethyllysine Mark by HP1 Chromodomain. Journal of the American Chemical Society, 2009, 131, 14928-14931.	6.6	22
544	Transcription termination by nuclear RNA polymerases. Genes and Development, 2009, 23, 1247-1269.	2.7	280
545	Epigenetics and the control of epithelial sodium channel expression in collecting duct. Kidney International, 2009, 75, 260-267.	2.6	52
546	Many human large intergenic noncoding RNAs associate with chromatin-modifying complexes and affect gene expression. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 11667-11672.	3.3	2,709
547	Histone H3 Modifications Associated With Differentiation and Long-Term Culture of Mesenchymal Adipose Stem Cells. Stem Cells and Development, 2009, 18, 725-736.	1.1	91
548	Identifying regulatory elements in eukaryotic genomes. Briefings in Functional Genomics & Proteomics, 2009, 8, 215-230.	3.8	87
549	NA-Seq: A Discovery Tool for the Analysis of Chromatin Structure and Dynamics during Differentiation. Developmental Cell, 2009, 16, 466-481.	3.1	55
550	A Hierarchy of H3K4me3 and H3K27me3 Acquisition in Spatial Gene Regulation in Xenopus Embryos. Developmental Cell, 2009, 17, 425-434.	3.1	206
551	Epigenetic gene regulation in stem cells and correlation to cancer. Differentiation, 2009, 78, 1-17.	1.0	70

щ		IF	Citations
#	ARTICLE Epigenomic profiling of cancer cells. International Journal of Biochemistry and Cell Biology, 2009, 41,		
552	127-135.	1.2	42
553	Inflammatory signalling as mediator of epigenetic modulation in tissue-specific chronic inflammation. International Journal of Biochemistry and Cell Biology, 2009, 41, 176-184.	1.2	117
554	Marking time: The dynamic role of chromatin and covalent modification in transcription. International Journal of Biochemistry and Cell Biology, 2009, 41, 155-163.	1.2	60
555	DNA methylomes, histone codes and miRNAs: Tying it all together. International Journal of Biochemistry and Cell Biology, 2009, 41, 87-95.	1.2	283
556	Epigenetics and human disease. International Journal of Biochemistry and Cell Biology, 2009, 41, 136-146.	1.2	99
557	Dynamic access of the glucocorticoid receptor to response elements in chromatin. International Journal of Biochemistry and Cell Biology, 2009, 41, 214-224.	1.2	37
558	Mechanisms that Specify Promoter Nucleosome Location and Identity. Cell, 2009, 137, 445-458.	13.5	376
559	Dimethylation of H3K4 by Set1 Recruits the Set3 Histone Deacetylase Complex to 5′ Transcribed Regions. Cell, 2009, 137, 259-272.	13.5	275
560	Androgen Receptor Regulates a Distinct Transcription Program in Androgen-Independent Prostate Cancer. Cell, 2009, 138, 245-256.	13.5	797
561	CTCF: Master Weaver of the Genome. Cell, 2009, 137, 1194-1211.	13.5	1,371
562	Genome-wide Mapping of HATs and HDACs Reveals Distinct Functions in Active and Inactive Genes. Cell, 2009, 138, 1019-1031.	13.5	1,174
563	Jarid2/Jumonji Coordinates Control of PRC2 Enzymatic Activity and Target Gene Occupancy in Pluripotent Cells. Cell, 2009, 139, 1290-1302.	13.5	474
564	Epigenetic mechanisms in schizophrenia. Biochimica Et Biophysica Acta - General Subjects, 2009, 1790, 869-877.	1.1	137
565	The role of histone H2A and H2B post-translational modifications in transcription: A genomic perspective. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2009, 1789, 37-44.	0.9	49
566	Jmjd2c histone demethylase enhances the expression of Mdm2 oncogene. Biochemical and Biophysical Research Communications, 2009, 389, 366-371.	1.0	55
567	Characterization of human epigenomes. Current Opinion in Genetics and Development, 2009, 19, 127-134.	1.5	144
568	Nuclear genome organization: common themes and individual patterns. Current Opinion in Genetics and Development, 2009, 19, 166-171.	1.5	37
569	Finding distal regulatory elements in the human genome. Current Opinion in Genetics and Development, 2009, 19, 541-549.	1.5	218

#	Article	IF	CITATIONS
570	Evolution of transcriptional control in mammals. Current Opinion in Genetics and Development, 2009, 19, 579-585.	1.5	47
571	Endogenous retroviral LTRs as promoters for human genes: A critical assessment. Gene, 2009, 448, 105-114.	1.0	261
572	Chromatin Signatures in Multipotent Human Hematopoietic Stem Cells Indicate the Fate of Bivalent Genes during Differentiation. Cell Stem Cell, 2009, 4, 80-93.	5.2	548
573	Glimpses of the Epigenetic Landscape. Cell Stem Cell, 2009, 4, 1-2.	5.2	36
574	Phosphorylation Dynamics during Early Differentiation of Human Embryonic Stem Cells. Cell Stem Cell, 2009, 5, 214-226.	5.2	301
575	A systems biology approach to understanding cis-regulatory module function. Seminars in Cell and Developmental Biology, 2009, 20, 856-862.	2.3	35
576	The stem cell—Chromatin connection. Seminars in Cell and Developmental Biology, 2009, 20, 1143-1148.	2.3	21
577	A multi-layer method to study genome-scale positions of nucleosomes. Genomics, 2009, 93, 140-145.	1.3	18
578	Generations of sequencing technologies. Genomics, 2009, 93, 105-111.	1.3	288
579	ChIP-seq: Using high-throughput sequencing to discover protein–DNA interactions. Methods, 2009, 48, 240-248.	1.9	455
580	RNA-Seq—quantitative measurement of expression through massively parallel RNA-sequencing. Methods, 2009, 48, 249-257.	1.9	414
581	Epigenetic background of neuronal fate determination. Progress in Neurobiology, 2009, 87, 98-117.	2.8	22
582	Identification of neuronal target genes for CCAAT/Enhancer Binding Proteins. Molecular and Cellular Neurosciences, 2009, 40, 313-327.	1.0	40
583	High-Resolution Mapping of Sequence-Directed Nucleosome Positioning on Genomic DNA. Journal of Molecular Biology, 2009, 390, 292-305.	2.0	27
584	Toxoplasma H2A Variants Reveal Novel Insights into Nucleosome Composition and Functions for this Histone Family. Journal of Molecular Biology, 2009, 392, 33-47.	2.0	62
585	Breaching the Boundaries that Safeguard against Repression. Molecular Cell, 2009, 34, 395-397.	4.5	4
586	H3K4me3 Stimulates the V(D)J RAG Complex for Both Nicking and Hairpinning in trans in Addition to Tethering in cis: Implications for Translocations. Molecular Cell, 2009, 34, 535-544.	4.5	111
587	Linking Cell Cycle to Histone Modifications: SBF and H2B Monoubiquitination Machinery and Cell-Cycle Regulation of H3K79 Dimethylation. Molecular Cell, 2009, 35, 626-641.	4.5	159

#	Article	IF	CITATIONS
588	Two Mammalian MOF Complexes Regulate Transcription Activation by Distinct Mechanisms. Molecular Cell, 2009, 36, 290-301.	4.5	151
589	Interaction of Transcriptional Regulators with Specific Nucleosomes across the Saccharomyces Genome. Molecular Cell, 2009, 35, 889-902.	4.5	110
590	Biased Chromatin Signatures around Polyadenylation Sites and Exons. Molecular Cell, 2009, 36, 245-254.	4.5	347
591	Genome-Wide Analysis of RNA-Protein Interactions in Plants. Methods in Molecular Biology, 2009, 553, 13-37.	0.4	38
592	High Throughput Characterization of Combinatorial Histone Codes. Molecular and Cellular Proteomics, 2009, 8, 2266-2284.	2.5	271
593	Evolution of Genomic Imprinting: Insights from Marsupials and Monotremes. Annual Review of Genomics and Human Genetics, 2009, 10, 241-262.	2.5	141
594	Cell Cycle Control of Kaposi's Sarcoma-Associated Herpesvirus Latency Transcription by CTCF-Cohesin Interactions. Journal of Virology, 2009, 83, 6199-6210.	1.5	46
595	Strategies for Epigenome Analysis. , 2009, , 3-18.		7
596	Next-generation DNA sequencing of paired-end tags (PET) for transcriptome and genome analyses. Genome Research, 2009, 19, 521-532.	2.4	286
597	Epigenetic Regulation in Human Brain—Focus on Histone Lysine Methylation. Biological Psychiatry, 2009, 65, 198-203.	0.7	206
598	Ontogenic expression of hepatic Ahr mRNA is associated with histone H3K4 di-methylation during mouse liver development. Toxicology Letters, 2009, 189, 184-190.	0.4	13
599	The State-of-the-Art of Chromatin Immunoprecipitation. Methods in Molecular Biology, 2009, 567, 1-25.	0.4	32
600	Global Repression of Cancer Gene Expression in a Zebrafish Model of Melanoma Is Linked to Epigenetic Regulation. Zebrafish, 2009, 6, 417-424.	0.5	48
601	Polycomb group-mediated gene silencing mechanisms: stability versus flexibility. Epigenomics, 2009, 1, 301-318.	1.0	5
602	Chromatin Immunoprecipitation Using Microarrays. Methods in Molecular Biology, 2009, 529, 279-295.	0.4	12
603	Next-Generation Sequencing: From Basic Research to Diagnostics. Clinical Chemistry, 2009, 55, 641-658.	1.5	668
604	Regulation of Stem Cell Pluripotency and Differentiation Involves a Mutual Regulatory Circuit of the Nanog, OCT4, and SOX2 Pluripotency Transcription Factors With Polycomb Repressive Complexes and Stem Cell microRNAs. Stem Cells and Development, 2009, 18, 1093-1108.	1.1	375
605	Transcriptional and epigenetic functions of histone variant H2A.ZThis paper is one of a selection of papers published in this Special Issue, entitled CSBMCB's 51st Annual Meeting– Epigenetics and Chromatin Dynamics, and has undergone the Journal's usual peer review process Biochemistry and Cell Biology. 2009. 87. 19-25.	0.9	50

#	Article	IF	CITATIONS
607	Paused Pol II captures enhancer activity and acts as a potent insulator. Genes and Development, 2009, 23, 1606-1612.	2.7	20
609	The multiple facets of histone H4-lysine 20 methylationThis paper is one of a selection of papers published in this Special Issue, entitled CSBMCB's 51st Annual Meeting– Epigenetics and Chromatin Dynamics, and has undergone the Journal's usual peer review process Biochemistry and Cell Biology, 2009. 87, 151-161.	0.9	66
610	Regulation of gene expression and cellular proliferation by histone H2A.ZThis paper is one of a selection of papers published in this Special Issue, entitled CSBMCB's 51st Annual Meeting– Epigenetics and Chromatin Dynamics, and has undergone the Journal's usual peer review process Biochemistry and Cell Biology, 2009, 87, 179-188.	0.9	53
611	Applications of Ultra-high-Throughput Sequencing. Methods in Molecular Biology, 2009, 553, 79-108.	0.4	72
615	CTCF binding site classes exhibit distinct evolutionary, genomic, epigenomic and transcriptomic features. Genome Biology, 2009, 10, R131.	13.9	72
616	Differential binding and co-binding pattern of FOXA1 and FOXA3 and their relation to H3K4me3 in HepG2 cells revealed by ChIP-seq. Genome Biology, 2009, 10, R129.	13.9	64
617	Defining the chromatin signature of inducible genes in T cells. Genome Biology, 2009, 10, R107.	13.9	30
618	Preferential binding of HIF-1 to transcriptionally active loci determines cell-type specific response to hypoxia. Genome Biology, 2009, 10, R113.	13.9	131
619	Genome-wide analysis of mono-, di- and trimethylation of histone H3 lysine 4 in Arabidopsis thaliana. Genome Biology, 2009, 10, R62.	13.9	504
620	The need for speed. Genome Biology, 2009, 10, 212.	13.9	12
621	EpiGRAPH: user-friendly software for statistical analysis and prediction of (epi)genomic data. Genome Biology, 2009, 10, R14.	13.9	48
622	Profiling RE1/REST-mediated histone modifications in the human genome. Genome Biology, 2009, 10, R9.	13.9	70
623	ChIP'ing the mammalian genome: technical advances and insights into functional elements. Genome Medicine, 2009, 1, 89.	3.6	16
624	A Decade of Cancer Gene Profiling: From Molecular Portraits to Molecular Function. Methods in Molecular Biology, 2009, 576, 61-87.	0.4	13
627	Short-Read Sequencing Technologies for Transcriptional Analyses. Annual Review of Plant Biology, 2009, 60, 305-333.	8.6	118
628	Chromatin Immunoprecipitation Assays. Methods in Molecular Biology, 2009, , .	0.4	6
629	Algorithms in Bioinformatics. Lecture Notes in Computer Science, 2009, , .	1.0	2
630	How does the periodicity associated with nucleosomal DNA reflect on its intrinsic curvature?. , 2009, , .		0

CITATION REPORT

#	Article	IF	CITATIONS
631	Advantages of next-generation sequencing versus the microarray in epigenetic research. Briefings in Functional Genomics & Proteomics, 2009, 8, 174-183.	3.8	218
632	Regulation of Gene Expression in Peripheral T Cells by Runx Transcription Factors. Advances in Immunology, 2009, 104, 1-23.	1.1	20
633	Connection between histone H2A variants and chromatin remodeling complexesThis paper is one of a selection of papers published in this Special Issue, entitled CSBMCB's 51st Annual Meeting– Epigenetics and Chromatin Dynamics, and has undergone the Journal's usual peer review process Biochemistry and Cell Biology, 2009, 87, 35-50.	0.9	63
634	Scoring overlapping and adjacent signals from genome-wide ChIP and DamID assays. Molecular BioSystems, 2009, 5, 1429.	2.9	13
635	Machine learning approach for classifying histone modifications. , 2009, , .		0
636	Divergent transcription: A new feature of active promoters. Cell Cycle, 2009, 8, 2557-2564.	1.3	172
637	Renal Ischemia-Induced Cholesterol Loading. American Journal of Pathology, 2009, 174, 54-62.	1.9	54
639	Acetylation of Vertebrate H2A.Z and Its Effect on the Structure of the Nucleosome. Biochemistry, 2009, 48, 5007-5017.	1.2	83
640	CDKN1C (p57KIP2) Is a Direct Target of EZH2 and Suppressed by Multiple Epigenetic Mechanisms in Breast Cancer Cells. PLoS ONE, 2009, 4, e5011.	1.1	155
641	Epigenetic regulation of vertebrate <i>Hox</i> genes: A dynamic equilibrium. Epigenetics, 2009, 4, 537-540.	1.3	52
642	Epigenetic marks in melanoma. Pigment Cell and Melanoma Research, 2009, 22, 14-29.	1.5	27
643	Nucleosomes are well positioned in exons and carry characteristic histone modifications. Genome Research, 2009, 19, 1732-1741.	2.4	274
644	Pervasive transcription of the eukaryotic genome: functional indices and conceptual implications. Briefings in Functional Genomics & Proteomics, 2009, 8, 407-423.	3.8	140
645	Epigenetic mechanisms in cancer. Biomarkers in Medicine, 2009, 3, 397-410.	0.6	32
646	Selective Gene Amplification for High-Throughput Sequencing. Recent Patents on DNA & Gene Sequences, 2009, 3, 29-38.	0.7	4
647	High-resolution mapping studies of chromatin and gene regulatory elements. Epigenomics, 2009, 1, 319-329.	1.0	5
648	Mechanisms of transcriptional repression by histone lysine methylation. International Journal of Developmental Biology, 2009, 53, 335-354.	0.3	163
649	Insights into the function of the human P-TEFb component CDK9 in the regulation of chromatin modifications and co-transcriptional mRNA processing. Cell Cycle, 2009, 8, 3636-3642.	1.3	55

#	Article	IF	CITATIONS
650	HIV integration site distributions in resting and activated CD4 + T cells infected in culture. Aids, 2009, 23, 1461-1471.	1.0	129
651	Expression of the leukemia oncogene Lmo2 is controlled by an array of tissue-specific elements dispersed over 100 kb and bound by Tal1/Lmo2, Ets, and Gata factors. Blood, 2009, 113, 5783-5792.	0.6	69
652	Transcriptome and Genome Characterization Using Massively Parallel Paired End Tag (PET) Sequencing Analysis. , 2009, , 41-60.		0
653	New Era of Genome-Wide Gene Expression Analysis. , 2009, , 61-77.		0
654	L1 Retrotransposon and Retinoblastoma: Molecular Linkages Between Epigenetics and Cancer. Current Molecular Medicine, 2010, 10, 511-521.	0.6	17
655	Histone Variant H2A.Z Can Serve as a New Target for Breast Cancer Therapy. Current Medicinal Chemistry, 2010, 17, 3155-3161.	1.2	38
656	Long Noncoding RNAs as Enhancers of Gene Expression. Cold Spring Harbor Symposia on Quantitative Biology, 2010, 75, 325-331.	2.0	72
657	Epigenetic mechanisms in lupus. Current Opinion in Rheumatology, 2010, 22, 478-482.	2.0	54
658	Intra―and interâ€chromosomal interactions correlate with CTCF binding genome wide. Molecular Systems Biology, 2010, 6, 426.	3.2	92
659	Next Generation Sequencing: Advances in Characterizing the Methylome. Genes, 2010, 1, 143-165.	1.0	4
660	Signatures of polycomb repression and reduced H3K4 trimethylation are associated with p15INK4b DNA methylation in AML. Blood, 2010, 115, 3098-3108.	0.6	80
661	Epigenetic chromatin states uniquely define the developmental plasticity of murine hematopoietic stem cells. Blood, 2010, 115, 247-256.	0.6	96
662	Profiling of histone H3 lysine 9 trimethylation levels predicts transcription factor activity and survival in acute myeloid leukemia. Blood, 2010, 116, 3564-3571.	0.6	90
663	Polycomb proteins in hematologic malignancies. Blood, 2010, 116, 5465-5475.	0.6	56
664	High-definition mapping of retroviral integration sites identifies active regulatory elements in human multipotent hematopoietic progenitors. Blood, 2010, 116, 5507-5517.	0.6	150
665	Epigenetic silencing of BIM in glucocorticoid poor-responsive pediatric acute lymphoblastic leukemia, and its reversal by histone deacetylase inhibition. Blood, 2010, 116, 3013-3022.	0.6	110
666	Next generation sequencing based approaches to epigenomics. Briefings in Functional Genomics, 2010, 9, 455-465.	1.3	60
667	Differentiation of Effector CD4 T Cell Populations. Annual Review of Immunology, 2010, 28, 445-489.	9.5	2,783

# 668	ARTICLE Regulation of herpes simplex virus type 1 thymidine kinase gene expression by thyroid hormone receptor in cultured neuronal cells. Journal of NeuroVirology, 2010, 16, 13-24.	IF 1.0	Citations
669	Analysis of the primary structure of chromatin with next-generation sequencing. Epigenomics, 2010, 2, 187-197.	1.0	11
670	Processing and analyzing ChIP-seq data: from short reads to regulatory interactions. Briefings in Functional Genomics, 2010, 9, 466-476.	1.3	15
671	Single Molecule Epigenetic Analysis in a Nanofluidic Channel. Analytical Chemistry, 2010, 82, 2480-2487.	3.2	110
672	Decoding the histone H4 lysine 20 methylation mark. Critical Reviews in Biochemistry and Molecular Biology, 2010, 45, 440-452.	2.3	52
673	Reversal of Histone Methylation: Biochemical and Molecular Mechanisms of Histone Demethylases. Annual Review of Biochemistry, 2010, 79, 155-179.	5.0	513
674	Histone methyltransferases: regulation of transcription and contribution to human disease. Journal of Molecular Medicine, 2010, 88, 1213-1220.	1.7	51
675	Role of Ucp1 enhancer methylation and chromatin remodelling in the control of Ucp1 expression in murine adipose tissue. Diabetologia, 2010, 53, 1164-1173.	2.9	68
676	Seq-ing LPS-Induced Enhancers. Immunity, 2010, 32, 296-298.	6.6	10
677	The Transcription Factor GATA3 Actively Represses RUNX3 Protein-Regulated Production of Interferon-Î ³ . Immunity, 2010, 32, 507-517.	6.6	151
678	Partitioning the C. elegans genome by nucleosome modification, occupancy, and positioning. Chromosoma, 2010, 119, 73-87.	1.0	55
679	Synaptonemal complex stability depends on repressive histone marks of the lateral element-associated repeat sequences. Chromosoma, 2010, 119, 41-58.	1.0	7
680	Chromatin insulators specifically associate with different levels of higher-order chromatin organization in Drosophila. Chromosoma, 2010, 119, 177-194.	1.0	19
681	CTCF shapes chromatin by multiple mechanisms: the impact of 20Âyears of CTCF research on understanding the workings of chromatin. Chromosoma, 2010, 119, 351-360.	1.0	85
682	Positional variations among heterogeneous nucleosome maps give dynamical information on chromatin. Chromosoma, 2010, 119, 391-404.	1.0	8
683	The impact of histone post-translational modifications on developmental gene regulation. Amino Acids, 2010, 39, 1087-1105.	1.2	24
684	A Method to Study the Epigenetic Chromatin States of Rare Hematopoietic Stem and Progenitor Cells; MiniChIP–Chip. Biological Procedures Online, 2010, 12, 1-17.	1.4	4
685	Genome-Wide Analysis of Epigenetic Modifications. Journal of Computer Science and Technology, 2010, 25, 35-41.	0.9	1

#	Article	IF	CITATIONS
686	Predicted methylation landscape of all CpG islands on the human genome. Science Bulletin, 2010, 55, 2353-2358.	1.7	0
687	Simulation of ChIP-Seq based on extra-sonication of IPed DNA fragments. Science Bulletin, 2010, 55, 2380-2389.	1.7	0
688	Regulation beyond genome sequences: DNA and histone methylation in embryonic stem cells. Frontiers in Biology, 2010, 5, 41-47.	0.7	0
689	Epigenetic regulation of neuronal dendrite and dendritic spine development. Frontiers in Biology, 2010, 5, 304-323.	0.7	24
690	Genome-wide identification and annotation of HIF-1α binding sites in two cell lines using massively parallel sequencing. The HUGO Journal, 2010, 4, 35-48.	4.1	43
691	ATP Dependent Chromatin Remodeling Enzymes in Embryonic Stem Cells. Stem Cell Reviews and Reports, 2010, 6, 62-73.	5.6	42
692	Epigenetics Lessons from Twins: Prospects for Autoimmune Disease. Clinical Reviews in Allergy and Immunology, 2010, 39, 30-41.	2.9	94
693	The Current State of Chromatin Immunoprecipitation. Molecular Biotechnology, 2010, 45, 87-100.	1.3	224
694	Characterization of the DOT1L Network: Implications of Diverse Roles for DOT1L. Protein Journal, 2010, 29, 213-223.	0.7	51
695	Prediction of nucleosome DNA formation potential and nucleosome positioning using increment of diversity combined with quadratic discriminant analysis. Chromosome Research, 2010, 18, 777-785.	1.0	19
696	Utilization of next-generation sequencing platforms in plant genomics and genetic variant discovery. Molecular Breeding, 2010, 25, 553-570.	1.0	112
697	Two polypyrimidine tracts in the nitric oxide synthase 2 gene: similar regulatory sequences with different properties. Molecular Biology Reports, 2010, 37, 2021-2030.	1.0	9
698	Genome-wide profiling of histone H3 lysine 9 acetylation and dimethylation in Arabidopsis reveals correlation between multiple histone marks and gene expression. Plant Molecular Biology, 2010, 72, 585-595.	2.0	167
699	Low-copy repeats on chromosome 22q11.2 show replication timing switches, DNA flexibility peaks and stress inducible asynchrony, sharing instability features with fragile sites. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2010, 686, 74-83.	0.4	11
700	Investigating micronutrients and epigenetic mechanisms in relation to inflammatory bowel disease. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2010, 690, 71-80.	0.4	36
701	The role of REST in transcriptional and epigenetic dysregulation in Huntington's disease. Neurobiology of Disease, 2010, 39, 28-39.	2.1	134
702	Systems toxicology approaches for understanding the joint effects of environmental chemical mixtures. Science of the Total Environment, 2010, 408, 3725-3734.	3.9	198
703	Interchromosomal association and gene regulation in trans. Trends in Genetics, 2010, 26, 188-197.	2.9	83

#	Article	IF	Citations
704	Gene regulation by nucleosome positioning. Trends in Genetics, 2010, 26, 476-483.	2.9	211
705	A statistical method for excluding non-variable CpG sites in high-throughput DNA methylation profiling. BMC Bioinformatics, 2010, 11, 227.	1.2	21
706	HPeak: an HMM-based algorithm for defining read-enriched regions in ChIP-Seq data. BMC Bioinformatics, 2010, 11, 369.	1.2	94
707	Application of machine learning methods to histone methylation ChIP-Seq data reveals H4R3me2 globally represses gene expression. BMC Bioinformatics, 2010, 11, 396.	1.2	74
708	Next generation tools for genomic data generation, distribution, and visualization. BMC Bioinformatics, 2010, 11, 455.	1.2	42
709	Epigenetic domains found in mouse embryonic stem cells via a hidden Markov model. BMC Bioinformatics, 2010, 11, 557.	1.2	16
710	An effective approach for identification of in vivo protein-DNA binding sites from paired-end ChIP-Seq data. BMC Bioinformatics, 2010, 11, 81.	1.2	21
711	Annotation of gene promoters by integrative data-mining of ChIP-seq Pol-II enrichment data. BMC Bioinformatics, 2010, 11, S65.	1.2	28
712	Touring Ensembl: A practical guide to genome browsing. BMC Genomics, 2010, 11, 295.	1.2	33
713	The ubiquitin-conjugating enzyme HR6B is required for maintenance of X chromosome silencing in mouse spermatocytes and spermatids. BMC Genomics, 2010, 11, 367.	1.2	35
714	Distributed probing of chromatin structure in vivo reveals pervasive chromatin accessibility for expressed and non-expressed genes during tissue differentiation in C. elegans. BMC Genomics, 2010, 11, 465.	1.2	21
715	Genome-wide promoter analysis of histone modifications in human monocyte-derived antigen presenting cells. BMC Genomics, 2010, 11, 642.	1.2	29
716	Statistics of protein-DNA binding and the total number of binding sites for a transcription factor in the mammalian genome. BMC Genomics, 2010, 11, S12.	1.2	13
717	Complex sense-antisense architecture of TNFAIP1/POLDIP2 on 17q11.2 represents a novel transcriptional structural-functional gene module involved in breast cancer progression. BMC Genomics, 2010, 11, S9.	1.2	38
718	Dynamic changes in genome-wide histone H3 lysine 4 methylation patterns in response to dehydration stress in Arabidopsis thaliana. BMC Plant Biology, 2010, 10, 238.	1.6	191
719	Promoter- and cell-specific epigenetic regulation of CD44, Cyclin D2, GLIPR1 and PTEN by Methyl-CpG binding proteins and histone modifications. BMC Cancer, 2010, 10, 297.	1.1	31
720	Overexpression of Chromatin Assembly Factor-1/p60 helps to predict the prognosis of melanoma patients. BMC Cancer, 2010, 10, 63.	1.1	35
721	Inference of hierarchical regulatory network of estrogen-dependent breast cancer through ChIP-based data. BMC Systems Biology, 2010, 4, 170.	3.0	40

	CITATION R	EPORT	
# 722	ARTICLE Role of triptolide in cell proliferation, cell cycle arrest, apoptosis and histone methylation in multiple myeloma U266 cells. European Journal of Pharmacology, 2010, 646, 1-11.	IF 1.7	Citations
723	Experimental approaches to the study of epigenomic dysregulation in ageing. Experimental Gerontology, 2010, 45, 255-268.	1.2	18
724	A Cellular Memory of Developmental History Generates Phenotypic Diversity in C. elegans. Current Biology, 2010, 20, 149-155.	1.8	111
725	IUGR decreases PPARÎ ³ and SETD8 Expression in neonatal rat lung and these effects are ameliorated by maternal DHA supplementation. Early Human Development, 2010, 86, 785-791.	0.8	76
726	PML-RARα/RXR Alters the Epigenetic Landscape in Acute Promyelocytic Leukemia. Cancer Cell, 2010, 17, 173-185.	7.7	276
727	An Integrated Network of Androgen Receptor, Polycomb, and TMPRSS2-ERG Gene Fusions in Prostate Cancer Progression. Cancer Cell, 2010, 17, 443-454.	7.7	743
728	PPARγ in adipocyte differentiation and metabolism – Novel insights from genomeâ€wide studies. FEBS Letters, 2010, 584, 3242-3249.	1.3	330
729	Long intronic GAA repeats causing Friedreich ataxia impede transcription elongation. EMBO Molecular Medicine, 2010, 2, 120-129.	3.3	113
730	PR‣et7â€mediated monomethylation of histone H4 lysine 20 at specific genomic regions induces transcriptional repression. Journal of Cellular Biochemistry, 2010, 110, 609-619.	1.2	64
731	Changes in histone acetylation and methylation that are important for persistent but not transient expression of <i>CCR4</i> in human CD4 ⁺ T cells. European Journal of Immunology, 2010, 40, 3183-3197.	1.6	7
732	Does CTCF mediate between nuclear organization and gene expression?. BioEssays, 2010, 32, 37-50.	1.2	150
733	Epigenetics and parental effects. BioEssays, 2010, 32, 818-827.	1.2	125
734	Setting and resetting of epigenetic marks in malignant transformation and development. BioEssays, 2010, 32, 669-679.	1.2	20
735	RNA as the substrate for epigenomeâ€environment interactions. BioEssays, 2010, 32, 548-552.	1.2	64
736	Form and function of dosageâ€compensated chromosomes – a chickenâ€andâ€egg relationship. BioEssays, 2010, 32, 709-717.	1.2	9
737	What an epigenome remembers. BioEssays, 2010, 32, 659-668.	1.2	59
738	Returning to the stem state: Epigenetics of recapitulating preâ€differentiation chromatin structure. BioEssays, 2010, 32, 791-799.	1.2	27
740	Epigenomics of T cell activation, differentiation, and memory. Current Opinion in Immunology, 2010, 22, 341-347.	2.4	91

#	Article	IF	CITATIONS
741	Modeling epigenetic modifications under multiple treatment conditions. Computational Statistics and Data Analysis, 2010, 54, 1179-1189.	0.7	0
742	Maintaining Cell Identity through Global Control of Genomic Organization. Immunity, 2010, 33, 12-24.	6.6	187
743	The CTCF insulator protein forms an unusual DNA structure. BMC Molecular Biology, 2010, 11, 101.	3.0	44
744	Identification of regulatory elements flanking human XIST reveals species differences. BMC Molecular Biology, 2010, 11, 20.	3.0	19
745	Sequence periodicity in nucleosomal DNA and intrinsic curvature. BMC Structural Biology, 2010, 10, S8.	2.3	5
746	The Drosophila homolog of the mammalian imprint regulator, CTCF, maintains the maternal genomic imprint in Drosophila melanogaster. BMC Biology, 2010, 8, 105.	1.7	15
747	SICTIN: Rapid footprinting of massively parallel sequencing data. BioData Mining, 2010, 3, 4.	2.2	10
748	Menin and RNF20 recruitment is associated with dynamic histone modifications that regulate signal transducer and activator of transcription 1 (STAT1)-activated transcription of the interferon regulatory factor 1 gene (IRF1). Epigenetics and Chromatin, 2010, 3, 16.	1.8	27
749	CTCF regulates the local epigenetic state of ribosomal DNA repeats. Epigenetics and Chromatin, 2010, 3, 19.	1.8	80
750	Distinguishing epigenetic marks of developmental and imprinting regulation. Epigenetics and Chromatin, 2010, 3, 2.	1.8	69
751	Global turnover of histone post-translational modifications and variants in human cells. Epigenetics and Chromatin, 2010, 3, 22.	1.8	114
752	Histone H3 lysine 4 methylation is associated with the transcriptional reprogramming efficiency of somatic nuclei by oocytes. Epigenetics and Chromatin, 2010, 3, 4.	1.8	38
753	A paucity of heterochromatin at functional human neocentromeres. Epigenetics and Chromatin, 2010, 3, 6.	1.8	83
754	Epigenetic histone modifications of human transposable elements: genome defense versus exaptation. Mobile DNA, 2010, 1, 2.	1.3	60
755	CTCF terminal segments are unstructured. Protein Science, 2010, 19, 1110-1116.	3.1	19
756	Global levels of histone modifications predict prostate cancer recurrence. Prostate, 2010, 70, 61-69.	1.2	194
757	A <i>Runx1</i> Intronic Enhancer Marks Hemogenic Endothelial Cells and Hematopoietic Stem Cells Â. Stem Cells, 2010, 28, 1869-1881.	1.4	83
758	Multiplex parallel pairâ€endâ€ditag sequencing approaches in system biology. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2010, 2, 224-234.	6.6	4

#	Article	IF	CITATIONS
759	DNA methylation and gene expression. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2010, 2, 362-371.	6.6	138
760	Genomeâ€wide maps of transcription regulatory elements. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2010, 2, 422-437.	6.6	22
761	Chromatin remodeling in the aging genome of Drosophila. Aging Cell, 2010, 9, 971-978.	3.0	165
762	Epigenetic control of plant immunity. Molecular Plant Pathology, 2010, 11, 563-576.	2.0	167
763	The role of DNA methylation, nucleosome occupancy and histone modifications in paramutation. Plant Journal, 2010, 63, 366-378.	2.8	54
764	Molecular basis of histone H3K36me3 recognition by the PWWP domain of Brpf1. Nature Structural and Molecular Biology, 2010, 17, 617-619.	3.6	192
765	Human RNA polymerase III transcriptomes and relationships to Pol II promoter chromatin and enhancer-binding factors. Nature Structural and Molecular Biology, 2010, 17, 620-628.	3.6	234
766	Pol II and its associated epigenetic marks are present at Pol III–transcribed noncoding RNA genes. Nature Structural and Molecular Biology, 2010, 17, 629-634.	3.6	161
767	Nuclear-localized tiny RNAs are associated with transcription initiation and splice sites in metazoans. Nature Structural and Molecular Biology, 2010, 17, 1030-1034.	3.6	146
768	Corecognition of DNA and a methylated histone tail by the MSL3 chromodomain. Nature Structural and Molecular Biology, 2010, 17, 1027-1029.	3.6	90
769	Reciprocal intronic and exonic histone modification regions in humans. Nature Structural and Molecular Biology, 2010, 17, 1495-1499.	3.6	111
770	H2A.Z nucleosomes enriched over active genes are homotypic. Nature Structural and Molecular Biology, 2010, 17, 1500-1507.	3.6	109
771	Epigenetic regulation of the human p53 gene promoter by the CTCF transcription factor in transformed cell lines. Oncogene, 2010, 29, 2217-2227.	2.6	95
772	Coordination of PAD4 and HDAC2 in the regulation of p53-target gene expression. Oncogene, 2010, 29, 3153-3162.	2.6	117
773	Carcinoma in situ testis displays permissive chromatin modifications similar to immature foetal germ cells. British Journal of Cancer, 2010, 103, 1269-1276.	2.9	78
774	Dual-specificity histone demethylase KIAA1718 (KDM7A) regulates neural differentiation through FGF4. Cell Research, 2010, 20, 154-165.	5.7	106
775	Dynamic regulation of alternative splicing and chromatin structure in Drosophila gonads revealed by RNA-seq. Cell Research, 2010, 20, 763-783.	5.7	107
776	Coordinated regulation of active and repressive histone methylations by a dual-specificity histone demethylase ceKDM7A from Caenorhabditis elegans. Cell Research, 2010, 20, 899-907.	5.7	29

#	Article	IF	CITATIONS
777	UTX mediates demethylation of H3K27me3 at muscle-specific genes during myogenesis. EMBO Journal, 2010, 29, 1401-1411.	3.5	191
778	High-resolution profiling of γH2AX around DNA double strand breaks in the mammalian genome. EMBO Journal, 2010, 29, 1446-1457.	3.5	442
779	JmjC enzyme KDM2A is a regulator of rRNA transcription in response to starvation. EMBO Journal, 2010, 29, 1510-1522.	3.5	98
780	Chromatin density and splicing destiny: on the cross-talk between chromatin structure and splicing. EMBO Journal, 2010, 29, 1629-1636.	3.5	139
781	Essential role of p18Hamlet/SRCAP-mediated histone H2A.Z chromatin incorporation in muscle differentiation. EMBO Journal, 2010, 29, 2014-2025.	3.5	72
782	Regulation of major histocompatibility complex class II gene expression, genetic variation and disease. Genes and Immunity, 2010, 11, 99-112.	2.2	122
783	Epigenetic regulatory mechanisms in vertebrate eye development and disease. Heredity, 2010, 105, 135-151.	1.2	74
784	Epigenetic regulation of development by histone lysine methylation. Heredity, 2010, 105, 24-37.	1.2	80
785	CHD7 cooperates with PBAF to control multipotent neural crest formation. Nature, 2010, 463, 958-962.	13.7	527
786	Chromatin signature of embryonic pluripotency is established during genome activation. Nature, 2010, 464, 922-926.	13.7	340
787	CpG islands influence chromatin structure via the CpG-binding protein Cfp1. Nature, 2010, 464, 1082-1086.	13.7	577
788	Widespread transcription at neuronal activity-regulated enhancers. Nature, 2010, 465, 182-187.	13.7	2,120
789	Brain function and chromatin plasticity. Nature, 2010, 465, 728-735.	13.7	240
790	Histone H4K20/H3K9 demethylase PHF8 regulates zebrafish brain and craniofacial development. Nature, 2010, 466, 503-507.	13.7	263
791	Discovery and characterization of chromatin states for systematic annotation of the human genome. Nature Biotechnology, 2010, 28, 817-825.	9.4	947
792	Linking cell signaling and the epigenetic machinery. Nature Biotechnology, 2010, 28, 1033-1038.	9.4	84
793	Tackling the epigenome: challenges and opportunities for collaboration. Nature Biotechnology, 2010, 28, 1039-1044.	9.4	82
794	The NIH Roadmap Epigenomics Mapping Consortium. Nature Biotechnology, 2010, 28, 1045-1048.	9.4	1,705

	CHAHON	KLPORT	
#	Article	IF	CITATIONS
795	Putting epigenome comparison into practice. Nature Biotechnology, 2010, 28, 1053-1056.	9.4	7
796	Consolidation of the cancer genome into domains of repressive chromatin by long-range epigenetic silencing (LRES) reduces transcriptional plasticity. Nature Cell Biology, 2010, 12, 235-246.	4.6	178
797	The histone H4 Lys 20 methyltransferase PR-Set7 regulates replication origins in mammalian cells. Nature Cell Biology, 2010, 12, 1086-1093.	4.6	254
798	Small-molecule-mediated G-quadruplex isolation from human cells. Nature Chemistry, 2010, 2, 1095-1098.	6.6	166
799	Transcriptional regulation by small RNAs at sequences downstream from 3′ gene termini. Nature Chemical Biology, 2010, 6, 621-629.	3.9	103
800	Nucleosome dynamics define transcriptional enhancers. Nature Genetics, 2010, 42, 343-347.	9.4	426
801	Deregulation of H3K27 methylation in cancer. Nature Genetics, 2010, 42, 100-101.	9.4	97
802	Epigenetic marks identify functional elements. Nature Genetics, 2010, 42, 282-284.	9.4	3
803	Protective hemoglobinopathies and Plasmodium falciparum transmission. Nature Genetics, 2010, 42, 284-285.	9.4	5
804	A global network of transcription factors, involving E2A, EBF1 and Foxo1, that orchestrates B cell fate. Nature Immunology, 2010, 11, 635-643.	7.0	475
805	Effector T cell plasticity: flexibility in the face of changing circumstances. Nature Immunology, 2010, 11, 674-680.	7.0	430
806	The Jmjd3-Irf4 axis regulates M2 macrophage polarization and host responses against helminth infection. Nature Immunology, 2010, 11, 936-944.	7.0	996
807	Chromatin profiling by directly sequencing small quantities of immunoprecipitated DNA. Nature Methods, 2010, 7, 47-49.	9.0	112
808	Covalent histone modifications — miswritten, misinterpreted and mis-erased in human cancers. Nature Reviews Cancer, 2010, 10, 457-469.	12.8	982
809	Licensed to elongate: a molecular mechanism for MLL-based leukaemogenesis. Nature Reviews Cancer, 2010, 10, 721-728.	12.8	151
810	Principles and challenges of genome-wide DNA methylation analysis. Nature Reviews Genetics, 2010, 11, 191-203.	7.7	1,432
811	Deconstructing repression: evolving models of co-repressor action. Nature Reviews Genetics, 2010, 11, 109-123.	7.7	466
812	Repeat expansion disease: progress and puzzles in disease pathogenesis. Nature Reviews Genetics, 2010, 11, 247-258.	7.7	425

# 813	ARTICLE Chromatin structure and the inheritance of epigenetic information. Nature Reviews Genetics, 2010, 11, 285-296.	IF 7.7	Citations 642
814	Next-generation genomics: an integrative approach. Nature Reviews Genetics, 2010, 11, 476-486.	7.7	554
815	Annotating non-coding regions of the genome. Nature Reviews Genetics, 2010, 11, 559-571.	7.7	398
816	Epigenetic regulation of the immune system in health and disease. Tissue Antigens, 2010, 76, 431-439.	1.0	54
818	Chromatin Remodeling. , 2010, , 359-375.		1
819	Orphan CpG Islands Identify Numerous Conserved Promoters in the Mammalian Genome. PLoS Genetics, 2010, 6, e1001134.	1.5	445
820	High Nucleosome Occupancy Is Encoded at Human Regulatory Sequences. PLoS ONE, 2010, 5, e9129.	1.1	163
821	Evaluation of Algorithm Performance in ChIP-Seq Peak Detection. PLoS ONE, 2010, 5, e11471.	1.1	244
822	Signal Transducers and Activators of Transcription-1 (STAT1) Regulates microRNA Transcription in Interferon Î ³ -Stimulated HeLa Cells. PLoS ONE, 2010, 5, e11794.	1.1	61
823	Complex Exon-Intron Marking by Histone Modifications Is Not Determined Solely by Nucleosome Distribution. PLoS ONE, 2010, 5, e12339.	1.1	64
824	Analysis of Jmjd6 Cellular Localization and Testing for Its Involvement in Histone Demethylation. PLoS ONE, 2010, 5, e13769.	1.1	67
825	The Structural Complexity of the Human BORIS Gene in Gametogenesis and Cancer. PLoS ONE, 2010, 5, e13872.	1.1	57
826	Comparative Analyses of SUV420H1 Isoforms and SUV420H2 Reveal Differences in Their Cellular Localization and Effects on Myogenic Differentiation. PLoS ONE, 2010, 5, e14447.	1.1	31
827	ZNF274 Recruits the Histone Methyltransferase SETDB1 to the 3′ Ends of ZNF Genes. PLoS ONE, 2010, 5, e15082.	1.1	147
828	Tiling Histone H3 Lysine 4 and 27 Methylation in Zebrafish Using High-Density Microarrays. PLoS ONE, 2010, 5, e15651.	1.1	27
829	Embryo and Endosperm Inherit Distinct Chromatin and Transcriptional States from the Female Gametes in <i>Arabidopsis</i> Â Â. Plant Cell, 2010, 22, 307-320.	3.1	160
830	The three-dimensional architecture of Hox cluster silencing. Nucleic Acids Research, 2010, 38, 7472-7484.	6.5	126
831	A Gibbs sampling strategy applied to the mapping of ambiguous short-sequence tags. Bioinformatics, 2010, 26, 2501-2508.	1.8	37

#	Article	IF	CITATIONS
832	CTCF Controls Expression and Chromatin Architecture of the Human Major Histocompatibility Complex Class II Locus. Molecular and Cellular Biology, 2010, 30, 4211-4223.	1.1	73
833	Coordinated activities of wild-type plus mutant EZH2 drive tumor-associated hypertrimethylation of lysine 27 on histone H3 (H3K27) in human B-cell lymphomas. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 20980-20985.	3.3	608
834	A SUMO-regulated activation function controls synergy of c-Myb through a repressor–activator switch leading to differential p300 recruitment. Nucleic Acids Research, 2010, 38, 4970-4984.	6.5	40
835	ICI 182,780 induces P-cadherin overexpression in breast cancer cells through chromatin remodelling at the promoter level: a role for C/EBPA in CDH3 gene activation. Human Molecular Genetics, 2010, 19, 2554-2566.	1.4	18
836	A link between H3K27me3 mark and exon length in the gene promoters of pluripotent and differentiated cells. Bioinformatics, 2010, 26, 855-859.	1.8	3
837	Dynamic and Selective Nucleosome Repositioning during Endotoxin Tolerance. Journal of Biological Chemistry, 2010, 285, 1259-1271.	1.6	69
838	Modern approaches for investigating epigenetic signaling pathways. Journal of Applied Physiology, 2010, 109, 927-933.	1.2	28
839	Genome-wide assessment of differential roles for p300 and CBP in transcription regulation. Nucleic Acids Research, 2010, 38, 5396-5408.	6.5	133
840	Histone Variant H2A.Z Regulates Centromere Silencing and Chromosome Segregation in Fission Yeast. Journal of Biological Chemistry, 2010, 285, 1909-1918.	1.6	50
841	Genome-wide analysis of histone modifications in human pancreatic islets. Genome Research, 2010, 20, 428-433.	2.4	106
842	IGFBP7 is a p53-responsive gene specifically silenced in colorectal cancer with CpG island methylator phenotype. Carcinogenesis, 2010, 31, 342-349.	1.3	90
843	CpG_MI: a novel approach for identifying functional CpG islands in mammalian genomes. Nucleic Acids Research, 2010, 38, e6-e6.	6.5	40
844	Transcription Factor NF-Y Induces Apoptosis in Cells Expressing Wild-Type p53 through E2F1 Upregulation and p53 Activation. Cancer Research, 2010, 70, 9711-9720.	0.4	36
845	<i>Drosophila</i> RB Proteins Repress Differentiation-Specific Genes via Two Different Mechanisms. Molecular and Cellular Biology, 2010, 30, 2563-2577.	1.1	16
846	Changes in H2A.Z occupancy and DNA methylation during B-cell lymphomagenesis. Genome Research, 2010, 20, 1383-1390.	2.4	112
847	Genome-Wide Distribution of MacroH2A1 Histone Variants in Mouse Liver Chromatin. Molecular and Cellular Biology, 2010, 30, 5473-5483.	1.1	60
848	Computational analysis of genome-wide DNA methylation during the differentiation of human embryonic stem cells along the endodermal lineage. Genome Research, 2010, 20, 1441-1450.	2.4	155
849	DNA methylation prevents CTCF-mediated silencing of the oncogene <i>BCL6</i> in B cell lymphomas. Journal of Experimental Medicine, 2010, 207, 1939-1950.	4.2	124

#	Article	IF	CITATIONS
850	Cell-Type-Specific Activation and Repression of PU.1 by a Complex of Discrete, Functionally Specialized <i>cis</i> -Regulatory Elements. Molecular and Cellular Biology, 2010, 30, 4922-4939.	1.1	48
851	A cis-regulatory site downregulates PTHLH in translocation t(8;12)(q13;p11.2) and leads to Brachydactyly Type E. Human Molecular Genetics, 2010, 19, 848-860.	1.4	67
852	Nuclear Role of WASp in the Pathogenesis of Dysregulated T _H 1 Immunity in Human Wiskott-Aldrich Syndrome. Science Translational Medicine, 2010, 2, 37ra44.	5.8	109
853	Ring1B and Suv39h1 delineate distinct chromatin states at bivalent genes during early mouse lineage commitment. Development (Cambridge), 2010, 137, 2483-2492.	1.2	102
854	Genome-Wide Profiling of the Core Clock Protein BMAL1 Targets Reveals a Strict Relationship with Metabolism. Molecular and Cellular Biology, 2010, 30, 5636-5648.	1.1	134
855	ZOOM Lite: next-generation sequencing data mapping and visualization software. Nucleic Acids Research, 2010, 38, W743-W748.	6.5	17
856	The Dnmt3a PWWP Domain Reads Histone 3 Lysine 36 Trimethylation and Guides DNA Methylation. Journal of Biological Chemistry, 2010, 285, 26114-26120.	1.6	445
857	Identification of a Promoter for the Human C1q-Tumor Necrosis Factor–Related Protein-5 Gene Associated with Late-Onset Retinal Degeneration. , 2010, 51, 5499.		13
858	Transcription and post-transcriptional regulation of spermatogenesis. Philosophical Transactions of the Royal Society B: Biological Sciences, 2010, 365, 1637-1651.	1.8	128
859	Methodological framework for functional characterization of plant microRNAs. Journal of Experimental Botany, 2010, 61, 2271-2280.	2.4	9
860	Transcriptional Attenuation in Colon Carcinoma Cells in Response to Butyrate. Cancer Prevention Research, 2010, 3, 1292-1302.	0.7	23
861	PHF8 Targets Histone Methylation and RNA Polymerase II To Activate Transcription. Molecular and Cellular Biology, 2010, 30, 3286-3298.	1.1	98
862	Defining the budding yeast chromatinâ€associated interactome. Molecular Systems Biology, 2010, 6, 448.	3.2	58
863	Mediation of CTCF transcriptional insulation by DEAD-box RNA-binding protein p68 and steroid receptor RNA activator SRA. Genes and Development, 2010, 24, 2543-2555.	2.7	231
864	Derepression of Polycomb targets during pancreatic organogenesis allows insulin-producing beta-cells to adopt a neural gene activity program. Genome Research, 2010, 20, 722-732.	2.4	146
865	The Evolution of Epitype. Plant Cell, 2010, 22, 1658-1666.	3.1	12
866	Cell type specificity of chromatin organization mediated by CTCF and cohesin. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 3651-3656.	3.3	244
867	<i>BCL6</i> promoter interacts with far upstream sequences with greatly enhanced activating histone modifications in germinal center B cells. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 11930-11935.	3.3	34

#	Article	IF	CITATIONS
868	Histone3 lysine4 trimethylation regulated by the facilitates chromatin transcription complex is critical for DNA cleavage in class switch recombination. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 22190-22195.	3.3	100
869	In Vivo Residue-specific Histone Methylation Dynamics. Journal of Biological Chemistry, 2010, 285, 3341-3350.	1.6	227
870	NuA4-dependent Acetylation of Nucleosomal Histones H4 and H2A Directly Stimulates Incorporation of H2A.Z by the SWR1 Complex. Journal of Biological Chemistry, 2010, 285, 15966-15977.	1.6	140
871	On the detection and refinement of transcription factor binding sites using ChIP-Seq data. Nucleic Acids Research, 2010, 38, 2154-2167.	6.5	91
872	De novo motif identification improves the accuracy of predicting transcription factor binding sites in ChIP-Seq data analysis. Nucleic Acids Research, 2010, 38, e126-e126.	6.5	62
873	ChlPing the cistrome of PXR in mouse liver. Nucleic Acids Research, 2010, 38, 7943-7963.	6.5	59
874	HRTBLDb: an informative data resource for hormone receptors target binding loci. Nucleic Acids Research, 2010, 38, D676-D681.	6.5	11
875	Epigenetic drugs for cancer treatment and prevention: mechanisms of action. Biomolecular Concepts, 2010, 1, 239-251.	1.0	15
876	Epigenetic Regulation of Pericentromeric Heterochromatin during Mammalian Meiosis. Cytogenetic and Genome Research, 2010, 129, 280-289.	0.6	15
877	Epigenetic propagation of CD4 expression is established by the <i>Cd4</i> proximal enhancer in helper T cells. Genes and Development, 2010, 24, 659-669.	2.7	58
878	Integrating multiple evidence sources to predict transcription factor binding in the human genome. Genome Research, 2010, 20, 526-536.	2.4	85
879	Polycomb Repressive Complex 2 and Trithorax modulate <i>Drosophila</i> longevity and stress resistance. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 169-174.	3.3	174
880	Deciphering the cancer imprintome. Briefings in Functional Genomics, 2010, 9, 329-339.	1.3	38
881	Comprehensive Analysis of the Palindromic Motif TCTCGCGAGA: A Regulatory Element of the HNRNPK Promoter. DNA Research, 2010, 17, 245-260.	1.5	39
882	Genome-wide identification of new imprinted genes. Briefings in Functional Genomics, 2010, 9, 304-314.	1.3	48
883	Cutting Edge: Intrinsic Programming of Thymic γÎT Cells for Specific Peripheral Tissue Localization. Journal of Immunology, 2010, 185, 7156-7160.	0.4	40
884	Histone H4 lysine 20 mono- and tri-methylation define distinct biologically processes in SV40 minichromosomes. Cell Cycle, 2010, 9, 1320-1332.	1.3	23
885	Epigenetics of the vascular endothelium. Journal of Applied Physiology, 2010, 109, 916-926.	1.2	71

#	Article	IF	CITATIONS
886	Chromatin Environment of Histone Variant H3.3 Revealed by Quantitative Imaging and Genome-scale Chromatin and DNA Immunoprecipitation. Molecular Biology of the Cell, 2010, 21, 1872-1884.	0.9	42
888	Next-generation Sequencing und hochparallele Genexpressionsanalyse in der klinischen Diagnostik / Next-generation sequencing and massively parallel analysis of gene expression: uses in clinical diagnostics. Laboratoriums Medizin, 2010, 34, 349-356.	0.1	1
889	Chromatin regulators: weaving epigenetic nets. Biomolecular Concepts, 2010, 1, 225-238.	1.0	2
890	H3K27me3 regulates BMP activity in developing spinal cord. Development (Cambridge), 2010, 137, 2915-2925.	1.2	84
891	The scaRNA2 is produced by an independent transcription unit and its processing is directed by the encoding region. Nucleic Acids Research, 2010, 38, 370-381.	6.5	22
892	Heterochromatin dysregulation in human diseases. Journal of Applied Physiology, 2010, 109, 232-242.	1.2	31
893	Cell-Specific Determinants of Peroxisome Proliferator-Activated Receptor Î ³ Function in Adipocytes and Macrophages. Molecular and Cellular Biology, 2010, 30, 2078-2089.	1.1	189
894	Histone modifications and chromatin organization in prostate cancer. Epigenomics, 2010, 2, 551-560.	1.0	71
895	Integrative epigenomic and genomic analysis of malignant pheochromocytoma. Experimental and Molecular Medicine, 2010, 42, 484.	3.2	32
896	Identification and characterization of putative methylation targets in theMAOAlocus using bioinformatic approaches. Epigenetics, 2010, 5, 325-342.	1.3	28
897	Hypoxic Repression of Endothelial Nitric-oxide Synthase Transcription Is Coupled with Eviction of Promoter Histones. Journal of Biological Chemistry, 2010, 285, 810-826.	1.6	134
898	ChIP-seq and Functional Analysis of the SOX2 Gene in Colorectal Cancers. OMICS A Journal of Integrative Biology, 2010, 14, 369-384.	1.0	61
899	Dimerization of a viral SET protein endows its function. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 18433-18438.	3.3	24
900	X chromosome-wide analyses of genomic DNA methylation states and gene expression in male and female neutrophils. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 3704-3709.	3.3	44
901	Genetic and Epigenetic Regulation and Expression Signatures of Glutathione S-Transferases in Developing Mouse Liver. Toxicological Sciences, 2010, 116, 32-43.	1.4	36
902	A signal–noise model for significance analysis of ChIP-seq with negative control. Bioinformatics, 2010, 26, 1199-1204.	1.8	131
903	Regulated post-transcriptional RNA cleavage diversifies the eukaryotic transcriptome. Genome Research, 2010, 20, 1639-1650.	2.4	76
904	Activating and inhibitory functions for the histone lysine methyltransferase G9a in T helper cell differentiation and function. Journal of Experimental Medicine, 2010, 207, 915-922.	4.2	113

#	Article	IF	CITATIONS
905	Chromatin Remodeling in Mammary Gland Differentiation and Breast Tumorigenesis. Cold Spring Harbor Perspectives in Biology, 2010, 2, a004515-a004515.	2.3	33
906	Lens epithelium-derived growth factor fusion proteins redirect HIV-1 DNA integration. Proceedings of the United States of America, 2010, 107, 3135-3140.	3.3	129
908	Epigenomics and ovarian carcinoma. Biomarkers in Medicine, 2010, 4, 543-570.	0.6	38
909	Epigenetic control of embryonic stem cell fate. Journal of Experimental Medicine, 2010, 207, 2287-2295.	4.2	125
910	ASXL1 Represses Retinoic Acid Receptor-mediated Transcription through Associating with HP1 and LSD1. Journal of Biological Chemistry, 2010, 285, 18-29.	1.6	83
911	CCCTC-binding Factor Acts Upstream of FOXA1 and Demarcates the Genomic Response to Estrogen*. Journal of Biological Chemistry, 2010, 285, 28604-28613.	1.6	35
912	Epigenetic regulation of WNT signaling in chronic lymphocytic leukemia. Epigenomics, 2010, 2, 53-70.	1.0	22
913	The Number of Vitamin D Receptor Binding Sites Defines the Different Vitamin D Responsiveness of the CYP24 Gene in Malignant and Normal Mammary Cells. Journal of Biological Chemistry, 2010, 285, 24174-24183.	1.6	37
914	Epithelial Cell Adhesion Molecule Regulation Is Associated with the Maintenance of the Undifferentiated Phenotype of Human Embryonic Stem Cells. Journal of Biological Chemistry, 2010, 285, 8719-8732.	1.6	114
915	Transforming Growth Factor β Promotes Complexes between Smad Proteins and the CCCTC-binding Factor on the H19 Imprinting Control Region Chromatin. Journal of Biological Chemistry, 2010, 285, 19727-19737.	1.6	30
916	Stefin B Interacts with Histones and Cathepsin L in the Nucleus. Journal of Biological Chemistry, 2010, 285, 10078-10086.	1.6	89
917	Kinetics of Re-establishing H3K79 Methylation Marks in Global Human Chromatin*. Journal of Biological Chemistry, 2010, 285, 32778-32786.	1.6	56
918	Structural and Biochemical Studies on the Chromo-barrel Domain of Male Specific Lethal 3 (MSL3) Reveal a Binding Preference for Mono- or Dimethyllysine 20 on Histone H4. Journal of Biological Chemistry, 2010, 285, 40879-40890.	1.6	41
919	p53 binds preferentially to genomic regions with high DNA-encoded nucleosome occupancy. Genome Research, 2010, 20, 1361-1368.	2.4	86
920	Allele-Specific H3K79 Di- versus Trimethylation Distinguishes Opposite Parental Alleles at Imprinted Regions. Molecular and Cellular Biology, 2010, 30, 2693-2707.	1.1	25
921	8q24 prostate, breast, and colon cancer risk loci show tissue-specific long-range interaction with <i>MYC</i> . Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 9742-9746.	3.3	353
922	Microarray-based Transcriptional and Epigenetic Profiling of Matrix Metalloproteinases, Collagens, and Related Genes in Cancer. Journal of Biological Chemistry, 2010, 285, 19647-19659.	1.6	47
923	The Human IL-3/Granulocyte-Macrophage Colony-Stimulating Factor Locus Is Epigenetically Silent in Immature Thymocytes and Is Progressively Activated during T Cell Development. Journal of Immunology, 2010, 184, 3043-3054.	0.4	28

#	Article	IF	CITATIONS
924	Pathology tissue–chromatin immunoprecipitation, coupled with high-throughput sequencing, allows the epigenetic profiling of patient samples. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 21535-21540.	3.3	63
925	Genomics of medulloblastoma: from Giemsa-banding to next-generation sequencing in 20 years. Neurosurgical Focus, 2010, 28, E6.	1.0	48
926	HHMD: the human histone modification database. Nucleic Acids Research, 2010, 38, D149-D154.	6.5	79
927	Epigenetic Regulatory Mechanisms Associated with Infertility. Obstetrics and Gynecology International, 2010, 2010, 1-7.	0.5	7
928	The GNUMAP algorithm: unbiased probabilistic mapping of oligonucleotides from next-generation sequencing. Bioinformatics, 2010, 26, 38-45.	1.8	122
929	PU.1 Binds to a Distal Regulatory Element That Is Necessary for B Cell-Specific Expression of CIITA. Journal of Immunology, 2010, 184, 5018-5028.	0.4	28
930	Learning a Weighted Sequence Model of the Nucleosome Core and Linker Yields More Accurate Predictions in Saccharomyces cerevisiae and Homo sapiens. PLoS Computational Biology, 2010, 6, e1000834.	1.5	20
931	Epigenetic Analysis of KSHV Latent and Lytic Genomes. PLoS Pathogens, 2010, 6, e1001013.	2.1	229
932	Arabidopsis thaliana Chromosome 4 Replicates in Two Phases That Correlate with Chromatin State. PLoS Genetics, 2010, 6, e1000982.	1.5	65
933	Natural Single-Nucleosome Epi-Polymorphisms in Yeast. PLoS Genetics, 2010, 6, e1000913.	1.5	14
934	Histone Deacetylases Play a Major Role in the Transcriptional Regulation of the Plasmodium falciparum Life Cycle. PLoS Pathogens, 2010, 6, e1000737.	2.1	135
935	Initial Genomics of the Human Nucleolus. PLoS Genetics, 2010, 6, e1000889.	1.5	324
936	H2A.Z Demarcates Intergenic Regions of the Plasmodium falciparum Epigenome That Are Dynamically Marked by H3K9ac and H3K4me3. PLoS Pathogens, 2010, 6, e1001223.	2.1	201
937	Characterization of a Novel WDR5-binding Site That Recruits RbBP5 through a Conserved Motif to Enhance Methylation of Histone H3 Lysine 4 by Mixed Lineage Leukemia Protein-1*. Journal of Biological Chemistry, 2010, 285, 32967-32976.	1.6	92
938	A Comprehensive Genetic Analysis of Candidate Genes Regulating Response to Trypanosoma congolense Infection in Mice. PLoS Neglected Tropical Diseases, 2010, 4, e880.	1.3	14
939	Integration Preferences of Wildtype AAV-2 for Consensus Rep-Binding Sites at Numerous Loci in the Human Genome. PLoS Pathogens, 2010, 6, e1000985.	2.1	72
940	Homotypic clusters of transcription factor binding sites are a key component of human promoters and enhancers. Genome Research, 2010, 20, 565-577.	2.4	203
941	Future Directions in Research on the Epigenetics of Aging. , 2010, , 433-446.		0

#	Article	IF	CITATIONS
942	Deciphering the Code for Retroviral Integration Target Site Selection. PLoS Computational Biology, 2010, 6, e1001008.	1.5	41
943	Mutational Analysis of the Poly(ADP-Ribosyl)ation Sites of the Transcription Factor CTCF Provides an Insight into the Mechanism of Its Regulation by Poly(ADP-Ribosyl)ation. Molecular and Cellular Biology, 2010, 30, 1199-1216.	1.1	77
944	Histone demethylase KDM5A is an integral part of the core Notch–RBP-J repressor complex. Genes and Development, 2010, 24, 590-601.	2.7	162
945	Discovering homotypic binding events at high spatial resolution. Bioinformatics, 2010, 26, 3028-3034.	1.8	43
946	Genetic and epigenetic influences on expression of spermine synthase and spermine oxidase in suicide completers. International Journal of Neuropsychopharmacology, 2010, 13, 725-736.	1.0	47
947	Single nucleosome ChIPs identify an extensive switch of acetyl marks on cell cycle promoters. Cell Cycle, 2010, 9, 2149-2159.	1.3	22
948	Random deposition of histone variants: A cellular mistake or a novel regulatory mechanism?. Epigenetics, 2010, 5, 368-372.	1.3	16
949	Crosstalk between histone modifications maintains the developmental pattern of gene expression on a tissue-specific locus. Epigenetics, 2010, 5, 273-281.	1.3	18
950	From chromatin to splicing: RNA-processing as a total artwork. Epigenetics, 2010, 5, 180-184.	1.3	24
951	Disparate chromatin landscapes and kinetics of inactivation impact differential regulation of p53 target genes. Cell Cycle, 2010, 9, 3428-3437.	1.3	18
952	Epigenetic alteration of microRNAs in DNMT3B-mutated patients of ICF syndrome. Epigenetics, 2010, 5, 427-443.	1.3	31
953	Chromosome 8q24-Associated Cancers and MYC. Genes and Cancer, 2010, 1, 555-559.	0.6	100
954	Tip60: Connecting chromatin to DNA damage signaling. Cell Cycle, 2010, 9, 930-936.	1.3	184
955	Reconciling the positive and negative roles of histone H2A.Z in gene transcription. Epigenetics, 2010, 5, 267-272.	1.3	94
956	A simple method for improving the specificity of anti-methyl histone antibodies. Epigenetics, 2010, 5, 392-395.	1.3	7
957	Gene-specific repression of the p53 target gene PUMA via intragenic CTCF–Cohesin binding. Genes and Development, 2010, 24, 1022-1034.	2.7	80
958	Chromatin and sequence features that define the fine and gross structure of genomic methylation patterns. Genome Research, 2010, 20, 972-980.	2.4	160
959	Meiotic silencing in Caenorhabditis elegans. International Review of Cell and Molecular Biology, 2010, 282, 91-134.	1.6	24

ARTICLE IF CITATIONS # Intronic elements in the Na+/I- symporter gene (NIS) interact with retinoic acid receptors and mediate 960 6.5 23 initiation of transcription. Nucleic Acids Research, 2010, 38, 3172-3185. Chromatin Remodeling around Nucleosome-Free Regions Leads to Repression of Noncoding RNA 1.1 Transcription. Molecular and Cellular Biology, 2010, 30, 5110-5122. LEDGF Hybrids Efficiently Retarget Lentiviral Integration Into Heterochromatin. Molecular Therapy, 962 3.7 144 2010, 18, 552-560. Epigenetic control of inducible gene expression in the immune system. Epigenomics, 2010, 2, 775-795. Epigenetic therapy: targeting histones and their modifications in human disease. Future Medicinal 964 1.1 11 Chemistry, 2010, 2, 543-548. Clucocorticoid Receptor Activates Poised FKBP51 Locus through Long-Distance Interactions. 3.7 Molecular Endocrinology, 2010, 24, 511-525. Trimethylation of histone H3 lysine 4 impairs methylation of histone H3 lysine 9. Epigenetics, 2010, 5, 966 1.3 64 767-775. Role of histone methylation and demethylation in adipogenesis and obesity. Organogenesis, 2010, 6, 967 0.4 90 24-32. Locus co-occupancy, nucleosome positioning, and H3K4me1 regulate the functionality of FOXA2-, 968 2.4 109 HNF4A-, and PDX1-bound loci in islets and liver. Genome Research, 2010, 20, 1037-1051. JASPAR 2010: the greatly expanded open-access database of transcription factor binding profiles. 6.5 529 Nucleic Acids Research, 2010, 38, D105-D110. Causal Relationship of Histone Modifications and Gene Expression Indicated by Variable Bayeasian 970 Network Methods. International Conference on Bioinformatics and Biomedical Engineering: 0.0 0 [proceedings] International Conference on Bioinformatics and Biomedical Engineering, 2010, . Switch Regions, Chromatin Accessibility and AID Targeting. Modecular Medicine and Medicinal, 2010, , 971 0.4 12-30. Statistical Issues in the Analysis of ChIP-Seq and RNA-Seq Data. Genes, 2010, 1, 317-334. 972 1.0 17 Next-Generation Sequencing Techniques for Eukaryotic Microorganisms: Sequencing-Based Solutions to Biological Problems. Eukaryotic Cell, 2010, 9, 1300-1310. 3.4 974 Molecular diagnostics in transplantation. Nature Reviews Nephrology, 2010, 6, 614-628. 4.1 80 Histone Modification Therapy of Cancer. Advances in Genetics, 2010, 70, 341-386. Cancer Epigenome. Advances in Genetics, 2010, 70, 247-276. 976 0.8 37 Epigenetics of Schizophrenia. Current Topics in Behavioral Neurosciences, 2010, 4, 611-628. 54

#	Article	IF	CITATIONS
978	Higher Organization and Histone Modification of the Plant Nucleus and Chromosome. Cytogenetic and Genome Research, 2010, 129, 55-63.	0.6	4
980	Chromatin Landscape Dictates HSF Binding to Target DNA Elements. PLoS Genetics, 2010, 6, e1001114.	1.5	194
981	Next Generation DNA Sequencing and the Future of Genomic Medicine. Genes, 2010, 1, 38-69.	1.0	60
982	Computational Analysis of ChIP-seq Data. Methods in Molecular Biology, 2010, 674, 143-159.	0.4	6
983	Arginine/lysine–methyl/methyl switches: biochemical role of histone arginine methylation in transcriptional regulation. Epigenomics, 2010, 2, 119-137.	1.0	53
984	Epigenetic control of the immune system: histone demethylation as a target for drug discovery. Drug Discovery Today: Technologies, 2010, 7, e67-e75.	4.0	8
985	Studying Histone Modifications and Their Genomic Functions by Employing Chromatin Immunoprecipitation and Immunoblotting. Methods in Cell Biology, 2010, 98, 35-56.	0.5	39
986	Genome-wide analysis of host-chromosome binding sites for Epstein-Barr Virus Nuclear Antigen 1 (EBNA1). Virology Journal, 2010, 7, 262.	1.4	74
987	Protocol: fine-tuning of a Chromatin Immunoprecipitation (ChIP) protocol in tomato. Plant Methods, 2010, 6, 11.	1.9	51
988	Targeting DOT1L action and interactions in leukemia: the role of DOT1L in transformation and development. Expert Opinion on Therapeutic Targets, 2010, 14, 405-418.	1.5	42
989	Transcriptional Activity Affects the H3K4me3 Level and Distribution in the Coding Region. Molecular and Cellular Biology, 2010, 30, 2933-2946.	1.1	38
990	Histone Variant H2A.Z Inhibits Transcription in Reconstituted Nucleosomes. Biochemistry, 2010, 49, 4018-4026.	1.2	16
991	Chatting histone modifications in mammals. Briefings in Functional Genomics, 2010, 9, 429-443.	1.3	102
992	The Role of the Transcription Factor CREB in Immune Function. Journal of Immunology, 2010, 185, 6413-6419.	0.4	638
993	Dispersed Chromosomal Stat5b-binding Elements Mediate Growth Hormone-activated Insulin-like Growth Factor-I Gene Transcription. Journal of Biological Chemistry, 2010, 285, 17636-17647.	1.6	54
994	Coordinated postnatal downâ€regulation of multiple growthâ€promoting genes: evidence for a genetic program limiting organ growth. FASEB Journal, 2010, 24, 3083-3092.	0.2	48
995	Chromatin in the Nuclear Landscape. Cold Spring Harbor Symposia on Quantitative Biology, 2010, 75, 11-22.	2.0	24
996	Integrating one-dimensional and three-dimensional maps of genomes. Journal of Cell Science, 2010, 123, 1979-1988.	1.2	63

#	Article	IF	CITATIONS
997	New Insights to Nuclear Receptor Gene Regulation from Analysis of their Response Elements in Target Genes. , 2010, , 419-437.		0
998	Developmental regulation and individual differences of neuronal H3K4me3 epigenomes in the prefrontal cortex. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 8824-8829.	3.3	218
999	Epigenome Mapping in Normal and Disease States. Circulation Research, 2010, 107, 327-339.	2.0	164
1000	A Functional Link between the Histone Demethylase PHF8 and the Transcription Factor ZNF711 in X-Linked Mental Retardation. Molecular Cell, 2010, 38, 165-178.	4.5	186
1001	Short RNAs Are Transcribed from Repressed Polycomb Target Genes and Interact with Polycomb Repressive Complex-2. Molecular Cell, 2010, 38, 675-688.	4.5	338
1002	Simple Combinations of Lineage-Determining Transcription Factors Prime cis-Regulatory Elements Required for Macrophage and B Cell Identities. Molecular Cell, 2010, 38, 576-589.	4.5	10,215
1003	The PARP Side of the Nucleus: Molecular Actions, Physiological Outcomes, and Clinical Targets. Molecular Cell, 2010, 39, 8-24.	4.5	738
1004	Human LSD2/KDM1b/AOF1 Regulates Gene Transcription by Modulating Intragenic H3K4me2 Methylation. Molecular Cell, 2010, 39, 222-233.	4.5	209
1005	PARP-1 Regulates Chromatin Structure and Transcription through a KDM5B-Dependent Pathway. Molecular Cell, 2010, 39, 736-749.	4.5	276
1006	H2A.Z Maintenance during Mitosis Reveals Nucleosome Shifting on Mitotically Silenced Genes. Molecular Cell, 2010, 39, 901-911.	4.5	136
1007	Analysis of Active and Inactive X Chromosome Architecture Reveals the Independent Organization ofÂ30Ânm and Large-Scale Chromatin Structures. Molecular Cell, 2010, 40, 397-409.	4.5	73
1008	Control of embryonic stem cell identity by nucleosome remodeling enzymes. Current Opinion in Genetics and Development, 2010, 20, 500-504.	1.5	16
1009	Oncogenic RAS alters the global and gene-specific histone modification pattern during epithelial–mesenchymal transition in colorectal carcinoma cells. International Journal of Biochemistry and Cell Biology, 2010, 42, 911-920.	1.2	32
1010	The molecular pathology of schizophrenia—Focus on histone and DNA modifications. Brain Research Bulletin, 2010, 83, 103-107.	1.4	37
1011	Aberrant Epigenetic Landscape in Cancer: How Cellular Identity Goes Awry. Developmental Cell, 2010, 19, 698-711.	3.1	529
1012	Differentiation-Specific Histone Modifications Reveal Dynamic Chromatin Interactions and Partners for the Intestinal Transcription Factor CDX2. Developmental Cell, 2010, 19, 713-726.	3.1	192
1013	Functional Analysis of CTCF During Mammalian Limb Development. Developmental Cell, 2010, 19, 819-830.	3.1	136
1014	Chromatin assembly on herpes simplex virus genomes during lytic infection. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2010, 1799, 217-222.	0.9	15

#	Article	IF	CITATIONS
1015	A novel mechanism of epigenetic regulation: Nucleosome-space occupancy. Biochemical and Biophysical Research Communications, 2010, 391, 884-889.	1.0	20
1016	CTCF is a DNA methylation-sensitive positive regulator of the INK/ARF locus. Biochemical and Biophysical Research Communications, 2010, 392, 129-134.	1.0	60
1017	The tumor suppressor Rb and its related Rbl2 genes are regulated by Utx histone demethylase. Biochemical and Biophysical Research Communications, 2010, 399, 238-244.	1.0	34
1018	Distinct Factors Control Histone Variant H3.3 Localization at Specific Genomic Regions. Cell, 2010, 140, 678-691.	13.5	1,069
1019	The In Vivo Pattern of Binding of RAG1 and RAG2 to Antigen Receptor Loci. Cell, 2010, 141, 419-431.	13.5	257
1020	Derivation of Pre-X Inactivation Human Embryonic Stem Cells under Physiological Oxygen Concentrations. Cell, 2010, 141, 872-883.	13.5	367
1021	Long Noncoding RNAs with Enhancer-like Function in Human Cells. Cell, 2010, 143, 46-58.	13.5	1,664
1022	Comparative Epigenomic Analysis of Murine and Human Adipogenesis. Cell, 2010, 143, 156-169.	13.5	460
1023	Global Epigenomic Analysis of Primary Human Pancreatic Islets Provides Insights into Type 2 Diabetes Susceptibility Loci. Cell Metabolism, 2010, 12, 443-455.	7.2	190
1024	Wilms Tumor Chromatin Profiles Highlight Stem Cell Properties and a Renal Developmental Network. Cell Stem Cell, 2010, 6, 591-602.	5.2	80
1025	Distinct Epigenomic Landscapes of Pluripotent and Lineage-Committed Human Cells. Cell Stem Cell, 2010, 6, 479-491.	5.2	747
1026	The Yin and Yang of Polycomb Repression in Regenerating Muscle. Cell Stem Cell, 2010, 7, 422-424.	5.2	1
1027	A New Cohesive Team to Mediate DNA Looping. Cell Stem Cell, 2010, 7, 424-426.	5.2	9
1028	Genome-wide mechanisms of nuclear receptor action. Trends in Endocrinology and Metabolism, 2010, 21, 3-9.	3.1	74
1029	Targeting DNA methylation for epigenetic therapy. Trends in Pharmacological Sciences, 2010, 31, 536-546.	4.0	275
1030	Histone methyltransferases in cancer. Seminars in Cell and Developmental Biology, 2010, 21, 209-220.	2.3	262
1031	Identification and Characterization of Human snoRNA Core Promoters. Genomics, 2010, 96, 50-56.	1.3	18
1032	Mechanisms Underlying Lineage Commitment and Plasticity of Helper CD4 ⁺ T Cells. Science, 2010, 327, 1098-1102.	6.0	1,151

#	Article	IF	Citations
1033	Interplay Between Different Epigenetic Modifications and Mechanisms. Advances in Genetics, 2010, 70, 101-141.	0.8	128
1034	Next-generation sequencing in aging research: Emerging applications, problems, pitfalls and possible solutions. Ageing Research Reviews, 2010, 9, 315-323.	5.0	98
1035	Histone lysine methylation: an epigenetic modification?. Epigenomics, 2010, 2, 151-161.	1.0	21
1036	The INO80 Family of Chromatin-Remodeling Enzymes: Regulators of Histone Variant Dynamics. Cold Spring Harbor Symposia on Quantitative Biology, 2010, 75, 35-42.	2.0	38
1037	Estrogen Receptor α Controls a Gene Network in Luminal-Like Breast Cancer Cells Comprising Multiple Transcription Factors and MicroRNAs. American Journal of Pathology, 2010, 176, 2113-2130.	1.9	151
1038	Mechanisms and functions of p38 MAPK signalling. Biochemical Journal, 2010, 429, 403-417.	1.7	1,342
1039	Evolutionarily conserved replication timing profiles predict long-range chromatin interactions and distinguish closely related cell types. Genome Research, 2010, 20, 761-770.	2.4	526
1040	Histone modification levels are predictive for gene expression. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 2926-2931.	3.3	664
1041	The distribution of repressive histone modifications on silenced FMR1 alleles provides clues to the mechanism of gene silencing in fragile X syndrome. Human Molecular Genetics, 2010, 19, 4634-4642.	1.4	76
1042	Human aging-associated DNA hypermethylation occurs preferentially at bivalent chromatin domains. Genome Research, 2010, 20, 434-439.	2.4	646
1043	A unique H3K4me2 profile marks tissue-specific gene regulation. Genome Research, 2010, 20, 1493-1502.	2.4	117
1044	An Omics Perspective on Cancer Research. , 2010, , .		20
1045	Bioinformatics approaches for genomics and post genomics applications of next-generation sequencing. Briefings in Bioinformatics, 2010, 11, 181-197.	3.2	141
1046	Epigenetics of Aging. , 2010, , .		10
1047	Epigenetics in cancer. Carcinogenesis, 2010, 31, 27-36.	1.3	2,119
1048	An Integrated System for DNA Sequencing by Synthesis Using Novel Nucleotide Analogues. Accounts of Chemical Research, 2010, 43, 551-563.	7.6	60
1050	Genomic Analyses of Hormone Signaling and Gene Regulation. Annual Review of Physiology, 2010, 72, 191-218.	5.6	78
1051	Genome Stability and Human Diseases. Sub-Cellular Biochemistry, 2010, , .	1.0	5

#	Article	IF	CITATIONS
1052	Grasping trimethylation of histone H3 at lysine 4. Epigenomics, 2010, 2, 395-406.	1.0	66
1055	The Genomic HyperBrowser: inferential genomics at the sequence level. Genome Biology, 2010, 11, R121.	13.9	78
1056	Caenorhabditis elegans chromosome arms are anchored to the nuclear membrane via discontinuous association with LEM-2. Genome Biology, 2010, 11, R120.	13.9	169
1057	ArchAlign: Coordinate-free chromatin alignment reveals novel architectures. Genome Biology, 2010, 11, R126.	13.9	18
1058	Estimating enrichment of repetitive elements from high-throughput sequence data. Genome Biology, 2010, 11, R69.	13.9	94
1059	Nucleosome rotational setting is associated with transcriptional regulation in promoters of tissue-specific human genes. Genome Biology, 2010, 11, R51.	13.9	14
1060	Monovalent and unpoised status of most genes in undifferentiated cell-enriched Drosophila testis. Genome Biology, 2010, 11, R42.	13.9	65
1061	Evidence-ranked motif identification. Genome Biology, 2010, 11, R19.	13.9	77
1062	Genome-wide prediction of transcription factor binding sites using an integrated model. Genome Biology, 2010, 11, R7.	13.9	100
1063	Behavioral Neurobiology of Schizophrenia and Its Treatment. Current Topics in Behavioral Neurosciences, 2010, , .	0.8	8
1064	Chromatin Regulatory Mechanisms in Pluripotency. Annual Review of Cell and Developmental Biology, 2010, 26, 503-532.	4.0	161
1065	Global Epigenetic and Transcriptional Trends among Two Rice Subspecies and Their Reciprocal Hybrids. Plant Cell, 2010, 22, 17-33.	3.1	514
1066	Integrative genome-wide approaches in embryonic stem cell research. Integrative Biology (United) Tj ETQq0 0 0 i	rgBT /Over 0.6	lock 10 Tf 50
1067	Improved prediction of transcription binding sites from chromatin modification data. , 2010, , .		0
1068	The Epigenetics of Suicide: Explaining the Biological Effects of Early Life Environmental Adversity. Archives of Suicide Research, 2010, 14, 291-310.	1.2	56
1069	DNA Architecture, Deformability, and Nucleosome Positioning. Journal of Biomolecular Structure and Dynamics, 2010, 27, 725-739.	2.0	33
1070	Gammaretroviral Integration into Nucleosomal Target DNA <i>In Vivo</i> . Journal of Virology, 2011, 85, 7393-7401.	1.5	64
1071	Reconstruction of Histone Modification Network from Next-generation Sequencing Data. , 2011, , .		3

#	Article	IF	CITATIONS
1072	Sequencing nucleic acids: from chemistry to medicine. Chemical Communications, 2011, 47, 7281.	2.2	26
1073	Tackling the challenging motif problem through hybrid particle swarm optimized alignment clustering. , 2011, , .		1
1074	Transcriptional regulation of haematopoietic transcription factors. Stem Cell Research and Therapy, 2011, 2, 6.	2.4	36
1075	Epigenetic regulation of satellite cell activation during muscle regeneration. Stem Cell Research and Therapy, 2011, 2, 18.	2.4	55
1076	Protein Arginine Methyltransferase Prmt5-Mep50 Methylates Histones H2A and H4 and the Histone Chaperone Nucleoplasmin in Xenopus laevis Eggs. Journal of Biological Chemistry, 2011, 286, 42221-42231.	1.6	49
1077	Chromatin signature analysis and prediction of genome-wide novel promoters using finite mixture model. , 2011, , .		1
1078	Chromatin structure of pluripotent stem cells and induced pluripotent stem cells. Briefings in Functional Genomics, 2011, 10, 37-49.	1.3	28
1079	Epigenetic-based companion diagnostics. Personalized Medicine, 2011, 8, 623-631.	0.8	1
1081	Epigenetic regulation of cardiovascular differentiation. Cardiovascular Research, 2011, 90, 404-412.	1.8	60
1082	<i>Drosophila</i> Set1 is the major histone H3 lysine 4 trimethyltransferase with role in transcription. EMBO Journal, 2011, 30, 2817-2828.	3.5	168
1083	Recognition of enhancer element–specific histone methylation by TIP60 in transcriptional activation. Nature Structural and Molecular Biology, 2011, 18, 1358-1365.	3.6	124
1084	Genome-wide chromatin occupancy analysis reveals a role for ASH2 in transcriptional pausing. Nucleic Acids Research, 2011, 39, 4628-4639.	6.5	34
1085	Structure and Mechanisms of Lysine Methylation Recognition by the Chromodomain in Gene Transcription. Biochemistry, 2011, 50, 1966-1980.	1.2	101
1086	Epigenetic mechanisms in diabetic vascular complications. Cardiovascular Research, 2011, 90, 421-429.	1.8	178
1087	Proteomic Investigation of Epigenetics in Neuropsychiatric Disorders: A Missing Link between Genetics and Behavior?. Journal of Proteome Research, 2011, 10, 58-65.	1.8	21
1088	Nucleosome Positioning in Saccharomyces cerevisiae. Microbiology and Molecular Biology Reviews, 2011, 75, 301-320.	2.9	108
1089	Alterations in chromatin are associated with increases in collagen III expression in aging nephropathy. American Journal of Physiology - Renal Physiology, 2011, 300, F531-F539.	1.3	15
1090	Epigenetic signatures distinguish multiple classes of enhancers with distinct cellular functions. Genome Research, 2011, 21, 1273-1283.	2.4	487

#	Article	IF	CITATIONS
1091	Broad chromosomal domains of histone modification patterns in <i>C. elegans</i> . Genome Research, 2011, 21, 227-236.	2.4	256
1092	Regulation of nucleosome landscape and transcription factor targeting at tissue-specific enhancers by BRG1. Genome Research, 2011, 21, 1650-1658.	2.4	160
1093	Epigenetic Studies of Psychosis: Current Findings, Methodological Approaches, and Implications for Postmortem Research. Biological Psychiatry, 2011, 69, 146-156.	0.7	104
1094	Transposon-mediated rewiring of gene regulatory networks contributed to the evolution of pregnancy in mammals. Nature Genetics, 2011, 43, 1154-1159.	9.4	400
1095	Interactions of Transcription Factors with Chromatin. Sub-Cellular Biochemistry, 2011, 52, 223-259.	1.0	4
1097	Chromatin dynamics and the repair of DNA double strand breaks. Cell Cycle, 2011, 10, 261-267.	1.3	144
1098	The Epigenome and Plant Development. Annual Review of Plant Biology, 2011, 62, 411-435.	8.6	172
1099	Polycomb Mechanisms and Epigenetic Control of Gene Activity. , 2011, , 107-121.		0
1100	Using MACS to Identify Peaks from ChIP‣eq Data. Current Protocols in Bioinformatics, 2011, 34, Unit 2.14.	25.8	203
1101	DNA methylation directly silences genes with non-CpG island promoters and establishes a nucleosome occupied promoter. Human Molecular Genetics, 2011, 20, 4299-4310.	1.4	172
1102	Biochemical Characterization of Human SET and MYND Domain-Containing Protein 2 Methyltransferase. Biochemistry, 2011, 50, 6488-6497.	1.2	43
1103	ChIP-Seq: technical considerations for obtaining high-quality data. Nature Immunology, 2011, 12, 918-922.	7.0	199
1104	Joint Binding of OTX2 and MYC in Promotor Regions Is Associated with High Gene Expression in Medulloblastoma. PLoS ONE, 2011, 6, e26058.	1.1	24
1105	Using CisGenome to Analyze ChIPâ€chip and ChIPâ€seq Data. Current Protocols in Bioinformatics, 2011, 33, Unit2.13.	25.8	34
1106	Transcriptional activity regulates alternative cleavage and polyadenylation. Molecular Systems Biology, 2011, 7, 534.	3.2	111
1108	Uncovering combinatorial interactions in chromatin. Epigenomics, 2011, 3, 371-379.	1.0	3
1109	Splicing enhances recruitment of methyltransferase HYPB/Setd2 and methylation of histone H3 Lys36. Nature Structural and Molecular Biology, 2011, 18, 977-983.	3.6	204
1110	The diverse functions of Dot1 and H3K79 methylation. Genes and Development, 2011, 25, 1345-1358.	2.7	492

#	Article	IF	CITATIONS
1111	Natural History of the Eukaryotic Chromatin Protein Methylation System. Progress in Molecular Biology and Translational Science, 2011, 101, 105-176.	0.9	65
1112	The DNMT3 Family of Mammalian De Novo DNA Methyltransferases. Progress in Molecular Biology and Translational Science, 2011, 101, 255-285.	0.9	150
1113	Composition and Epigenetic Markers of Heterochromatin in the Aphid <i>Aphis nerii</i> (Hemiptera: Aphididae). Cytogenetic and Genome Research, 2011, 133, 67-77.	0.6	26
1114	PeakRanger: A cloud-enabled peak caller for ChIP-seq data. BMC Bioinformatics, 2011, 12, 139.	1.2	142
1115	ReadDB Provides Efficient Storage for Mapped Short Reads. BMC Bioinformatics, 2011, 12, 278.	1.2	0
1116	Homeobox gene Rhox5 is regulated by epigenetic mechanisms in cancer and stem cells and promotes cancer growth. Molecular Cancer, 2011, 10, 63.	7.9	13
1117	Effects of RNA interference-mediated gene silencing of JMJD2A on human breast cancer cell line MDA-MB-231 in vitro. Journal of Experimental and Clinical Cancer Research, 2011, 30, 90.	3.5	46
1118	Epigenetic Aspects of Chronic Diseases. , 2011, , .		3
1119	Genomic Approaches to Deconstruct Pluripotency. Annual Review of Genomics and Human Genetics, 2011, 12, 165-185.	2.5	33
1120	DNA Methylation and Cancer. , 2011, 67, 1-23.		89
1121	Yeast Systems Biology. Methods in Molecular Biology, 2011, , .	0.4	7
1122	A Handbook of Transcription Factors. Sub-Cellular Biochemistry, 2011, , .	1.0	14
1123	Identifying dispersed epigenomic domains from ChIP-Seq data. Bioinformatics, 2011, 27, 870-871.	1.8	163
1124	From stem cell to red cell: regulation of erythropoiesis at multiple levels by multiple proteins, RNAs, and chromatin modifications. Blood, 2011, 118, 6258-6268.	0.6	353
1125	Epigenetics and Disease. , 2011, , .		5
1126	Revealing histone variant induced changes via quantitative proteomics. Critical Reviews in Biochemistry and Molecular Biology, 2011, 46, 284-294.	2.3	29
1127	H3K9 methyltransferase G9a and the related molecule GLP. Genes and Development, 2011, 25, 781-788.	2.7	473
1128	Techniques to Study DNA Methylation and Histone Modification. , 2011, , 21-39.		3

ARTICLE IF CITATIONS High-Throughput Sequencing., 2011,, 461-478. 1129 8 RNA. Methods in Molecular Biology, 2011, , . 0.4 MM-ChIP enables integrative analysis of cross-platform and between-laboratory ChIP-chip or ChIP-seq 1131 13.9 22 data. Genome Biology, 2011, 12, R11. A statistical framework for modeling gene expression using chromatin features and application to modENCODE datasets. Genome Biology, 2011, 12, R15. 13.9 A Statistical Framework for the Analysis of ChIP-Seq Data. Journal of the American Statistical 1133 100 1.8 Association, 2011, 106, 891-903. Child Health, Developmental Plasticity, and Epigenetic Programming. Endocrine Reviews, 2011, 32, 1134 8.9 533 159-224. Androgen Action. Methods in Molecular Biology, 2011, , . 1135 0.4 2 Human Pluripotent Stem Cells. Methods in Molecular Biology, 2011, , . 1136 0.4 1138 High-Resolution Genome-wide Mapping of the Primary Structure of Chromatin. Cell, 2011, 144, 175-186. 13.5 151 Functional and Mechanistic Diversity of Distal Transcription Enhancers. Cell, 2011, 144, 327-339. 13.5 718 An Epigenetic Signature for Monoallelic Olfactory Receptor Expression. Cell, 2011, 145, 555-570. 1140 13.5257 Mapping Rare and Common Causal Alleles for Complex Human Diseases. Cell, 2011, 147, 57-69. 1141 13.5 100 Combinatorial Patterning of Chromatin Regulators Uncovered by Genome-wide Location Analysis in 1142 13.5 303 Human Cells. Cell, 2011, 147, 1628-1639. Polycomb-Repressed Genes Have Permissive Enhancers that Initiate Reprogramming. Cell, 2011, 147, 1143 13.5 161 1283-1294. Comprehensive Genome-wide Protein-DNA Interactions Detected at Single-Nucleotide Resolution. Cell, 1144 13.5 684 2011, 147, 1408-1419. Conserved Function of lincRNAs in Vertebrate Embryonic Development despite Rapid Sequence 1145 1,072 Evolution. Cell, 2011, 147, 1537-1550. Hypoxia causes epigenetic gene regulation in macrophages by attenuating Jumonji histone demethylase 1146 1.4 109 activity. Cytokine, 2011, 53, 256-262. Transcriptional repressors, corepressors and chromatin modifying enzymes in T cell development. 1147 1.4 Cytokine, 2011, 53, 271-281.

#	Article	IF	CITATIONS
1148	A Wt1-Controlled Chromatin Switching Mechanism Underpins Tissue-Specific Wnt4 Activation and Repression. Developmental Cell, 2011, 21, 559-574.	3.1	146
1149	Prepatterning of Developmental Gene Expression by Modified Histones before Zygotic Genome Activation. Developmental Cell, 2011, 21, 993-1004.	3.1	188
1150	Sequence and epigenetic determinants in the regulation of the Math6 gene by Neurogenin3. Differentiation, 2011, 82, 66-76.	1.0	9
1151	Chromatin higher-order structures and gene regulation. Current Opinion in Genetics and Development, 2011, 21, 175-186.	1.5	373
1152	Locking the genome: nuclear organization and cell fate. Current Opinion in Genetics and Development, 2011, 21, 167-174.	1.5	68
1153	Epigenetic regulation of transposable element derived human gene promoters. Gene, 2011, 475, 39-48.	1.0	42
1154	Computational analysis suggests a highly bendable, fragile structure for nucleosomal DNA. Gene, 2011, 476, 10-14.	1.0	4
1155	Genome-wide interplay of nuclear receptors with the epigenome. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2011, 1812, 818-823.	1.8	23
1156	Long-range DNA interactions are specifically altered by locked nucleic acid-targeting of a CTCF binding site. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2011, 1809, 24-33.	0.9	5
1157	The effect of CD4 receptor downregulation and its downstream signaling molecules on HIV-1 latency. Biochemical and Biophysical Research Communications, 2011, 404, 646-651.	1.0	7
1158	Characterization of histone H3K27 modifications in the β-globin locus. Biochemical and Biophysical Research Communications, 2011, 405, 210-215.	1.0	10
1159	H3K4 tri-methylation provides an epigenetic signature of active enhancers. EMBO Journal, 2011, 30, 4198-4210.	3.5	265
1160	CTCF-promoted RNA polymerase II pausing links DNA methylation to splicing. Nature, 2011, 479, 74-79.	13.7	853
1161	Methylation screening of reciprocal genome-wide UPDs identifies novel human-specific imprinted genesâ€. Human Molecular Genetics, 2011, 20, 3188-3197.	1.4	55
1162	Reprogramming transcription by distinct classes of enhancers functionally defined by eRNA. Nature, 2011, 474, 390-394.	13.7	777
1163	Multilineage Priming of Enhancer Repertoires Precedes Commitment to the B and Myeloid Cell Lineages in Hematopoietic Progenitors. Immunity, 2011, 35, 413-425.	6.6	125
1164	Genome-wide Analyses of Transcription Factor GATA3-Mediated Gene Regulation in Distinct T Cell Types. Immunity, 2011, 35, 299-311.	6.6	293
1165	NF-κB Induction of the SUMO Protease SENP2: A Negative Feedback Loop to Attenuate Cell Survival Response to Genotoxic Stress. Molecular Cell, 2011, 43, 180-191.	4.5	75

		IATION REPORT	
#	Article	IF	CITATIONS
1166	Mechanisms and Consequences of Alternative Polyadenylation. Molecular Cell, 2011, 43, 853-866.	4.5	626
1167	High-grade neuroendocrine carcinomas of the lung highly express enhancer of zeste homolog 2, but carcinoids do not. Human Pathology, 2011, 42, 867-872.	1.1	22
1168	Epigenetic, transcriptional and posttranscriptional regulation of the tyrosine hydroxylase gene. International Journal of Developmental Neuroscience, 2011, 29, 873-883.	0.7	50
1169	OPERating ON Chromatin, a Colorful Language where Context Matters. Journal of Molecular Biology, 2011, 409, 36-46.	2.0	321
1170	Transcriptional regulation of mammalian miRNA genes. Genomics, 2011, 97, 1-6.	1.3	147
1171	Genome-wide profiling of DNA methylation in human cancer cells. Genomics, 2011, 98, 280-287.	1.3	42
1172	Epigenetic methodologies for behavioral scientists. Hormones and Behavior, 2011, 59, 407-416.	1.0	13
1173	Genome-wide Maps of Histone Modifications Unwind InÂVivo Chromatin States of the Hair Follicle Lineage. Cell Stem Cell, 2011, 9, 219-232.	5.2	187
1174	Androgen receptor-driven chromatin looping in prostate cancer. Trends in Endocrinology and Metabolism, 2011, 22, 474-480.	3.1	45
1175	Epigenetic Mechanisms in Cognition. Neuron, 2011, 70, 813-829.	3.8	434
1176	MicroRNA regulation of neural plasticity and memory. Neurobiology of Learning and Memory, 2011, 90 89-94.	6, 1.0	158
1177	Maintaining CD4–CD8 lineage integrity in T cells: Where plasticity serves versatility. Seminars in Immunology, 2011, 23, 360-367.	2.7	7
1178	PPARs and Lipid Ligands in Inflammation and Metabolism. Chemical Reviews, 2011, 111, 6321-6340.	23.0	151
1179	Molecular mechanisms of genomic imprinting and clinical implications for cancer. Expert Reviews in Molecular Medicine, 2011, 13, e2.	1.6	66
1180	Deep-sequencing identification of the genomic targets of the cytidine deaminase AID and its cofactor RPA in B lymphocytes. Nature Immunology, 2011, 12, 62-69.	7.0	249
1181	Enhancer function: new insights into the regulation of tissue-specific gene expression. Nature Reviews Genetics, 2011, 12, 283-293.	7.7	768
1182	A User's Guide to the Encyclopedia of DNA Elements (ENCODE). PLoS Biology, 2011, 9, e1001046.	2.6	1,257
1183	A chemical probe selectively inhibits G9a and GLP methyltransferase activity in cells. Nature Chemical Biology, 2011, 7, 566-574.	3.9	465

#	Article	IF	CITATIONS
1184	Epigenetics, Stem Cells, and Cellular Differentiation. , 2011, , 315-328.		1
1185	Expression of distinct RNAs from 3′ untranslated regions. Nucleic Acids Research, 2011, 39, 2393-2403.	6.5	185
1186	Chromatin Remodelling and RNA Processing. , 2011, , .		2
1188	Role of Signaling Pathways and Epigenetic Factors in Lineage Determination During Human Embryonic Stem Cell Differentiation. , 2011, , .		2
1189	Chromosomal Position Effects and Gene Variegation. , 2011, , 77-105.		1
1190	Chromatin Modifications Distinguish Genomic Features and Physical Organization of the Nucleus. , 2011, , 159-171.		0
1191	Biologic characteristics of premalignant breast disease. Cancer Biomarkers, 2011, 9, 177-192.	0.8	15
1192	Modeling regulatory motifs. , 0, , 126-147.		0
1193	Next generation quantitative genetics in plants. Frontiers in Plant Science, 2011, 2, 77.	1.7	11
1194	Assessing Epigenetic Information. , 2011, , 173-181.		5
1195	Understanding the Molecular Circuitry of Cell Lineage Specification in the Early Mouse Embryo. Genes, 2011, 2, 420-448.	1.0	16
1196	Comparison of Four ChIP-Seq Analytical Algorithms Using Rice Endosperm H3K27 Trimethylation Profiling Data. PLoS ONE, 2011, 6, e25260.	1.1	54
1197	H3 Lysine 4 Is Acetylated at Active Gene Promoters and Is Regulated by H3 Lysine 4 Methylation. PLoS Genetics, 2011, 7, e1001354.	1.5	175
1198	Identification of Lysine 37 of Histone H2B as a Novel Site of Methylation. PLoS ONE, 2011, 6, e16244.	1.1	29
1199	Mayday SeaSight: Combined Analysis of Deep Sequencing and Microarray Data. PLoS ONE, 2011, 6, e16345.	1.1	17
1200	Multiple Wnt/ß-Catenin Responsive Enhancers Align with the MYC Promoter through Long-Range Chromatin Loops. PLoS ONE, 2011, 6, e18966.	1.1	44
1201	Heterochromatic Genes Undergo Epigenetic Changes and Escape Silencing in Immunodeficiency, Centromeric Instability, Facial Anomalies (ICF) Syndrome. PLoS ONE, 2011, 6, e19464.	1.1	30
1202	Genomic Organization of H2Av Containing Nucleosomes in Drosophila Heterochromatin. PLoS ONE, 2011, 6, e20511.	1.1	7

#	Article	IF	CITATIONS
1203	Interplay between SIN3A and STAT3 Mediates Chromatin Conformational Changes and GFAP Expression during Cellular Differentiation. PLoS ONE, 2011, 6, e22018.	1.1	48
1204	High Resolution Detection and Analysis of CpG Dinucleotides Methylation Using MBD-Seq Technology. PLoS ONE, 2011, 6, e22226.	1.1	69
1205	Stage-Specific Histone Modification Profiles Reveal Global Transitions in the Xenopus Embryonic Epigenome. PLoS ONE, 2011, 6, e22548.	1.1	37
1206	The UBC9 E2 SUMO Conjugating Enzyme Binds the PR-Set7 Histone Methyltransferase to Facilitate Target Gene Repression. PLoS ONE, 2011, 6, e22785.	1.1	10
1207	Systematic Clustering of Transcription Start Site Landscapes. PLoS ONE, 2011, 6, e23409.	1.1	59
1208	Tree-Based Position Weight Matrix Approach to Model Transcription Factor Binding Site Profiles. PLoS ONE, 2011, 6, e24210.	1.1	21
1209	High Resolution Analysis of the Chromatin Landscape of the IgE Switch Region in Human B Cells. PLoS ONE, 2011, 6, e24571.	1.1	12
1210	AMD, an Automated Motif Discovery Tool Using Stepwise Refinement of Gapped Consensuses. PLoS ONE, 2011, 6, e24576.	1.1	33
1211	Regulation of DCC Localization by HTZ-1/H2A.Z and DPY-30 Does not Correlate with H3K4 Methylation Levels. PLoS ONE, 2011, 6, e25973.	1.1	8
1212	Clobal Mapping of H3K4me1 and H3K4me3 Reveals the Chromatin State-Based Cell Type-Specific Gene Regulation in Human Treg Cells. PLoS ONE, 2011, 6, e27770.	1.1	32
1213	Glioma Stem Cell Maintenance: The Role of the Microenvironment. Current Pharmaceutical Design, 2011, 17, 2386-2401.	0.9	76
1214	Reversible Epigenetic Modifications of the Two Cardiac Myosin Heavy Chain Genes During Changes in Expression. Gene Expression, 2011, 15, 51-59.	0.5	17
1215	Genetic Analysis Implicates the Set3/Hos2 Histone Deacetylase in the Deposition and Remodeling of Nucleosomes Containing H2A.Z. Genetics, 2011, 187, 1053-1066.	1.2	23
1216	Maternal malnutrition and placental insufficiency induce global downregulation of gene expression in fetal kidneys. Journal of Developmental Origins of Health and Disease, 2011, 2, 124-133.	0.7	16
1217	MYB transcriptionally regulates the miR-155 host gene in chronic lymphocytic leukemia. Blood, 2011, 117, 3816-3825.	0.6	128
1218	The MMSET histone methyl transferase switches global histone methylation and alters gene expression in t(4;14) multiple myeloma cells. Blood, 2011, 117, 211-220.	0.6	300
1219	The host genomic environment of the provirus determines the abundance of HTLV-1–infected T-cell clones. Blood, 2011, 117, 3113-3122.	0.6	273
1220	Gene induction and repression during terminal erythropoiesis are mediated by distinct epigenetic changes. Blood, 2011, 118, e128-e138.	0.6	103

#	Article	IF	CITATIONS
1221	PLU1 histone demethylase decreases the expression of KAT5 and enhances the invasive activity of the cells. Biochemical Journal, 2011, 437, 555-564.	1.7	22
1222	Histone Methyltransferase PR-Set7 and Histone Variant H2A.Z, Induced during Hepatocarcinogenesis, Repress the Promoter Activity of the Tumor Marker Gene and the Ras-Induced Colony Formation Activity. Journal of Health Science, 2011, 57, 264-273.	0.9	2
1225	Human genetics and genomics a decade after the release of the draft sequence of the human genome. Human Genomics, 2011, 5, 577.	1.4	86
1226	Helper T-cell differentiation and plasticity: insights from epigenetics. Immunology, 2011, 134, 235-245.	2.0	96
1227	Histone methylation is a critical regulator of the abnormal expression of POU5F1 and RASSF1A in testis cancer cell lines. Journal of Developmental and Physical Disabilities, 2011, 34, 110-123.	3.6	21
1228	Chromatin Architecture and the Regulation of Nuclear Receptor Inducible Transcription. Journal of Neuroendocrinology, 2011, 23, 94-106.	1.2	13
1229	Control of nuclear receptor function by local chromatin structure. FEBS Journal, 2011, 278, 2211-2230.	2.2	35
1230	Structure and function of active chromatin and DNase I hypersensitive sites. FEBS Journal, 2011, 278, 2182-2210.	2.2	110
1231	Molecular mechanisms of T ell tolerance. Immunological Reviews, 2011, 241, 133-144.	2.8	70
1232	Nuclear adaptor Ldb1 regulates a transcriptional program essential for the maintenance of hematopoietic stem cells. Nature Immunology, 2011, 12, 129-136.	7.0	91
1233	Cancer epigenetics reaches mainstream oncology. Nature Medicine, 2011, 17, 330-339.	15.2	1,102
1234	Genome-scale analysis of replication timing: from bench to bioinformatics. Nature Protocols, 2011, 6, 870-895.	5.5	110
1235	Unravelling the complexity of metastasis — molecular understanding and targeted therapies. Nature Reviews Cancer, 2011, 11, 735-748.	12.8	318
1236	Charting histone modifications and the functional organization of mammalian genomes. Nature Reviews Genetics, 2011, 12, 7-18.	7.7	1,019
1237	Recombination centres and the orchestration of V(D)J recombination. Nature Reviews Immunology, 2011, 11, 251-263.	10.6	486
1238	Genomic views of STAT function in CD4+ T helper cell differentiation. Nature Reviews Immunology, 2011, 11, 239-250.	10.6	251
1239	Epigenetics of haematopoietic cell development. Nature Reviews Immunology, 2011, 11, 478-488.	10.6	151
1240	Functional dissection of an enhancer-like element located within the second intron of the human U2AF1L4 gene. Biochemistry (Moscow), 2011, 76, 951-957.	0.7	Ο

#	Article	IF	CITATIONS
1241	Mapping of INS promoter interactions reveals its role in long-range regulation of SYT8 transcription. Nature Structural and Molecular Biology, 2011, 18, 372-378.	3.6	55
1242	Histone H3 lysine 9 trimethylation and HP1Î ³ favor inclusion of alternative exons. Nature Structural and Molecular Biology, 2011, 18, 337-344.	3.6	228
1243	Impact of chromatin structure on sequence variability in the human genome. Nature Structural and Molecular Biology, 2011, 18, 510-515.	3.6	66
1244	Genome-wide CTCF distribution in vertebrates defines equivalent sites that aid the identification of disease-associated genes. Nature Structural and Molecular Biology, 2011, 18, 708-714.	3.6	95
1245	Histone onco-modifications. Oncogene, 2011, 30, 3391-3403.	2.6	261
1246	The HDAC class I-specific inhibitor entinostat (MS-275) effectively relieves epigenetic silencing of the LAT2 gene mediated by AML1/ETO. Oncogene, 2011, 30, 3062-3072.	2.6	45
1247	Regulation of chromatin by histone modifications. Cell Research, 2011, 21, 381-395.	5.7	4,442
1248	Chromatin condensation via the condensin II complex is required for peripheral T-cell quiescence. EMBO Journal, 2011, 30, 263-276.	3.5	130
1249	Distinct roles of GCN5/PCAF-mediated H3K9ac and CBP/p300-mediated H3K18/27ac in nuclear receptor transactivation. EMBO Journal, 2011, 30, 249-262.	3.5	655
1250	Epigenetic engineering shows H3K4me2 is required for HJURP targeting and CENP-A assembly on a synthetic human kinetochore. EMBO Journal, 2011, 30, 328-340.	3.5	264
1251	Phospho-MED1-enhanced UBE2C locus looping drives castration-resistant prostate cancer growth. EMBO Journal, 2011, 30, 2405-2419.	3.5	108
1252	The androgen receptor fuels prostate cancer by regulating central metabolism and biosynthesis. EMBO Journal, 2011, 30, 2719-2733.	3.5	530
1253	Extensive chromatin remodelling and establishment of transcription factor â€~hotspots' during early adipogenesis. EMBO Journal, 2011, 30, 1459-1472.	3.5	300
1254	Transcriptional repression and DNA looping associated with a novel regulatory element in the final exon of the lymphotoxin-β gene. Genes and Immunity, 2011, 12, 126-135.	2.2	13
1255	Applications of next generation sequencing in molecular ecology of non-model organisms. Heredity, 2011, 107, 1-15.	1.2	930
1256	Comprehensive analysis of the chromatin landscape in Drosophila melanogaster. Nature, 2011, 471, 480-485.	13.7	781
1257	The Polycomb complex PRC2 and its mark in life. Nature, 2011, 469, 343-349.	13.7	2,783
1258	Initial impact of the sequencing of the human genome. Nature, 2011, 470, 187-197.	13.7	919

		CITATION REPORT		
#	Article		IF	CITATIONS
1259	Mapping and analysis of chromatin state dynamics in nine human cell types. Nature, 202	11, 473, 43-49.	13.7	2,630
1260	Epigenetic regulation of osteoclast differentiation. Annals of the New York Academy of S 1240, 7-13.	Sciences, 2011,	1.8	45
1261	Unraveling the Glioma Epigenome—From Molecular Mechanisms to Novel Biomarkers Targets. Brain Pathology, 2011, 21, 619-632.	and Therapeutic	2.1	38
1262	Coupling mitosis to DNA replication: The emerging role of the histone H4-lysine 20 meth PR-Set7. Trends in Cell Biology, 2011, 21, 452-460.	ıyltransferase	3.6	46
1263	Genome-wide transcription factor binding: beyond direct target regulation. Trends in Ge 27, 141-148.	netics, 2011,	2.9	187
1264	Genome organization in and around the nucleolus. Trends in Genetics, 2011, 27, 149-15	6.	2.9	181
1265	Pioneer factors: directing transcriptional regulators within the chromatin environment. T Genetics, 2011, 27, 465-474.	rends in	2.9	138
1266	Effect of PCR extension temperature on high-throughput sequencing. Molecular and Bio Parasitology, 2011, 176, 64-67.	chemical	0.5	19
1267	Epigenetic regulation of spermidine/spermine N1-acetyltransferase (SAT1) in Suicide. Jou Psychiatric Research, 2011, 45, 1229-1235.	ırnal of	1.5	60
1268	Epigenetic modifications in plants: an evolutionary perspective. Current Opinion in Plant 14, 179-186.	Biology, 2011,	3.5	170
1269	A comparison of two cell regulatory models entailing high dimensional attractors represe phenotype. Progress in Biophysics and Molecular Biology, 2011, 106, 443-449.	enting	1.4	21
1270	Occupancy of chromatin organizers in the Epstein–Barr virus genome. Virology, 2011,	. 415, 1-5.	1.1	38
1271	Identification of cis regulatory features in the embryonic zebrafish genome through larg profiling of H3K4me1 and H3K4me3 binding sites. Developmental Biology, 2011, 357, 4		0.9	76
1272	Elf5 regulation in the Trophectoderm. Developmental Biology, 2011, 360, 343-350.		0.9	27
1273	Nuclear factor I revealed as family of promoter binding transcription activators. BMC Ge 12, 181.	nomics, 2011,	1.2	48
1274	A compendium of genome-wide hematopoietic transcription factor maps supports the id gene regulatory control mechanisms. Experimental Hematology, 2011, 39, 531-541.	lentification of	0.2	43
1275	Histone arginine methylation. FEBS Letters, 2011, 585, 2024-2031.		1.3	405
1276	Every methyl counts – Epigenetic calculus. FEBS Letters, 2011, 585, 2001-2007.		1.3	31

ARTICLE IF CITATIONS # Transcriptional and epigenetic networks in haematological malignancy. FEBS Letters, 2011, 585, 1277 1.3 32 2100-2111. Polycomb proteins in mammalian cell differentiation and plasticity. FEBS Letters, 2011, 585, 2067-2077. 1278 1.3 Ubâ€family modifications at the replication fork: Regulating PCNAâ€interacting components. FEBS Letters, 1279 1.3 21 2011, 585, 2920-2928. Histone lysine methylation and demethylation pathways in cancer. Biochimica Et Biophysica Acta: 214 Reviews on Cancer, 2011, 1815, 75-89. Genome-wide analysis of OCT4 binding sites in glioblastoma cancer cells. Journal of Zhejiang 1281 1.3 11 University: Science B, 2011, 12, 812-819. Transcription initiation platforms and CTF recruitment at tissue-specific enhancers and promoters. Nature Structural and Molecular Biology, 2011, 18, 956-963. 3.6 296 DNA double-strand breaks induced by high NaCl occur predominantly in gene deserts. Proceedings of 1283 3.3 48 the National Academy of Sciences of the United States of America, 2011, 108, 20796-20801. Epigenetic Mechanisms in Inflammation. Journal of Dental Research, 2011, 90, 9-17. 1284 2.5 221 1285 Determinants of nucleosome organization in primary human cells. Nature, 2011, 474, 516-520. 13.7 567 Epigenetic regulation by nuclear receptors. Epigenomics, 2011, 3, 59-72. 1.0 29 Epigenomics of human embryonic stem cells and induced pluripotent stem cells: insights into 1287 3.6 49 pluripotency and implications for disease. Genome Medicine, 2011, 3, 36. CTCF, cohesin, and histone variants: connecting the genome. Biochemistry and Cell Biology, 2011, 89, 1288 505-513. Transcriptional control of embryonic and induced pluripotent stem cells. Epigenomics, 2011, 3, 323-343. 1289 1.0 13 From bench to bedside: Targeting epigenetics for cancer therapy. Clinical Oncology and Cancer Research, 2011, 8, 191-201. 1290 0.1 Matters of life and death: the role of chromatin remodeling proteins in retinal neuron survival. 1291 0.2 16 Journal of Ocular Biology, Diseases, and Informatics, 2011, 4, 111-120. Epigenetic regulation in cell reprogramming revealed by genome-wide analysis. Epigenomics, 2011, 3, 1292 73-81. Studying the epigenome using next generation sequencing. Journal of Medical Genetics, 2011, 48, 1293 1.5108 721-730. 1294 Base-calling for next-generation sequencing platforms. Briefings in Bioinformatics, 2011, 12, 489-497. 3.2

#	Article	IF	CITATIONS
1295	Cohesin Regulates MHC Class II Genes through Interactions with MHC Class II Insulators. Journal of Immunology, 2011, 187, 4236-4244.	0.4	31
1296	CTCF-mediated functional chromatin interactome in pluripotent cells. Nature Genetics, 2011, 43, 630-638.	9.4	567
1297	CTCF function is modulated by neighboring DNA binding factors. Biochemistry and Cell Biology, 2011, 89, 459-468.	0.9	57
1298	Genome-Wide Identification of Transcription Factor-Binding Sites in Plants Using Chromatin Immunoprecipitation Followed by Microarray (ChIP-chip) or Sequencing (ChIP-seq). Methods in Molecular Biology, 2011, 876, 173-188.	0.4	55
1299	Insulation of tumor suppressor genes by the nuclear factor CTCF. Biochemistry and Cell Biology, 2011, 89, 479-488.	0.9	18
1300	Double-strand break-induced transcriptional silencing is associated with loss of tri-methylation at H3K4. Chromosome Research, 2011, 19, 883-899.	1.0	57
1301	Transcriptional silencing of N-Myc downstream-regulated gene 1 (NDRG1) in metastatic colon cancer cell line SW620. Clinical and Experimental Metastasis, 2011, 28, 127-135.	1.7	32
1302	Chromatin modifications that support acetylcholine receptor gene activation are established during muscle cell determination and differentiation. Molecular Biology Reports, 2011, 38, 1277-1285.	1.0	1
1303	Evaluation and comparison of the insulation efficiency of three enhancer-blocking insulators in plants. Plant Cell, Tissue and Organ Culture, 2011, 105, 405-414.	1.2	20
1304	Drosophila melanogaster heterochromatin protein HP1b plays important roles in transcriptional activation and development. Chromosoma, 2011, 120, 97-108.	1.0	20
1305	Cutting Edge: The Etiology of Autoimmune Thyroid Diseases. Clinical Reviews in Allergy and Immunology, 2011, 41, 190-197.	2.9	88
1306	Integration of Metabolic Reactions and Gene Regulation. Molecular Biotechnology, 2011, 47, 70-82.	1.3	8
1307	Epigenetic Regulation of Vascular Endothelial Biology/Pathobiology and Response to Fluid Shear Stress. Cellular and Molecular Bioengineering, 2011, 4, 560-578.	1.0	4
1308	3C-based methods to detect long-range chromatin interactions. Frontiers in Biology, 2011, 6, 76-81.	0.7	4
1309	Advances in Epigenetics and Epigenomics for Neurodegenerative Diseases. Current Neurology and Neuroscience Reports, 2011, 11, 464-473.	2.0	72
1310	Cancer associated epigenetic transitions identified by genome-wide histone methylation binding profiles in human colorectal cancer samples and paired normal mucosa. BMC Cancer, 2011, 11, 450.	1.1	30
1311	Clustered ChIP-Seq-defined transcription factor binding sites and histone modifications map distinct classes of regulatory elements. BMC Biology, 2011, 9, 80.	1.7	30
1312	Fish the ChIPs: a pipeline for automated genomic annotation of ChIP-Seq data. Biology Direct, 2011, 6, 51.	1.9	12

#	Article	IF	CITATIONS
1313	Pinpointing transcription factor binding sites from ChIP-seq data with SeqSite. BMC Systems Biology, 2011, 5, S3.	3.0	6
1314	Quantification of histone modification ChIP-seq enrichment for data mining and machine learning applications. BMC Research Notes, 2011, 4, 288.	0.6	10
1315	Generation of bivalent chromatin domains during cell fate decisions. Epigenetics and Chromatin, 2011, 4, 9.	1.8	54
1316	Histone modification profiles are predictive for tissue/cell-type specific expression of both protein-coding and microRNA genes. BMC Bioinformatics, 2011, 12, 155.	1.2	36
1317	Predicting functionally important SNP classes based on negative selection. BMC Bioinformatics, 2011, 12, 26.	1.2	12
1318	An integrated ChIP-seq analysis platform with customizable workflows. BMC Bioinformatics, 2011, 12, 277.	1.2	80
1319	ChIPseqR: analysis of ChIP-seq experiments. BMC Bioinformatics, 2011, 12, 39.	1.2	19
1320	A motif-independent metric for DNA sequence specificity. BMC Bioinformatics, 2011, 12, 408.	1.2	18
1321	Exploratory analysis of genomic segmentations with Segtools. BMC Bioinformatics, 2011, 12, 415.	1.2	20
1322	Lineage-specific evolution of the vertebrate Otopetringene family revealed by comparative genomic analyses. BMC Evolutionary Biology, 2011, 11, 23.	3.2	16
1323	The SOX2 response program in glioblastoma multiforme: an integrated ChIP-seq, expression microarray, and microRNA analysis. BMC Genomics, 2011, 12, 11.	1.2	141
1324	ChIP-chip versus ChIP-seq: Lessons for experimental design and data analysis. BMC Genomics, 2011, 12, 134.	1.2	128
1325	Chromatin structure characteristics of pre-miRNA genomic sequences. BMC Genomics, 2011, 12, 329.	1.2	13
1326	The differential disease regulome. BMC Genomics, 2011, 12, 353.	1.2	9
1327	Tight associations between transcription promoter type and epigenetic variation in histone positioning and modification. BMC Genomics, 2011, 12, 416.	1.2	14
1328	Prediction of RNA Polymerase II recruitment, elongation and stalling from histone modification data. BMC Genomics, 2011, 12, 544.	1.2	31
1329	A co-ordinated interaction between CTCF and ER in breast cancer cells. BMC Genomics, 2011, 12, 593.	1.2	58
1330	Combinatorial patterns of histone modifications in <i>Saccharomyces.cerevisiae</i> . Yeast, 2011, 28, 683-691.	0.8	13

		CITATION REPORT		
#	Article		IF	CITATIONS
1331	Exploring genomic profiles of hepatocellular carcinoma. Molecular Carcinogenesis, 201	1, 50, 235-243.	1.3	61
1332	RARÎ ³ is required for correct deposition and removal of Suz12 and H2A.Z in embryonic Journal of Cellular Physiology, 2011, 226, 293-298.	stem cells.	2.0	24
1333	Epigenetic control of macrophage polarization. European Journal of Immunology, 2011	, 41, 2490-2493.	1.6	100
1334	The hunt for the epiallele. Environmental and Molecular Mutagenesis, 2011, 52, 1-11.		0.9	28
1335	Integration profile of retroviral vector in gene therapy treated patients is cellâ€specific gene expression and chromatin conformation of target cell. EMBO Molecular Medicine		3.3	95
1336	<i>cis</i> â€regulatory mutations are a genetic cause of human limb malformations. De Dynamics, 2011, 240, 920-930.	evelopmental	0.8	68
1337	Wnt antagonist <i>DKK1</i> acts as a tumor suppressor gene that induces apoptosis a proliferation in human renal cell carcinoma. International Journal of Cancer, 2011, 128,	and inhibits 1793-1803.	2.3	97
1339	Decoding Genomes at High Speed: Implications for Science and Medicine. Angewandte International Edition, 2011, 50, 12406-12410.	Chemie -	7.2	12
1340	Dynamics of Polycomb and Trithorax activities during development. Birth Defects Rese Clinical and Molecular Teratology, 2011, 91, 781-787.	arch Part A:	1.6	7
1341	Epigenetic regulation in neural crest development. Birth Defects Research Part A: Clinic Molecular Teratology, 2011, 91, 788-796.	al and	1.6	15
1342	Diabetic embryopathy: A role for the epigenome?. Birth Defects Research Part A: Clinica Teratology, 2011, 91, 770-780.	al and Molecular	1.6	37
1343	Towards cracking the epigenetic code using a combination of highâ€ŧhroughput epige quantitative mass spectrometryâ€based proteomics. BioEssays, 2011, 33, 547-551.	nomics and	1.2	17
1344	Structure and Function of Mammalian DNA Methyltransferases. ChemBioChem, 2011,	12, 206-222.	1.3	561
1345	Histone Tails: Ideal Motifs for Probing Epigenetics through Chemical Biology Approache ChemBioChem, 2011, 12, 236-252.	25.	1.3	33
1346	Structure and Function of Histone H3 Lysine 9 Methyltransferases and Demethylases. (2011, 12, 254-263.	ChemBioChem,	1.3	75
1347	Spreading Chromatin into Chemical Biology. ChemBioChem, 2011, 12, 264-279.		1.3	67
1348	Application of ChIP-Seq and Related Techniques to the Study of Immune Function. Imm 830-842.	ıunity, 2011, 34,	6.6	60
1349	Regulation of major histocompatibility complex class II genes. Current Opinion in Immu 81-87.	inology, 2011, 23,	2.4	80

#	Article	IF	CITATIONS
1350	A top-down linguistic approach to the analysis of genomic sequences: The metabotropic glutamate receptors 1 and 5 in human and in mouse as a case study. Journal of Theoretical Biology, 2011, 270, 134-142.	0.8	1
1351	Identification of key mechanisms controlling gene expression in Leishmania infected macrophages using genome-wide promoter analysis. Infection, Genetics and Evolution, 2011, 11, 769-777.	1.0	2
1352	Multi-scale coding of genomic information: From DNA sequence to genome structure and function. Physics Reports, 2011, 498, 45-188.	10.3	108
1353	Genome-wide identification of conserved regulatory function in diverged sequences. Genome Research, 2011, 21, 1139-1149.	2.4	72
1354	PTGS2 (Prostaglandin Endoperoxide Synthase-2) Expression in Term Human Amnion in Vivo Involves Rapid mRNA Turnover, Polymerase-II 5′-Pausing, and Glucocorticoid Transrepression. Endocrinology, 2011, 152, 2113-2122.	1.4	12
1355	EpiRegNet: Constructing epigenetic regulatory network from high throughput gene expression data for humans. Epigenetics, 2011, 6, 1505-1512.	1.3	19
1356	Initiating RNA Polymerase II and TIPs as hallmarks of enhancer activity and tissue-specificity. Transcription, 2011, 2, 263-268.	1.7	33
1357	Where splicing joins chromatin. Nucleus, 2011, 2, 182-188.	0.6	54
1358	Histone methylation in myelodysplastic syndromes. Epigenomics, 2011, 3, 193-205.	1.0	12
1359	Epigenome sequencing comes of age in development, differentiation and disease mechanism research. Epigenomics, 2011, 3, 207-220.	1.0	7
1360	Chromatin landscape. Epigenetics, 2011, 6, 9-15.	1.3	90
1361	The Epigenetic Landscape of Lineage Choice: Lessons From the Heritability of Cd4 and Cd8 Expression. Current Topics in Microbiology and Immunology, 2011, 356, 165-188.	0.7	11
1362	Bivalent histone modifications in stem cells poise miRNA loci for CpG island hypermethylation in human cancer. Epigenetics, 2011, 6, 1344-1353.	1.3	16
1363	Dynamics of bivalent chromatin domains upon drug induced reactivation and resilencing in cancer cells. Epigenetics, 2011, 6, 1138-1148.	1.3	7
1364	Roles of chromatin insulator proteins in higher-order chromatin organization and transcription regulation. Nucleus, 2011, 2, 358-369.	0.6	43
1365	Pre-mRNA splicing is a determinant of histone H3K36 methylation. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 13564-13569.	3.3	175
1366	Lysine Methylation and Functional Modulation of Androgen Receptor by Set9 Methyltransferase. Molecular Endocrinology, 2011, 25, 433-444.	3.7	75
1367	Cutting Edge: Persistently Open Chromatin at Effector Gene Loci in Resting Memory CD8+ T Cells Independent of Transcriptional Status. Journal of Immunology, 2011, 186, 2705-2709.	0.4	74

#	Article	IF	CITATIONS
1368	Recognition of Unmodified Histone H3 by the First PHD Finger of Bromodomain-PHD Finger Protein 2 Provides Insights into the Regulation of Histone Acetyltransferases Monocytic Leukemic Zinc-finger Protein (MOZ) and MOZ-related factor (MORF). Journal of Biological Chemistry, 2011, 286, 36944-36955.	1.6	56
1369	Notice of Retraction: Chromatin Organization in Different Types of Splicing Events. , 2011, , .		0
1371	Dna Systems for B-Z Transition and Their Significance as Epigenetic Model: The Fundamental Role of the Methyl Group. Nucleosides, Nucleotides and Nucleic Acids, 2011, 30, 918-944.	0.4	7
1372	Repeat Expansion Affects Both Transcription Initiation and Elongation in Friedreich Ataxia Cells. Journal of Biological Chemistry, 2011, 286, 4209-4215.	1.6	79
1373	G4 motifs correlate with promoter-proximal transcriptional pausing in human genes. Nucleic Acids Research, 2011, 39, 4975-4983.	6.5	101
1374	A method to sequence and quantify DNA integration for monitoring outcome in gene therapy. Nucleic Acids Research, 2011, 39, e72-e72.	6.5	64
1375	The Histone Modifications Governing TFF1 Transcription Mediated by Estrogen Receptor. Journal of Biological Chemistry, 2011, 286, 13925-13936.	1.6	51
1376	Histone H4 Lys 20 monomethylation by histone methylase SET8 mediates Wnt target gene activation. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 3116-3123.	3.3	147
1377	Chromatin Dynamics of Gene Activation and Repression in Response to Interferon α (IFNα) Reveal New Roles for Phosphorylated and Unphosphorylated Forms of the Transcription Factor STAT2. Journal of Biological Chemistry, 2011, 286, 20217-20227.	1.6	51
1378	EpiChIP: gene-by-gene quantification of epigenetic modification levels. Nucleic Acids Research, 2011, 39, e27-e27.	6.5	36
1379	Reversal of Heterochromatic Silencing of Quiescent Herpes Simplex Virus Type 1 by ICPO. Journal of Virology, 2011, 85, 3424-3435.	1.5	33
1380	Genes for embryo development are packaged in blocks of multivalent chromatin in zebrafish sperm. Genome Research, 2011, 21, 578-589.	2.4	175
1381	The Histone Methyltransferase and Putative Oncoprotein MMSET Is Overexpressed in a Large Variety of Human Tumors. Clinical Cancer Research, 2011, 17, 2919-2933.	3.2	118
1382	Sequential Monte Carlo multiple testing. Bioinformatics, 2011, 27, 3235-3241.	1.8	33
1383	Histone H4K20me3 and HP1α are late heterochromatin markers in development, but present in undifferentiated embryonic stem cells. Journal of Cell Science, 2011, 124, 1878-1890.	1.2	79
1384	Novel Variant of Thyroglobulin Promoter Triggers Thyroid Autoimmunity through an Epigenetic Interferon α-modulated Mechanism. Journal of Biological Chemistry, 2011, 286, 31168-31179.	1.6	69
1385	Genome-wide analysis of the relationships between DNasel HS, histone modifications and gene expression reveals distinct modes of chromatin domains. Nucleic Acids Research, 2011, 39, 7428-7443.	6.5	52
1386	Gene Expression Differences Among Primates Are Associated With Changes in a Histone Epigenetic Modification. Genetics, 2011, 187, 1225-1234.	1.2	89

#	Article	IF	CITATIONS
1387	Have a break: determinants of meiotic DNA double strand break (DSB) formation and processing in plants. Journal of Experimental Botany, 2011, 62, 1545-1563.	2.4	69
1388	Genome-Wide Analysis Reveals Unique Regulation of Transcription of Th2-Specific Genes by GATA3. Journal of Immunology, 2011, 186, 6378-6389.	0.4	53
1389	Coordinated histone modifications are associated with gene expression variation within and between species. Genome Research, 2011, 21, 590-598.	2.4	140
1390	Inhibition of Suppressive T Cell Factor 1 (TCF-1) Isoforms in Naive CD4+ T Cells Is Mediated by IL-4/STAT6 Signaling. Journal of Biological Chemistry, 2011, 286, 919-928.	1.6	29
1391	Ab initio identification of transcription start sites in the Rhesus macaque genome by histone modification and RNA-Seq. Nucleic Acids Research, 2011, 39, 1408-1418.	6.5	19
1392	Histone H3 trimethylation at lysine 36 is associated with constitutive and facultative heterochromatin. Genome Research, 2011, 21, 1426-1437.	2.4	101
1393	Cocaine dynamically regulates heterochromatin and repetitive element unsilencing in nucleus accumbens. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 3035-3040.	3.3	179
1394	The Linker Region of MacroH2A Promotes Self-association of Nucleosomal Arrays. Journal of Biological Chemistry, 2011, 286, 23852-23864.	1.6	47
1395	H3K36 Methylation Antagonizes PRC2-mediated H3K27 Methylation. Journal of Biological Chemistry, 2011, 286, 7983-7989.	1.6	450
1396	Wide-ranging functions of E2F4 in transcriptional activation and repression revealed by genome-wide analysis. Nucleic Acids Research, 2011, 39, 3558-3573.	6.5	132
1397	Long-Range Epigenetic Silencing Associates with Deregulation of Ikaros Targets in Colorectal Cancer Cells. Molecular Cancer Research, 2011, 9, 1139-1151.	1.5	47
1398	Chromosome-Wide Analysis of Parental Allele-Specific Chromatin and DNA Methylation. Molecular and Cellular Biology, 2011, 31, 1757-1770.	1.1	46
1399	SCF ^{FBXO22} Regulates Histone H3 Lysine 9 and 36 Methylation Levels by Targeting Histone Demethylase KDM4A for Ubiquitin-Mediated Proteasomal Degradation. Molecular and Cellular Biology, 2011, 31, 3687-3699.	1.1	81
1400	The analysis on the combinations of histone modifications at the promoter region of gene in Saccharomyces.cerevisiae. , 2011, , .		0
1401	Genome-wide characterization of transcriptional start sites in humans by integrative transcriptome analysis. Genome Research, 2011, 21, 775-789.	2.4	122
1402	Epigenetic switch involved in activation of pioneer factor FOXA1-dependent enhancers. Genome Research, 2011, 21, 555-565.	2.4	196
1403	Widespread signatures of recent selection linked to nucleosome positioning in the human lineage. Genome Research, 2011, 21, 1777-1787.	2.4	65
1404	Euchromatic Subdomains in Rice Centromeres Are Associated with Genes and Transcription. Plant Cell, 2011, 23, 4054-4064.	3.1	51

#	Article	IF	Citations
1405	USP10 deubiquitylates the histone variant H2A.Z and both are required for androgen receptor-mediated gene activation. Nucleic Acids Research, 2011, 39, 3529-3542.	6.5	111
1406	Tissue-specific regulation of mouse MicroRNA genes in endoderm-derived tissues. Nucleic Acids Research, 2011, 39, 454-463.	6.5	51
1407	DNA methyltransferase 3b preferentially associates with condensed chromatin. Nucleic Acids Research, 2011, 39, 874-888.	6.5	34
1408	Systematic bias in high-throughput sequencing data and its correction by BEADS. Nucleic Acids Research, 2011, 39, e103-e103.	6.5	137
1409	Substance-specific and shared transcription and epigenetic changes in the human hippocampus chronically exposed to cocaine and alcohol. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 6626-6631.	3.3	214
1410	Genetic framework for GATA factor function in vascular biology. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 13641-13646.	3.3	96
1411	Brain-specific Expression of N-Acetylglucosaminyltransferase IX (GnT-IX) Is Regulated by Epigenetic Histone Modifications. Journal of Biological Chemistry, 2011, 286, 31875-31884.	1.6	45
1412	Sequential changes at differentiation gene promoters as they become active in a stem cell lineage. Development (Cambridge), 2011, 138, 2441-2450.	1.2	49
1413	Identifying transcriptional start sites of human microRNAs based on high-throughput sequencing data. Nucleic Acids Research, 2011, 39, 9345-9356.	6.5	149
1414	In the loop: long range chromatin interactions and gene regulation. Briefings in Functional Genomics, 2011, 10, 3-10.	1.3	71
1415	PROMoter uPstream Transcripts share characteristics with mRNAs and are produced upstream of all three major types of mammalian promoters. Nucleic Acids Research, 2011, 39, 7179-7193.	6.5	139
1416	Rapid innovation in ChIP-seq peak-calling algorithms is outdistancing benchmarking efforts. Briefings in Bioinformatics, 2011, 12, 626-633.	3.2	40
1417	Long-Distance Regulation of Fetal VδGene Segment TRDV4 by the Tcrd Enhancer. Journal of Immunology, 2011, 187, 2484-2491.	0.4	20
1418	Human Th1 and Th17 Cells Exhibit Epigenetic Stability at Signature Cytokine and Transcription Factor Loci. Journal of Immunology, 2011, 187, 5615-5626.	0.4	109
1419	Transcriptional and epigenetic regulation of the p53 tumor suppressor gene. Epigenetics, 2011, 6, 1068-1077.	1.3	92
1420	DOT1L regulates dystrophin expression and is critical for cardiac function. Genes and Development, 2011, 25, 263-274.	2.7	129
1421	Posttranslational Histone Modifications and the Neurobiology of Psychosis. , 2011, , 1-21.		0
1422	Global Identification of Androgen Response Elements. Methods in Molecular Biology, 2011, 776, 255-273.	0.4	14

#	Article	IF	CITATIONS
1423	A manually curated ChIP-seq benchmark demonstrates room for improvement in current peak-finder programs. Nucleic Acids Research, 2011, 39, e25-e25.	6.5	62
1424	Selective targeting of histone methylation. Cell Cycle, 2011, 10, 413-424.	1.3	32
1425	Class I and III HDACs and loss of active chromatin features contribute to epigenetic silencing of <i>CDX1</i> and <i>EPHB</i> tumor suppressor genes in colorectal cancer. Epigenetics, 2011, 6, 610-622.	1.3	24
1426	Epigenomic and RNA structural correlates of polyadenylation. RNA Biology, 2011, 8, 529-537.	1.5	20
1427	Dynamic nature of transcriptional regulation of nuclear receptor target genes in the context of chromatin organization. Dermato-Endocrinology, 2011, 3, 125-129.	1.9	2
1428	In vitro functional effects of XPC gene rare variants from bladder cancer patients. Carcinogenesis, 2011, 32, 516-521.	1.3	10
1429	The Decade of the Epigenomes?. Genes and Cancer, 2011, 2, 680-687.	0.6	16
1430	The histone methyltransferase Set7/9 promotes myoblast differentiation and myofibril assembly. Journal of Cell Biology, 2011, 194, 551-565.	2.3	99
1431	NF-Y affects histone acetylation and H2A.Z deposition in cell cycle promoters. Epigenetics, 2011, 6, 526-534.	1.3	15
1432	RB regulation of developmental transcriptional programs. Fly, 2011, 5, 115-118.	0.9	1
1433	Drosophila dosage compensation. Fly, 2011, 5, 147-154.	0.9	26
1434	An Evolutionarily Conserved TNF-α–Responsive Enhancer in the Far Upstream Region of Human <i>CCL2</i> Locus Influences Its Gene Expression. Journal of Immunology, 2011, 186, 7025-7038.	0.4	13
1435	Direct Recruitment of Insulin Receptor and ERK Signaling Cascade to Insulin-Inducible Gene Loci. Diabetes, 2011, 60, 127-137.	0.3	39
1436	Genomic Profiling of HMGN1 Reveals an Association with Chromatin at Regulatory Regions. Molecular and Cellular Biology, 2011, 31, 700-709.	1.1	44
1437	JmjN interacts with JmjC to ensure selective proteolysis of Gis1 by the proteasome. Microbiology (United Kingdom), 2011, 157, 2694-2701.	0.7	28
1438	Stable and dynamic nucleosome states during a meiotic developmental process. Genome Research, 2011, 21, 875-884.	2.4	75
1439	TbISWI Regulates Multiple Polymerase I (Pol I)-Transcribed Loci and Is Present at Pol II Transcription Boundaries in Trypanosoma brucei. Eukaryotic Cell, 2011, 10, 964-976.	3.4	35
1440	Patterns of Histone H3 Lysine 27 Monomethylation and Erythroid Cell Type-specific Gene Expression. Journal of Biological Chemistry, 2011, 286, 39457-39465.	1.6	22

#	Article	IF	CITATIONS
1441	CTCF Promotes Muscle Differentiation by Modulating the Activity of Myogenic Regulatory Factors. Journal of Biological Chemistry, 2011, 286, 12483-12494.	1.6	48
1442	Functional Analysis of KAP1 Genomic Recruitment. Molecular and Cellular Biology, 2011, 31, 1833-1847.	1.1	99
1443	Human Polymerase-Associated Factor complex (PAFc) connects the Super Elongation Complex (SEC) to RNA polymerase II on chromatin. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, E636-45.	3.3	160
1444	A Novel Disrupter of Telomere Silencing 1-like (DOT1L) Interaction Is Required for Signal Transducer and Activator of Transcription 1 (STAT1)-activated Gene Expression. Journal of Biological Chemistry, 2011, 286, 41195-41204.	1.6	12
1445	Human imprinted retrogenes exhibit non-canonical imprint chromatin signatures and reside in non-imprinted host genes. Nucleic Acids Research, 2011, 39, 4577-4586.	6.5	22
1446	The Structure of NSD1 Reveals an Autoregulatory Mechanism Underlying Histone H3K36 Methylation. Journal of Biological Chemistry, 2011, 286, 8361-8368.	1.6	157
1447	Mouse Rankl Expression Is Regulated in T Cells by c-Fos through a Cluster of Distal Regulatory Enhancers Designated the T Cell Control Region. Journal of Biological Chemistry, 2011, 286, 20880-20891.	1.6	42
1448	EZH1 and EZH2 cogovern histone H3K27 trimethylation and are essential for hair follicle homeostasis and wound repair. Genes and Development, 2011, 25, 485-498.	2.7	332
1449	IL-2 Regulates Expression of <i>C-MAF</i> in Human CD4 T Cells. Journal of Immunology, 2011, 187, 3721-3729.	0.4	29
1450	The complex transcription regulatory landscape of our genome: control in three dimensions. EMBO Journal, 2011, 30, 4345-4355.	3.5	59
1451	Role of the PWWP Domain of Lens Epithelium-derived Growth Factor (LEDGF)/p75 Cofactor in Lentiviral Integration Targeting. Journal of Biological Chemistry, 2011, 286, 41812-41826.	1.6	39
1452	Epigenetic virtues of chromodomains. Critical Reviews in Biochemistry and Molecular Biology, 2011, 46, 507-526.	2.3	56
1453	The Brd4 Extraterminal Domain Confers Transcription Activation Independent of pTEFb by Recruiting Multiple Proteins, Including NSD3. Molecular and Cellular Biology, 2011, 31, 2641-2652.	1.1	450
1454	Tissue-specific prediction of directly regulated genes. Bioinformatics, 2011, 27, 2354-2360.	1.8	7
1455	Predicting promoter activities of primary human DNA sequences. Nucleic Acids Research, 2011, 39, e75-e75.	6.5	10
1456	Discovering Transcription Factor Binding Sites in Highly Repetitive Regions of Genomes with Multi-Read Analysis of ChIP-Seq Data. PLoS Computational Biology, 2011, 7, e1002111.	1.5	73
1457	Epigenetically coordinated GATA2 binding is necessary for endothelium-specific <i>endomucin</i> expression. EMBO Journal, 2011, 30, 2582-2595.	3.5	68
1458	Mechanisms of Histone Modifications. , 2011, , 25-45.		7

	CHATION N		
#	Article	IF	CITATIONS
1459	Sculpting Chromatin Beyond the Double Helix. Current Topics in Developmental Biology, 2011, 96, 57-83.	1.0	25
1460	Transcription Initiation Patterns Indicate Divergent Strategies for Gene Regulation at the Chromatin Level. PLoS Genetics, 2011, 7, e1001274.	1.5	124
1461	A New Isoform of the Histone Demethylase JMJD2A/KDM4A Is Required for Skeletal Muscle Differentiation. PLoS Genetics, 2011, 7, e1001390.	1.5	59
1462	Expression of P. falciparum var Genes Involves Exchange of the Histone Variant H2A.Z at the Promoter. PLoS Pathogens, 2011, 7, e1001292.	2.1	95
1463	Apoptosis and DNA Methylation. Cancers, 2011, 3, 1798-1820.	1.7	25
1464	DNA methylation status predicts cell type-specific enhancer activity. EMBO Journal, 2011, 30, 3028-3039.	3.5	203
1465	The tumour antigen PRAME is a subunit of a Cul2 ubiquitin ligase and associates with active NFY promoters. EMBO Journal, 2011, 30, 3786-3798.	3.5	59
1466	Epigenetic Regulation of Learning and Memory by Drosophila EHMT/G9a. PLoS Biology, 2011, 9, e1000569.	2.6	185
1467	Dual role of FoxA1 in androgen receptor binding to chromatin, androgen signalling and prostate cancer. EMBO Journal, 2011, 30, 3962-3976.	3.5	318
1468	Jarid1b targets genes regulating development and is involved in neural differentiation. EMBO Journal, 2011, 30, 4586-4600.	3.5	183
1469	DNA Methylation and Histone Modifications Regulate De Novo Shoot Regeneration in Arabidopsis by Modulating WUSCHEL Expression and Auxin Signaling. PLoS Genetics, 2011, 7, e1002243.	1.5	201
1470	T-Cell Identity and Epigenetic Memory. Current Topics in Microbiology and Immunology, 2011, 356, 117-143.	0.7	13
1471	Polycomb-mediated repression during terminal differentiation: what don't you want to be when you grow up?: Figure 1 Genes and Development, 2011, 25, 997-1003.	2.7	17
1472	Chromatin Insulators: A Role in Nuclear Organization and Gene Expression. Advances in Cancer Research, 2011, 110, 43-76.	1.9	54
1473	Loss of H2A.Z Is Not Sufficient to Determine Transcriptional Activity of Snf2-Related CBP Activator Protein or p400 Complexes. International Journal of Cell Biology, 2011, 2011, 1-8.	1.0	8
1474	Combinatorial chromatin modification patterns in the human genome revealed by subspace clustering. Nucleic Acids Research, 2011, 39, 4063-4075.	6.5	49
1475	Characterization of STAT6 Target Genes in Human B Cells and Lung Epithelial Cells. DNA Research, 2011, 18, 379-392.	1.5	20
1476	Plant homeodomain fingers form a helping hand for transcription. Epigenetics, 2011, 6, 4-8.	1.3	52

#	Article	IF	CITATIONS
1477	Coordination of KSHV Latent and Lytic Gene Control by CTCF-Cohesin Mediated Chromosome Conformation. PLoS Pathogens, 2011, 7, e1002140.	2.1	100
1478	Mouse PRDM9 DNA-Binding Specificity Determines Sites of Histone H3 Lysine 4 Trimethylation for Initiation of Meiotic Recombination. PLoS Biology, 2011, 9, e1001176.	2.6	187
1479	Epigenetic Regulation by Lysine Demethylase 5 (KDM5) Enzymes in Cancer. Cancers, 2011, 3, 1383-1404.	1.7	136
1480	Epigenetic Regulation of Glucose Transporters in Non-Small Cell Lung Cancer. Cancers, 2011, 3, 1550-1565.	1.7	26
1481	Mechanisms Establishing TLR4-Responsive Activation States of Inflammatory Response Genes. PLoS Genetics, 2011, 7, e1002401.	1.5	146
1482	A High-Resolution Whole-Genome Map of Key Chromatin Modifications in the Adult Drosophila melanogaster. PLoS Genetics, 2011, 7, e1002380.	1.5	51
1483	The Motility of a Human Parasite, Toxoplasma gondii, Is Regulated by a Novel Lysine Methyltransferase. PLoS Pathogens, 2011, 7, e1002201.	2.1	92
1484	Epigenetic profile of the euchromatic region of human Y chromosome. Nucleic Acids Research, 2011, 39, 3594-3606.	6.5	19
1485	Epigenetic silencing of the oncogenic miR-17-92 cluster during PU.1-directed macrophage differentiation. EMBO Journal, 2011, 30, 4450-4464.	3.5	85
1486	Profiling RNA Polymerase II Using the Fast Chromatin Immunoprecipitation Method. Methods in Molecular Biology, 2011, 703, 219-234.	0.4	5
1487	Target Genes of Vitamin D. , 2011, , 211-226.		2
1488	A rank-based statistical test for measuring synergistic effects between two gene sets. Bioinformatics, 2011, 27, 2399-2405.	1.8	3
1489	The chromatin-binding protein HMGN3 stimulates histone acetylation and transcription across the <i>Glyt1</i> gene. Biochemical Journal, 2012, 442, 495-505.	1.7	17
1490	CTCFBSDB 2.0: a database for CTCF-binding sites and genome organization. Nucleic Acids Research, 2012, 41, D188-D194.	6.5	143
1491	The histone methyltransferase Setd8 acts in concert with c-Myc and is required to maintain skin. EMBO Journal, 2012, 31, 616-629.	3.5	71
1492	Spi-1/PU.1 activates transcription through clustered DNA occupancy in erythroleukemia. Nucleic Acids Research, 2012, 40, 8927-8941.	6.5	20
1493	Tackling Skeletal Muscle Cells Epigenome in the Next-Generation Sequencing Era. Comparative and Functional Genomics, 2012, 2012, 1-8.	2.0	3
1494	Predictive Models of Gene Regulation from High-Throughput Epigenomics Data. Comparative and Functional Genomics, 2012, 2012, 1-13.	2.0	10

# 1495	ARTICLE Genome-Wide RNA Polymerase II Profiles and RNA Accumulation Reveal Kinetics of Transcription and Associated Epigenetic Changes During Diurnal Cycles. PLoS Biology, 2012, 10, e1001442.	IF 2.6	CITATIONS
1496	Proximity of H2A.Z containing nucleosome to the transcription start site influences gene expression levels in the mammalian liver and brain. Nucleic Acids Research, 2012, 40, 8965-8978.	6.5	41
1497	H4K20me1 Contributes to Downregulation of X-Linked Genes for C. elegans Dosage Compensation. PLoS Genetics, 2012, 8, e1002933.	1.5	70
1498	Analysis of active chromatin modifications in early mammalian embryos reveals uncoupling of H2A.Z acetylation and H3K36 trimethylation from embryonic genome activation. Epigenetics, 2012, 7, 747-757.	1.3	67
1499	Detecting genomic indel variants with exact breakpoints in single- and paired-end sequencing data using SplazerS. Bioinformatics, 2012, 28, 619-627.	1.8	95
1500	Genome-Wide Localization of Protein-DNA Binding and Histone Modification by a Bayesian Change-Point Method with ChIP-seq Data. PLoS Computational Biology, 2012, 8, e1002613.	1.5	68
1501	Gene Reactivation by 5-Aza-2′-Deoxycytidine–Induced Demethylation Requires SRCAP–Mediated H2A.Z Insertion to Establish Nucleosome Depleted Regions. PLoS Genetics, 2012, 8, e1002604.	1.5	52
1502	Two Distinct Repressive Mechanisms for Histone 3 Lysine 4 Methylation through Promoting 3â€2-End Antisense Transcription. PLoS Genetics, 2012, 8, e1002952.	1.5	131
1503	Deposition of Histone Variant H2A.Z within Gene Bodies Regulates Responsive Genes. PLoS Genetics, 2012, 8, e1002988.	1.5	329
1504	Transcription Elongation and Tissue-Specific Somatic CAG Instability. PLoS Genetics, 2012, 8, e1003051.	1.5	56
1505	Molecular and Epigenetic Mechanisms of MLL in Human Leukemogenesis. Cancers, 2012, 4, 904-944.	1.7	34
1506	<i>Candida albicans</i> : A Model Organism for Studying Fungal Pathogens. , 2012, 2012, 1-15.		105
1507	MLL1, a Histone H3K4 Methyltransferase, Regulates the Expression of TNFα-mediated NF-κB Downstream Genes. Journal of Cell Science, 2012, 125, 4058-66.	1.2	63
1508	GMD: measuring the distance between histograms with applications on high-throughput sequencing reads. Bioinformatics, 2012, 28, 1164-1165.	1.8	16
1509	Transcriptional Regulation of Rod Photoreceptor Homeostasis Revealed by In Vivo NRL Targetome Analysis. PLoS Genetics, 2012, 8, e1002649.	1.5	99
1510	Hepatic ontogeny and tissue distribution of mRNAs of epigenetic modifiers in mice using RNA-sequencing. Epigenetics, 2012, 7, 914-929.	1.3	31
1511	Single Molecule Tools Elucidate H2A.Z Nucleosome Composition. Journal of Cell Science, 2012, 125, 2954-64.	1.2	39
1512	Computational inference of mRNA stability from histone modification and transcriptome profiles. Nucleic Acids Research, 2012, 40, 6414-6423.	6.5	16

#	Article	IF	CITATIONS
1513	Mouse model of endemic Burkitt translocations reveals the long-range boundaries of <i>lg</i> -mediated oncogene deregulation. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 10972-10977.	3.3	25
1514	Chromatin signature discovery via histone modification profile alignments. Nucleic Acids Research, 2012, 40, 10642-10656.	6.5	19
1515	An insulator loop resides between the synthetically interacting elements of the human/rat conserved breast cancer susceptibility locus MCS5A/Mcs5a. Nucleic Acids Research, 2012, 40, 132-147.	6.5	34
1516	Retargeting transposon insertions by the adeno-associated virus Rep protein. Nucleic Acids Research, 2012, 40, 6693-6712.	6.5	57
1517	Genome-wide analyses reveal the extent of opportunistic STAT5 binding that does not yield transcriptional activation of neighboring genes. Nucleic Acids Research, 2012, 40, 4461-4472.	6.5	38
1518	Acetylation of H2A.Z is a key epigenetic modification associated with gene deregulation and epigenetic remodeling in cancer. Genome Research, 2012, 22, 307-321.	2.4	155
1519	Epigenetic regulation by RARα maintains ligand-independent transcriptional activity. Nucleic Acids Research, 2012, 40, 102-115.	6.5	49
1520	Higher-Order Chromatin Regulation and Differential Gene Expression in the Human Tumor Necrosis Factor/Lymphotoxin Locus in Hepatocellular Carcinoma Cells. Molecular and Cellular Biology, 2012, 32, 1529-1541.	1.1	26
1521	High-resolution mapping of open chromatin in the rice genome. Genome Research, 2012, 22, 151-162.	2.4	205
1522	Genome-wide characterization of Foxa2 targets reveals upregulation of floor plate genes and repression of ventrolateral genes in midbrain dopaminergic progenitors. Development (Cambridge), 2012, 139, 2625-2634.	1.2	55
1523	Mutation of A677 in histone methyltransferase EZH2 in human B-cell lymphoma promotes hypertrimethylation of histone H3 on lysine 27 (H3K27). Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 2989-2994.	3.3	445
1524	Replicating and transcribing on twisted roads of chromatin. Briefings in Functional Genomics, 2012, 11, 188-204.	1.3	7
1525	A highly efficient and effective motif discovery method for ChIP-seq/ChIP-chip data using positional information. Nucleic Acids Research, 2012, 40, e50-e50.	6.5	32
1526	Association of the interferon-β gene with pericentromeric heterochromatin is dynamically regulated during virus infection through a YY1-dependent mechanism. Nucleic Acids Research, 2012, 40, 4396-4411.	6.5	8
1527	<i>SLC45A3-ELK4</i> Chimera in Prostate Cancer: Spotlight on <i>cis</i> -Splicing. Cancer Discovery, 2012, 2, 582-585.	7.7	40
1528	Cell type–specific genomics of Drosophila neurons. Nucleic Acids Research, 2012, 40, 9691-9704.	6.5	138
1529	WRAD: enabler of the SET1-family of H3K4 methyltransferases. Briefings in Functional Genomics, 2012, 11, 217-226.	1.3	114
1530	Total kinetic analysis reveals how combinatorial methylation patterns are established on lysines 27 and 36 of histone H3. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 13549-13554.	3.3	129

#	Article	IF	CITATIONS
1531	Integrated analysis identifies a class of androgen-responsive genes regulated by short combinatorial long-range mechanism facilitated by CTCF. Nucleic Acids Research, 2012, 40, 4754-4764.	6.5	39
1532	Epigenetics and stroke risk – beyond the static DNA code. Advances in Genomics and Genetics, 2012, , 67.	0.8	2
1533	The chromatin insulator CTCF and the emergence of metazoan diversity. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 17507-17512.	3.3	161
1534	H2B monoubiquitylation is a 5′-enriched active transcription mark and correlates with exon–intron structure in human cells. Genome Research, 2012, 22, 1026-1035.	2.4	60
1535	Improved predictions of transcription factor binding sites using physicochemical features of DNA. Nucleic Acids Research, 2012, 40, e175-e175.	6.5	30
1536	Regulation of u-PAR gene expression by H2A.Z is modulated by the MEK–ERK/AP-1 pathway. Nucleic Acids Research, 2012, 40, 600-613.	6.5	17
1537	HIF-1α-induced histone demethylase JMJD2B contributes to the malignant phenotype of colorectal cancer cells via an epigenetic mechanism. Carcinogenesis, 2012, 33, 1664-1673.	1.3	80
1538	dKDM5/LID regulates H3K4me3 dynamics at the transcription-start site (TSS) of actively transcribed developmental genes. Nucleic Acids Research, 2012, 40, 9493-9505.	6.5	47
1539	FANCJ coordinates two pathways that maintain epigenetic stability at G-quadruplex DNA. Nucleic Acids Research, 2012, 40, 1485-1498.	6.5	184
1540	Choline Nutrition Programs Brain Development Via DNA and Histone Methylation. Central Nervous System Agents in Medicinal Chemistry, 2012, 12, 82-94.	0.5	75
1541	The p400/Brd8 Chromatin Remodeling Complex Promotes Adipogenesis by Incorporating Histone Variant H2A.Z at PPARÎ ³ Target Genes. Endocrinology, 2012, 153, 5796-5808.	1.4	20
1542	Gene-Specific Patterns of Coregulator Requirements by Estrogen Receptor-α in Breast Cancer Cells. Molecular Endocrinology, 2012, 26, 955-966.	3.7	62
1543	PRC2 directly methylates GATA4 and represses its transcriptional activity. Genes and Development, 2012, 26, 37-42.	2.7	232
1544	Cell-type specific and combinatorial usage of diverse transcription factors revealed by genome-wide binding studies in multiple human cells. Genome Research, 2012, 22, 9-24.	2.4	119
1545	A multiplicity of factors contributes to selective RNA polymerase III occupancy of a subset of RNA polymerase III genes in mouse liver. Genome Research, 2012, 22, 666-680.	2.4	56
1546	Liganded Thyroid Hormone Receptor Induces Nucleosome Removal and Histone Modifications to Activate Transcription during Larval Intestinal Cell Death and Adult Stem Cell Development. Endocrinology, 2012, 153, 961-972.	1.4	44
1547	Local chromatin dynamics of transcription factors imply cell-lineage specific functions during cellular differentiation. Epigenetics, 2012, 7, 55-62.	1.3	5
1548	Experimental and Computational Challenges from Array-Based to Sequence-Based ChIP Techniques. Current Bioinformatics, 2012, 7, 447-453.	0.7	2

# 1549	ARTICLE Involvement of long noncoding RNAs in diseases affecting the central nervous system. RNA Biology, 2012, 9, 860-870.	IF 1.5	Citations 93
1550	The relationship between gene transcription and combinations of histone modifications. , 2012, , .		0
1551	Epigenetic priors for identifying active transcription factor binding sites. Bioinformatics, 2012, 28, 56-62.	1.8	103
1552	ΔNp63α represses anti-proliferative genes via H2A.Z deposition. Genes and Development, 2012, 26, 2325-2336.	2.7	51
1553	Whole-genome bisulfite DNA sequencing of a DNMT3B mutant patient. Epigenetics, 2012, 7, 542-550.	1.3	68
1554	Silencing of <i>Wnt5a</i> during colon cancer metastasis involves histone modifications. Epigenetics, 2012, 7, 551-558.	1.3	41
1555	CTCF-dependent chromatin insulator as a built-in attenuator of angiogenesis. Transcription, 2012, 3, 73-77.	1.7	10
1556	The endoglycosidase heparanase enters the nucleus of T lymphocytes and modulates H3 methylation at actively transcribed genes via the interplay with key chromatin modifying enzymes. Transcription, 2012, 3, 130-145.	1.7	58
1557	Mapping enhancer and promoter interactions. Cell Research, 2012, 22, 789-790.	5.7	7
1558	Dense Chromatin Activates Polycomb Repressive Complex 2 to Regulate H3 Lysine 27 Methylation. Science, 2012, 337, 971-975.	6.0	240
1559	Epigenetics of drug abuse: predisposition or response. Pharmacogenomics, 2012, 13, 1149-1160.	0.6	104
1560	Nextâ€generation sequencing applications for wheat crop improvement. American Journal of Botany, 2012, 99, 365-371.	0.8	98
1561	T-bet and GATA3 orchestrate Th1 and Th2 differentiation through lineage-specific targeting of distal regulatory elements. Nature Communications, 2012, 3, 1268.	5.8	292
1562	The Chromatin Fingerprint of Gene Enhancer Elements. Journal of Biological Chemistry, 2012, 287, 30888-30896.	1.6	77
1563	Uncovering Transcription Factor Modules Using One- and Three-dimensional Analyses. Journal of Biological Chemistry, 2012, 287, 30914-30921.	1.6	7
1564	Identification and Characterization of Nardilysin as a Novel Dimethyl H3K4-binding Protein Involved in Transcriptional Regulation. Journal of Biological Chemistry, 2012, 287, 10089-10098.	1.6	31
1565	Integration of Hi-C and ChIP-seq data reveals distinct types of chromatin linkages. Nucleic Acids Research, 2012, 40, 7690-7704.	6.5	94
1566	Identification of Core DNA Elements That Target Somatic Hypermutation. Journal of Immunology, 2012, 189, 5314-5326.	0.4	26

#	Article	IF	CITATIONS
1567	Application of Ultra-High Throughput Sequencing and Microarray Technologies in Pharmacogenomics Testing. , 2012, , 143-159.		2
1568	SMYD3 Promotes Cancer Invasion by Epigenetic Upregulation of the Metalloproteinase <i>MMP-9</i> . Cancer Research, 2012, 72, 810-820.	0.4	161
1569	Quantitative Assessment of Chromatin Immunoprecipitation Grade Antibodies Directed against Histone Modifications Reveals Patterns of Co-occurring Marks on Histone Protein Molecules. Molecular and Cellular Proteomics, 2012, 11, 128-137.	2.5	71
1570	Common Genetic Variation in the 3′- <i>BCL11B</i> Gene Desert Is Associated With Carotid-Femoral Pulse Wave Velocity and Excess Cardiovascular Disease Risk. Circulation: Cardiovascular Genetics, 2012, 5, 81-90.	5.1	90
1571	POLYPHEMUS: R package for comparative analysis of RNA polymerase II ChIP-seq profiles by non-linear normalization. Nucleic Acids Research, 2012, 40, e30-e30.	6.5	7
1572	H3K4 demethylation by Jarid1a and Jarid1b contributes to retinoblastoma-mediated gene silencing during cellular senescence. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 8971-8976.	3.3	141
1573	Retinoic acid and androgen receptors combine to achieve tissue specific control of human prostatic transglutaminase expression: a novel regulatory network with broader significance. Nucleic Acids Research, 2012, 40, 4825-4840.	6.5	26
1574	Pre-B cell to macrophage transdifferentiation without significant promoter DNA methylation changes. Nucleic Acids Research, 2012, 40, 1954-1968.	6.5	37
1575	Term myometrium is characterized by increased activating epigenetic modifications at the progesterone receptor-A promoter. Molecular Human Reproduction, 2012, 18, 401-409.	1.3	29
1576	Aberrant epigenetic landscape in intellectual disability. Progress in Brain Research, 2012, 197, 53-71.	0.9	23
1577	The Histone Demethylase Jhdm1a Regulates Hepatic Gluconeogenesis. PLoS Genetics, 2012, 8, e1002761.	1.5	20
1578	Gentechnische Methoden. , 2012, , .		9
1579	Changes of the Nucleolus Architecture in Absence of the Nuclear Factor CTCF. Cytogenetic and Genome Research, 2012, 136, 89-96.	0.6	12
1580	Regulation of GATA Factor Expression Is Distinct between Erythroid and Mast Cell Lineages. Molecular and Cellular Biology, 2012, 32, 4742-4755.	1.1	21
1581	A fully Bayesian hidden Ising model for ChIP-seq data analysis. Biostatistics, 2012, 13, 113-128.	0.9	15
1582	Proteome analysis of protein partners to nucleosomes containing canonical H2A or the variant histones H2A.Z or H2A.X. Biological Chemistry, 2012, 393, 47-61.	1.2	14
1583	17AAG Treatment Accelerates Doxorubicin Induced Cellular Senescence: Hsp90 Interferes with Enforced Senescence of Tumor Cells. Drug Target Insights, 2012, 6, DTI.S9943.	0.9	11
1584	Genome-Scale Technology Driven Advances to Research into Normal and Malignant Haematopoiesis. Scientifica, 2012, 2012, 1-11.	0.6	0

#	Article	IF	CITATIONS
1585	Transcriptional activation of the <i>IL31</i> gene by NFAT and STAT6. Journal of Leukocyte Biology, 2011, 91, 245-257.	1.5	24
1586	Defining the molecular blueprint that drives CD8+ T cell differentiation in response to infection. Frontiers in Immunology, 2012, 3, 371.	2.2	23
1587	Genomic and bioinformatics tools to understand the biology of signal transducers and activators of transcription. Hormone Molecular Biology and Clinical Investigation, 2012, 10, 207-10.	0.3	0
1588	Diabetes-induced Epigenetic Signature in Vascular Cells. Endocrine, Metabolic and Immune Disorders - Drug Targets, 2012, 12, 107-117.	0.6	7
1589	Epigenetic Control and Cancer: The Potential of Histone Demethylases as Therapeutic Targets. Pharmaceuticals, 2012, 5, 963-990.	1.7	18
1590	Epigenetic Alterations in Bladder Cancer and Their Potential Clinical Implications. Advances in Urology, 2012, 2012, 1-11.	0.6	24
1591	DBTSS: DataBase of Transcriptional Start Sites progress report in 2012. Nucleic Acids Research, 2012, 40, D150-D154.	6.5	112
1592	Linking prenatal maternal adversity to developmental outcomes in infants: The role of epigenetic pathways. Development and Psychopathology, 2012, 24, 1361-1376.	1.4	383
1593	Finding a Balance: How Diverse Dosage Compensation Strategies Modify Histone H4 to Regulate Transcription. Genetics Research International, 2012, 2012, 1-12.	2.0	5
1594	Integrative analysis of the zinc finger transcription factor Lame duck in the <i>Drosophila</i> myogenic gene regulatory network. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 20768-20773.	3.3	23
1595	<i>Tcra</i> gene recombination is supported by a <i>Tcra</i> enhancer- and CTCF-dependent chromatin hub. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E3493-502.	3.3	79
1596	Role of Runt-related Transcription Factor 3 (RUNX3) in Transcription Regulation of Natural Cytotoxicity Receptor 1 (NCR1/NKp46), an Activating Natural Killer (NK) Cell Receptor. Journal of Biological Chemistry, 2012, 287, 7324-7334.	1.6	32
1597	A Conserved Function for the H2A.Z C Terminus. Journal of Biological Chemistry, 2012, 287, 19148-19157.	1.6	32
1598	Signal analysis for genome-wide maps of histone modifications measured by ChIP-seq. Bioinformatics, 2012, 28, 1062-1069.	1.8	12
1599	CTCF Occupation of the Herpes Simplex Virus 1 Genome Is Disrupted at Early Times Postreactivation in a Transcription-Dependent Manner. Journal of Virology, 2012, 86, 12741-12759.	1.5	32
1600	Genome-wide prediction and analysis of human chromatin boundary elements. Nucleic Acids Research, 2012, 40, 511-529.	6.5	39
1601	Developmental regulation of N-terminal H2B methylation in Drosophila melanogaster. Nucleic Acids Research, 2012, 40, 1536-1549.	6.5	28
1602	The 19S proteasome subcomplex promotes the targeting of NuA4 HAT to the promoters of ribosomal protein genes to facilitate the recruitment of TFIID for transcriptional initiation in vivo. Nucleic Acids Research, 2012, 40, 1969-1983.	6.5	38

#	Article	IF	CITATIONS
1603	A novel ab initio identification system of transcriptional regulation motifs in genome DNA sequences based on direct comparison scheme of signal/noise distributions. Nucleic Acids Research, 2012, 40, 8835-8848.	6.5	7
1604	Epigenetic regulation of human cis -natural antisense transcripts. Nucleic Acids Research, 2012, 40, 1438-1445.	6.5	45
1605	Minireview: Applications of Next-Generation Sequencing on Studies of Nuclear Receptor Regulation and Function. Molecular Endocrinology, 2012, 26, 1651-1659.	3.7	9
1606	A Novel Bayesian Change-point Algorithm for Genome-wide Analysis of Diverse ChIPseq Data Types. Journal of Visualized Experiments, 2012, , e4273.	0.2	4
1607	Recent Advance in Epigenetics - Application to The Regulation of Osteoclast Differentiation. Current Rheumatology Reviews, 2012, 8, 103-108.	0.4	2
1608	On the Limitations of Biological Knowledge. Current Genomics, 2012, 13, 574-587.	0.7	15
1609	Chromatin measurements reveal contributions of synthesis and decay to steadyâ€state mRNA levels. Molecular Systems Biology, 2012, 8, 593.	3.2	48
1610	Genotyping-by-Sequencing in Plants. Biology, 2012, 1, 460-483.	1.3	315
1611	Chromatin accessibility, p300, and histone acetylation define PML-RARα and AML1-ETO binding sites in acute myeloid leukemia. Blood, 2012, 120, 3058-3068.	0.6	60
1612	Dynamic epigenetic enhancer signatures reveal key transcription factors associated with monocytic differentiation states. Blood, 2012, 119, e161-e171.	0.6	139
1613	Cancer Epigenomics. , 2012, , 129-159.		2
1614	The Application of the Next-Generation Sequencing Technologies in Cancer Research. , 2012, , 227-258.		0
1615	The role of WDR5 in silencing human fetal globin gene expression. Haematologica, 2012, 97, 1632-1640.	1.7	12
1617	Chromatin modification by SUMO-1 stimulates the promoters of translation machinery genes. Nucleic Acids Research, 2012, 40, 10172-10186.	6.5	64
1618	Enhancer-associated H3K4 monomethylation by Trithorax-related, the <i>Drosophila</i> homolog of mammalian Mll3/Mll4. Genes and Development, 2012, 26, 2604-2620.	2.7	327
1619	Pre-mRNA splicing: Role of epigenetics and implications in disease. Advances in Biological Regulation, 2012, 52, 377-388.	1.4	36
1620	LSD1 inhibition: a therapeutic strategy in cancer?. Expert Opinion on Therapeutic Targets, 2012, 16, 1239-1249.	1.5	112
1621	Histone H2A.Z inheritance during the cell cycle and its impact on promoter organization and dynamics. Nature Structural and Molecular Biology, 2012, 19, 1076-1083.	3.6	97

#	Article	IF	CITATIONS
1622	Histone Lysine Methylation Dynamics: Establishment, Regulation, and Biological Impact. Molecular Cell, 2012, 48, 491-507.	4.5	975
1623	Epigenetic mechanisms in antiâ€cancer actions of bioactive food components – the implications in cancer prevention. British Journal of Pharmacology, 2012, 167, 279-297.	2.7	157
1624	Threeâ€dimensional architecture of the IgH locus facilitates class switch recombination. Annals of the New York Academy of Sciences, 2012, 1267, 86-94.	1.8	25
1625	A High Throughput Scintillation Proximity Imaging Assay for Protein Methyltransferases. Combinatorial Chemistry and High Throughput Screening, 2012, 15, 359-371.	0.6	25
1626	The expanding scope of DNA sequencing. Nature Biotechnology, 2012, 30, 1084-1094.	9.4	280
1627	Interplay Between Social Experiences and the Genome: Epigenetic Consequences for Behavior. Advances in Genetics, 2012, 77, 33-57.	0.8	61
1628	ChIA-PET analysis of transcriptional chromatin interactions. Methods, 2012, 58, 289-299.	1.9	83
1629	Epigenetics of Host–Pathogen Interactions: The Road Ahead and the Road Behind. PLoS Pathogens, 2012, 8, e1003007.	2.1	205
1630	Mechanistic Links Between ATM and Histone Methylation Codes During DNA Repair. Progress in Molecular Biology and Translational Science, 2012, 110, 263-288.	0.9	16
1631	Genome-wide Epigenetic Data Facilitate Understanding of Disease Susceptibility Association Studies. Journal of Biological Chemistry, 2012, 287, 30932-30940.	1.6	49
1632	Epigenetic Regulation of Gene Expression in Keratinocytes. Journal of Investigative Dermatology, 2012, 132, 2505-2521.	0.3	111
1633	Mutant p53 is a transcriptional co-factor that binds to G-rich regulatory regions of active genes and generates transcriptional plasticity. Cell Cycle, 2012, 11, 3290-3303.	1.3	57
1634	Genome-wide Studies of CCCTC-binding Factor (CTCF) and Cohesin Provide Insight into Chromatin Structure and Regulation. Journal of Biological Chemistry, 2012, 287, 30906-30913.	1.6	88
1635	RNF8 regulates active epigenetic modifications and escape gene activation from inactive sex chromosomes in post-meiotic spermatids. Genes and Development, 2012, 26, 2737-2748.	2.7	108
1636	<i>Trans</i> -tail regulation of MLL4-catalyzed H3K4 methylation by H4R3 symmetric dimethylation is mediated by a tandem PHD of MLL4. Genes and Development, 2012, 26, 2749-2762.	2.7	181
1637	Blood chromatin as a biosensor of the epigenetic milieu: a tool for studies in living psychiatric patients. Epigenomics, 2012, 4, 551-559.	1.0	15
1638	PR-Set7 and H4K20me1: at the crossroads of genome integrity, cell cycle, chromosome condensation, and transcription. Genes and Development, 2012, 26, 325-337.	2.7	264
1639	DNA Methylation, H2A.Z, and the Regulation of Constitutive Expression. Cold Spring Harbor Symposia on Quantitative Biology, 2012, 77, 147-154.	2.0	47

#	Article	IF	CITATIONS
1640	A beginners guide to SNP calling from high-throughput DNA-sequencing data. Human Genetics, 2012, 131, 1541-1554.	1.8	92
1641	On WD40 proteins: Propelling our knowledge of transcriptional control?. Epigenetics, 2012, 7, 815-822.	1.3	61
1642	ESAT6 differentially inhibits IFNâ€Ĵ³â€inducible class II transactivator isoforms in both a TLR2â€dependent and â€independent manner. Immunology and Cell Biology, 2012, 90, 411-420.	1.0	35
1643	Morphine Epigenomically Regulates Behavior through Alterations in Histone H3 Lysine 9 Dimethylation in the Nucleus Accumbens. Journal of Neuroscience, 2012, 32, 17454-17464.	1.7	115
1644	Phosphorylated and sumoylation-deficient progesterone receptors drive proliferative gene signatures during breast cancer progression. Breast Cancer Research, 2012, 14, R95.	2.2	87
1645	Dissecting the regulatory architecture of gene expression QTLs. Genome Biology, 2012, 13, R7.	13.9	188
1646	What can epigenomics do for you?. Genome Biology, 2012, 13, 420.	13.9	9
1647	H2A.Z landscapes and dual modifications in pluripotent and multipotent stem cells underlie complex genome regulatory functions. Genome Biology, 2012, 13, R85.	13.9	166
1648	Non-genotoxic carcinogen exposure induces defined changes in the 5-hydroxymethylome. Genome Biology, 2012, 13, R93.	13.9	74
1649	Human genes with CpG island promoters have a distinct transcription-associated chromatin organization. Genome Biology, 2012, 13, R110.	13.9	98
1650	Proteogenomic characterization and mapping of nucleosomes decoded by Brd and HP1 proteins. Genome Biology, 2012, 13, R68.	13.9	81
1651	The mouse DXZ4 homolog retains Ctcf binding and proximity to Pls3 despite substantial organizational differences compared to the primate macrosatellite. Genome Biology, 2012, 13, R70.	13.9	39
1652	Classification of human genomic regions based on experimentally determined binding sites of more than 100 transcription-related factors. Genome Biology, 2012, 13, R48.	13.9	233
1653	The GENCODE pseudogene resource. Genome Biology, 2012, 13, R51.	13.9	273
1654	Cell type-specific binding patterns reveal that TCF7L2 can be tethered to the genome by association with GATA3. Genome Biology, 2012, 13, R52.	13.9	109
1655	Molecular biology techniques for the surgeon. World Journal of Surgical Procedures, 2012, 2, 5.	0.1	0
1656	Human Histone H3K79 Methyltransferase DOT1L Methyltransferase Binds Actively Transcribing RNA Polymerase II to Regulate Gene Expression. Journal of Biological Chemistry, 2012, 287, 39698-39709.	1.6	96
1657	Histone tail acetylation in brain occurs in an unpredictable fashion after death. Cell and Tissue Banking, 2012, 13, 597-606.	0.5	8

#	Article	IF	CITATIONS
1658	HACking the centromere chromatin code: insights from human artificial chromosomes. Chromosome Research, 2012, 20, 505-519.	1.0	40
1659	Calculation of nucleosomal DNA deformation energy: its implication for nucleosome positioning. Chromosome Research, 2012, 20, 889-902.	1.0	11
1660	Memetic algorithms for de novo motif-finding in biomedical sequences. Artificial Intelligence in Medicine, 2012, 56, 1-17.	3.8	3
1661	c-Myc Is a Universal Amplifier of Expressed Genes in Lymphocytes and Embryonic Stem Cells. Cell, 2012, 151, 68-79.	13.5	907
1662	First Exon Length Controls Active Chromatin Signatures and Transcription. Cell Reports, 2012, 2, 62-68.	2.9	159
1663	ChAP-MS: A Method for Identification of Proteins and Histone Posttranslational Modifications at a Single Genomic Locus. Cell Reports, 2012, 2, 198-205.	2.9	110
1664	Three Distinct Patterns of Histone H3Y41 Phosphorylation Mark Active Genes. Cell Reports, 2012, 2, 470-477.	2.9	54
1665	Linking DNA Methyltransferases to Epigenetic Marks and Nucleosome Structure Genome-wide in Human Tumor Cells. Cell Reports, 2012, 2, 1411-1424.	2.9	96
1666	Candida albicans Infection Affords Protection against Reinfection via Functional Reprogramming of Monocytes. Cell Host and Microbe, 2012, 12, 223-232.	5.1	926
1667	A conserved regulatory element located far downstream of the <i>gls</i> locus modulates <i>gls</i> expression through chromatin loop formation during myogenesis. FEBS Letters, 2012, 586, 3464-3470.	1.3	7
1668	The Transcription Factors Thpok and LRF Are Necessary and Partly Redundant for T Helper Cell Differentiation. Immunity, 2012, 37, 622-633.	6.6	39
1669	The Transcription Factor T-bet Is Induced by Multiple Pathways and Prevents an Endogenous Th2 Cell Program during Th1 Cell Responses. Immunity, 2012, 37, 660-673.	6.6	269
1670	Methyltransferase Inhibitor Adenosine Dialdehyde Suppresses Androgen Receptor Expression and Prostate Cancer Growth. Journal of Urology, 2012, 188, 300-306.	0.2	11
1671	Experimental approaches to identify cellular G-quadruplex structures and functions. Methods, 2012, 57, 84-92.	1.9	40
1672	Endophenotypes as a measure of suicidality. Journal of Applied Genetics, 2012, 53, 389-413.	1.0	14
1673	Epigenetics in the Central Nervous System. Current Geriatrics Reports, 2012, 1, 190-198.	1.1	2
1674	AID targeting is dependent on RNA polymerase II pausing. Seminars in Immunology, 2012, 24, 281-286.	2.7	42

#	Article	IF	CITATIONS
1676	ChIP-seq guidelines and practices of the ENCODE and modENCODE consortia. Genome Research, 2012, 22, 1813-1831.	2.4	1,708
1677	Chromatin Remodeling. Methods in Molecular Biology, 2012, , .	0.4	2
1678	Pharmacogene regulatory elements: from discovery to applications. Genome Medicine, 2012, 4, 45.	3.6	18
1679	Dissecting complex epigenetic alterations in human lupus. Arthritis Research and Therapy, 2012, 15, 201.	1.6	23
1680	Epigenetic changes in fetal hypothalamic energy regulating pathways are associated with maternal undernutrition and twinning. FASEB Journal, 2012, 26, 1694-1703.	0.2	110
1681	Peak detection of histone modifications based on ChIP-seq data in human genome. , 2012, , .		0
1682	Deep sequencing of subcellular RNA fractions shows splicing to be predominantly co-transcriptional in the human genome but inefficient for lncRNAs. Genome Research, 2012, 22, 1616-1625.	2.4	401
1683	CALM/AF10-positive leukemias show upregulation of genes involved in chromatin assembly and DNA repair processes and of genes adjacent to the breakpoint at 10p12. Leukemia, 2012, 26, 1012-1019.	3.3	35
1684	UVA-induced epigenetic regulation of P16INK4a in human epidermal keratinocytes and skin tumor derived cells. Photochemical and Photobiological Sciences, 2012, 11, 180-190.	1.6	30
1685	Ubiquitous heterogeneity and asymmetry of the chromatin environment at regulatory elements. Genome Research, 2012, 22, 1735-1747.	2.4	168
1686	Ordered Arrays of Native Chromatin Molecules for High-Resolution Imaging and Analysis. ACS Nano, 2012, 6, 7928-7934.	7.3	28
1687	Dynamic interaction between TAL1 oncoprotein and LSD1 regulates TAL1 function in hematopoiesis and leukemogenesis. Oncogene, 2012, 31, 5007-5018.	2.6	62
1688	p53-Independent regulation of p21Waf1/Cip1 expression and senescence by PRMT6. Nucleic Acids Research, 2012, 40, 9534-9542.	6.5	86
1689	Identification of a chronic obstructive pulmonary disease genetic determinant that regulates HHIP. Human Molecular Genetics, 2012, 21, 1325-1335.	1.4	143
1690	Genomic impact of cigarette smoke, with application to three smoking-related diseases. Critical Reviews in Toxicology, 2012, 42, 877-889.	1.9	63
1691	A unique H2A histone variant occupies the transcriptional start site of active genes. Nature Structural and Molecular Biology, 2012, 19, 25-30.	3.6	91
1692	Chimeric Transcript Generated by cis-Splicing of Adjacent Genes Regulates Prostate Cancer Cell Proliferation. Cancer Discovery, 2012, 2, 598-607.	7.7	137
1693	Enhancers: emerging roles in cell fate specification. EMBO Reports, 2012, 13, 423-430.	2.0	124

#	Article	IF	CITATIONS
1694	Somatic histone H3 alterations in pediatric diffuse intrinsic pontine gliomas and non-brainstem glioblastomas. Nature Genetics, 2012, 44, 251-253.	9.4	1,402
1695	Characterization of genome-wide enhancer-promoter interactions reveals co-expression of interacting genes and modes of higher order chromatin organization. Cell Research, 2012, 22, 490-503.	5.7	238
1696	Δ <i>Np63</i> knockout mice reveal its indispensable role as a master regulator of epithelial development and differentiation. Development (Cambridge), 2012, 139, 772-782.	1.2	245
1697	The GENCODE v7 catalog of human long noncoding RNAs: Analysis of their gene structure, evolution, and expression. Genome Research, 2012, 22, 1775-1789.	2.4	4,428
1698	Profiles of Epigenetic Histone Post-translational Modifications at Type 1 Diabetes Susceptible Genes. Journal of Biological Chemistry, 2012, 287, 16335-16345.	1.6	90
1699	Identification of Natural and Artificial DNA Substrates for Light-Activated LOV–HTH Transcription Factor EL222. Biochemistry, 2012, 51, 10024-10034.	1.2	59
1700	Histone H2A variants in nucleosomes and chromatin: more or less stable?. Nucleic Acids Research, 2012, 40, 10719-10741.	6.5	248
1701	Large chromatin domains in pluripotent and differentiated cells. Acta Biochimica Et Biophysica Sinica, 2012, 44, 48-53.	0.9	5
1702	Next generation sequencing in epigenetics: Insights and challenges. Seminars in Cell and Developmental Biology, 2012, 23, 192-199.	2.3	83
1703	Chronic Pain: Emerging Evidence for the Involvement of Epigenetics. Neuron, 2012, 73, 435-444.	3.8	240
1704	Histone Demethylases KDM4B and KDM6B Promotes Osteogenic Differentiation of Human MSCs. Cell Stem Cell, 2012, 11, 50-61.	5.2	264
1705	Transcriptional networks and chromatin remodeling controlling adipogenesis. Trends in Endocrinology and Metabolism, 2012, 23, 56-64.	3.1	234
1706	Exploring the application of high-throughput genomics technologies in the field of maternal-embryo communication. Theriogenology, 2012, 77, 717-737.	0.9	6
1707	Noncoding Transcription at Enhancers: General Principles and Functional Models. Annual Review of Genetics, 2012, 46, 1-19.	3.2	348
1708	Nuclear Organization and Genome Function. Annual Review of Cell and Developmental Biology, 2012, 28, 163-187.	4.0	99
1709	Epigenetic Signatures of Autism. Archives of General Psychiatry, 2012, 69, 314.	13.8	174
1710	A High-Throughput Chromatin Immunoprecipitation Approach Reveals Principles of Dynamic Gene Regulation in Mammals. Molecular Cell, 2012, 47, 810-822.	4.5	375
1711	Differential DNase I hypersensitivity reveals factor-dependent chromatin dynamics. Genome Research, 2012, 22, 1015-1025.	2.4	161

#	Article	IF	CITATIONS
1712	Discovering transcription factor regulatory targets using gene expression and binding data. Bioinformatics, 2012, 28, 206-213.	1.8	32
1713	Segmentation by sequestration. Nature Reviews Genetics, 2012, 13, 595-595.	7.7	0
1714	Modeling gene expression using chromatin features in various cellular contexts. Genome Biology, 2012, 13, R53.	13.9	231
1715	Three Murine Leukemia Virus Integration Regions within 100 Kilobases Upstream of <i>c-myb</i> Are Proximal to the 5′ Regulatory Region of the Gene through DNA Looping. Journal of Virology, 2012, 86, 10524-10532.	1.5	21
1716	Dynamic and Coordinated Epigenetic Regulation of Developmental Transitions in the Cardiac Lineage. Cell, 2012, 151, 206-220.	13.5	555
1717	Cohesins Repress Kaposi's Sarcoma-Associated Herpesvirus Immediate Early Gene Transcription during Latency. Journal of Virology, 2012, 86, 9454-9464.	1.5	67
1718	CpG island structure and trithorax/polycomb chromatin domains in human cells. Genomics, 2012, 100, 320-326.	1.3	35
1719	Mitochondrial regulation of epigenetics and its role in human diseases. Epigenetics, 2012, 7, 326-334.	1.3	129
1720	Genome-wide mapping of nucleosome positioning and DNA methylation within individual DNA molecules. Genome Research, 2012, 22, 2497-2506.	2.4	381
1721	Integration of ChIP-seq and machine learning reveals enhancers and a predictive regulatory sequence vocabulary in melanocytes. Genome Research, 2012, 22, 2290-2301.	2.4	64
1722	Dynamic MicroRNA Gene Transcription and Processing during T Cell Development. Journal of Immunology, 2012, 188, 3257-3267.	0.4	80
1723	The RNA polymerase II CTD coordinates transcription and RNA processing. Genes and Development, 2012, 26, 2119-2137.	2.7	513
1724	Emerging Epigenetic Targets and Therapies in Cancer Medicine. Cancer Discovery, 2012, 2, 405-413.	7.7	106
1725	KAP1 regulates gene networks controlling Tâ€cell development and responsiveness. FASEB Journal, 2012, 26, 4561-4575.	0.2	45
1726	Chromatin insulator elements: establishing barriers to set heterochromatin boundaries. Epigenomics, 2012, 4, 67-80.	1.0	63
1727	UHRF1 Double Tudor Domain and the Adjacent PHD Finger Act Together to Recognize K9me3-Containing Histone H3 Tail. Journal of Molecular Biology, 2012, 415, 318-328.	2.0	87
1728	Histone modification profiles characterize function-specific gene regulation. Journal of Theoretical Biology, 2012, 310, 132-142.	0.8	12
1729	Functional Association of Gdown1 with RNA Polymerase II Poised on Human Genes. Molecular Cell, 2012, 45, 38-50.	4.5	114

#	Article	IF	CITATIONS
1730	Cell-Type-Specific Control of Enhancer Activity by H3K9 Trimethylation. Molecular Cell, 2012, 46, 408-423.	4.5	91
1731	Independence of Repressive Histone Marks and Chromatin Compaction during Senescent Heterochromatic Layer Formation. Molecular Cell, 2012, 47, 203-214.	4.5	258
1732	The Histone Methyltransferase Wbp7 Controls Macrophage Function through GPI Glycolipid Anchor Synthesis. Immunity, 2012, 36, 572-585.	6.6	79
1733	Lessons from senescence: Chromatin maintenance in non-proliferating cells. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2012, 1819, 322-331.	0.9	60
1734	Precise deposition of histone H2A.Z in chromatin for genome expression and maintenance. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2012, 1819, 290-302.	0.9	94
1735	Discovering genome regulation with 3C and 3C-related technologies. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2012, 1819, 401-410.	0.9	34
1736	Epigenetic regulation of adipogenesis by histone methylation. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2012, 1819, 727-732.	0.9	80
1737	Co-transcriptional regulation of alternative pre-mRNA splicing. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2012, 1819, 673-683.	0.9	79
1738	The dual lives of bidirectional promoters. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2012, 1819, 688-693.	0.9	50
1739	Nicotinamide treatment reduces the levels of histone H3K4 trimethylation in the promoter of the mper1 circadian clock gene and blocks the ability of dexamethasone to induce the acute response. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2012, 1819, 877-884.	0.9	10
1740	Functional elements demarcated by histone modifications in breast cancer cells. Biochemical and Biophysical Research Communications, 2012, 418, 475-482.	1.0	28
1741	Cloning and characterization of the human SH3BP2 promoter. Biochemical and Biophysical Research Communications, 2012, 425, 25-32.	1.0	5
1742	Interaction between Î ³ -radiation and dietary folate starvation metabolically reprograms global hepatic histone H3 methylation at lysine 4 and lysine 27 residues. Food and Chemical Toxicology, 2012, 50, 464-472.	1.8	6
1743	Histone H2A.Z prepares the prostate specific antigen (PSA) gene for androgen receptor-mediated transcription and is upregulated in a model of prostate cancer progression. Cancer Letters, 2012, 315, 38-47.	3.2	55
1744	Extensive Promoter-Centered Chromatin Interactions Provide a Topological Basis for Transcription Regulation. Cell, 2012, 148, 84-98.	13.5	1,096
1745	Dynamic Transformations of Genome-wide Epigenetic Marking and Transcriptional Control Establish T Cell Identity. Cell, 2012, 149, 467-482.	13.5	313
1746	Cancer Epigenetics: From Mechanism to Therapy. Cell, 2012, 150, 12-27.	13.5	2,521
1747	Histone H3R2 Symmetric Dimethylation and Histone H3K4 Trimethylation Are Tightly Correlated in Eukaryotic Genomes. Cell Reports, 2012, 1, 83-90.	2.9	69

		CITATION RE	EPORT	
#	Article		IF	CITATIONS
1748	Transcriptional drivers of the T-cell lineage program. Current Opinion in Immunology, 20	12, 24, 132-138.	2.4	66
1749	Epigenetic mechanisms in tumorigenesis, tumor cell heterogeneity and drug resistance. Resistance Updates, 2012, 15, 21-38.	Drug	6.5	261
1750	Combinatorial complexity in chromatin structure and function: revisiting the histone co Opinion in Genetics and Development, 2012, 22, 148-155.	de. Current	1.5	245
1751	Targeting Epigenetic Readers in Cancer. New England Journal of Medicine, 2012, 367, 6	47-657.	13.9	363
1752	Epigenetic landscape and miRNA involvement during neural crest development. Develop Dynamics, 2012, 241, 1849-1856.	omental	0.8	28
1753	A yeast twoâ€hybrid screen identifies histone H2A.Z as a transcription factor ZNF24 int of Cellular Biochemistry, 2012, 113, 3411-3418.	eractor. Journal	1.2	4
1754	Predicting tissue specific cis-regulatory modules in the human genome using pairs of co motifs. BMC Bioinformatics, 2012, 13, 25.	-occurring	1.2	22
1755	A signal processing approach for enriched region detection in RNA polymerase II ChIP-se Bioinformatics, 2012, 13, S2.	q data. BMC	1.2	7
1756	Epigenetic features are significantly associated with alternative splicing. BMC Genomics	, 2012, 13, 123.	1.2	61
1757	Finding combinatorial histone code by semi-supervised biclustering. BMC Genomics, 20	12, 13, 301.	1.2	12
1758	Marek's disease virus infection induces widespread differential chromatin marks in i lines. BMC Genomics, 2012, 13, 557.	nbred chicken	1.2	17
1759	Euchromatin islands in large heterochromatin domains are enriched for CTCF binding ar differentially DNA-methylated regions. BMC Genomics, 2012, 13, 566.	d	1.2	40
1760	Limitations and possibilities of low cell number ChIP-seq. BMC Genomics, 2012, 13, 645		1.2	80
1761	Histone demethylase GASC1 - a potential prognostic and predictive marker in invasive b BMC Cancer, 2012, 12, 516.	reast cancer.	1.1	26
1762	â€~Sifting the significance from the data' - the impact of high-throughput genomic t human genetics and health care. Human Genomics, 2012, 6, 11.	echnologies on	1.4	5
1763	Electric oscillation and coupling of chromatin regulate chromosome packaging and tran eukaryotic cells. Theoretical Biology and Medical Modelling, 2012, 9, 27.	scription in	2.1	17
1764	HERV-H RNA is abundant in human embryonic stem cells and a precise marker for plurip Retrovirology, 2012, 9, 111.	otency.	0.9	188
1765	HRP-2 determines HIV-1 integration site selection in LEDGF/p75 depleted cells. Retroviro	blogy, 2012, 9, 84.	0.9	57

#	Article	IF	CITATIONS
1766	The influence of DNA sequence on epigenome-induced pathologies. Epigenetics and Chromatin, 2012, 5, 11.	1.8	19
1767	A genome-wide screen in human embryonic stem cells reveals novel sites of allele-specific histone modification associated with known disease loci. Epigenetics and Chromatin, 2012, 5, 6.	1.8	20
1768	The male germ cell gene regulator CTCFL is functionally different from CTCF and binds CTCF-like consensus sites in a nucleosome composition-dependent manner. Epigenetics and Chromatin, 2012, 5, 8.	1.8	80
1769	On the epigenetics of vascular regulation and disease. Clinical Epigenetics, 2012, 4, 7.	1.8	49
1770	Histone H3K79 methyltransferase Dot1L is directly activated by thyroid hormone receptor during Xenopus metamorphosis. Cell and Bioscience, 2012, 2, 25.	2.1	39
1771	ISWI contributes to ArsI insulator function in development of the sea urchin. Development (Cambridge), 2012, 139, 3613-3622.	1.2	15
1772	Stressâ€associated <scp>H</scp> 3 <scp>K</scp> 4 methylation accumulates during postnatal development and aging of rhesus macaque brain. Aging Cell, 2012, 11, 1055-1064.	3.0	44
1773	Next Generation Microarray Bioinformatics. Methods in Molecular Biology, 2012, , .	0.4	8
1774	Alterations in Histone H4 Lysine 20 Methylation: Implications for Cancer Detection and Prevention. Antioxidants and Redox Signaling, 2012, 17, 365-374.	2.5	18
1775	Genome-wide Chromatin Immunoprecipitation-Sequencing in Plasmodium. Methods in Molecular Biology, 2012, 923, 321-333.	0.4	14
1776	Identifying Functional Annotation for Noncoding Genomic Sequences. Current Protocols in Human Genetics, 2012, 72, Unit1.10.	3.5	5
1777	Disentangling the Many Layers of Eukaryotic Transcriptional Regulation. Annual Review of Genetics, 2012, 46, 43-68.	3.2	222
1778	ChIP-Seq Data Analysis: Identification of Protein–DNA Binding Sites with SISSRs Peak-Finder. Methods in Molecular Biology, 2012, 802, 305-322.	0.4	38
1779	Crossâ€ŧalk between <scp>DNA</scp> methylation and active histone modifications regulates aberrant expression of <scp>ZAP</scp> 70 in <scp>CLL</scp> . Journal of Cellular and Molecular Medicine, 2012, 16, 2074-2084.	1.6	10
1780	Epigenetic Epidemiology of Type 1 Diabetes. , 2012, , 377-400.		2
1781	Epigenetic Epidemiology of Obesity, Type 2 Diabetes, and Metabolic Disorders. , 2012, , 401-421.		Ο
1783	What does our genome encode?. Genome Research, 2012, 22, 1602-1611.	2.4	107
1784	Nuclear Receptor 5A (NR5A) Family Regulates 5-Aminolevulinic Acid Synthase 1 (ALAS1) Gene Expression in Steroidogenic Cells. Endocrinology, 2012, 153, 5522-5534.	1.4	30

	CITATION	N REPORT	
#	Article	IF	CITATIONS
1785	Epigenetics and Regeneration. Current Topics in Microbiology and Immunology, 2012, 367, 237-252.	0.7	3
1786	Cdc6: A multi-functional molecular switch with critical role in carcinogenesis. Transcription, 2012, 3, 124-129.	1.7	31
1787	Mapping Protein–DNA Interactions Using ChIP-Sequencing. Methods in Molecular Biology, 2012, 809, 157-173.	0.4	20
1788	Methods and Strategies to Determine Epigenetic Variation in Human Disease. , 2012, , 7-27.		2
1790	Ezh2 maintains a key phase of muscle satellite cell expansion but does not regulate terminal differentiation. Journal of Cell Science, 2013, 126, 565-579.	1.2	77
1791	Global mapping of H3K4me3 and H3K27me3 reveals chromatin state-based regulation of human monocyte-derived dendritic cells in different environments. Genes and Immunity, 2012, 13, 311-320.	2.2	43
1792	Sparkling Insights into Enhancer Structure, Function, and Evolution. Current Topics in Developmental Biology, 2012, 98, 97-120.	1.0	22
1793	Control of Proinflammatory Gene Programs by Regulated Trimethylation and Demethylation of Histone H4K20. Molecular Cell, 2012, 48, 28-38.	4.5	193
1794	The molecular basis of the memory T cell response: differential gene expression and its epigenetic regulation. Nature Reviews Immunology, 2012, 12, 306-315.	10.6	274
1795	Transcription control by long non-coding RNAs. Transcription, 2012, 3, 78-86.	1.7	23
1796	Long distance relationships: Enhancer–promoter communication and dynamic gene transcription. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2012, 1819, 1217-1227.	0.9	75
1797	Intergenic region between TATA-box binding protein and proteasome subunit C3 genes of Medaka function as the bidirectional promoter in vitro and in vivo. Gene, 2012, 511, 177-186.	1.0	3
1798	The Association Between H3K4me3 and Antisense Transcription. Genomics, Proteomics and Bioinformatics, 2012, 10, 74-81.	3.0	12
1799	Comparative Analyses of H3K4 and H3K27 Trimethylations Between the Mouse Cerebrum and Testis. Genomics, Proteomics and Bioinformatics, 2012, 10, 82-93.	3.0	22
1800	Epigenetic regulation of pancreas development and function. Seminars in Cell and Developmental Biology, 2012, 23, 693-700.	2.3	31
1801	Epigenetic modifications and diabetic nephropathy. Kidney Research and Clinical Practice, 2012, 31, 139-150.	0.9	11
1802	Identifying ChIP-seq enrichment using MACS. Nature Protocols, 2012, 7, 1728-1740.	5.5	1,471
1803	Genome-Wide Mapping of Nucleosome Occupancy, Histone Modifications, and Gene Expression Using Next-Generation Sequencing Technology. Methods in Enzymology, 2012, 513, 297-313.	0.4	24

#	Article	IF	CITATIONS
1804	Localized and Temporal Gene Regulation in Heart Development. Current Topics in Developmental Biology, 2012, 100, 171-201.	1.0	11
1805	Chromatin signatures of active enhancers. Nucleus, 2012, 3, 126-131.	0.6	70
1806	Systematic evaluation of factors influencing ChIP-seq fidelity. Nature Methods, 2012, 9, 609-614.	9.0	156
1809	Identifying Differential Histone Modification Sites from ChIPâ€seq Data. Methods in Molecular Biology, 2012, 802, 293-303.	0.4	10
1810	tDNA insulators and the emerging role of TFIIIC in genome organization. Transcription, 2012, 3, 277-284.	1.7	54
1811	Alterations of Histone Modifications in Cancer. , 2012, , 53-87.		5
1812	Recruitment of RPL11 at promoter sites of p53-regulated genes upon nucleolar stress through NEDD8 and in an Mdm2-dependent manner. Oncogene, 2012, 31, 3060-3071.	2.6	67
1813	DNA Methylation and Histone Modifications Are Associated with Repression of the Inhibin $\hat{I}\pm$ Promoter in the Rat Corpus Luteum. Endocrinology, 2012, 153, 4905-4917.	1.4	23
1814	Epigenetics of Solid Cancer Stem Cells. Methods in Molecular Biology, 2012, 863, 15-31.	0.4	17
1815	Genetic and epigenetic mechanisms in thyroid autoimmunity. Immunologic Research, 2012, 54, 204-213.	1.3	109
1816	Application of a systems approach to study developmental gene regulation. Biophysical Reviews, 2012, 4, 245-253.	1.5	2
1817	Spreading of X chromosome inactivation via a hierarchy of defined Polycomb stations. Genome Research, 2012, 22, 1864-1876.	2.4	143
1818	Integrative functional genomics identifies an enhancer looping to the <i>SOX9</i> gene disrupted by the 17q24.3 prostate cancer risk locus. Genome Research, 2012, 22, 1437-1446.	2.4	115
1819	Modeling the relative relationship of transcription factor binding and histone modifications to gene expression levels in mouse embryonic stem cells. Nucleic Acids Research, 2012, 40, 553-568.	6.5	145
1820	The von Hippel–Lindau tumor suppressor protein regulates gene expression and tumor growth through histone demethylase JARID1C. Oncogene, 2012, 31, 776-786.	2.6	133
1824	Primordial Germ Cells in Mice. Cold Spring Harbor Perspectives in Biology, 2012, 4, a008375-a008375.	2.3	308
1826	Histone H3K9 methyltransferase G9a represses PPARÎ ³ expression and adipogenesis. EMBO Journal, 2012, 32, 45-59.	3.5	162
1831	Bromodomain-containing Protein 4 (BRD4) Regulates RNA Polymerase II Serine 2 Phosphorylation in Human CD4+ T Cells. Journal of Biological Chemistry. 2012. 287. 43137-43155.	1.6	164

#	Article	IF	Citations
1832	Transcriptional Architecture and Chromatin Landscape of the Core Circadian Clock in Mammals. Science, 2012, 338, 349-354.	6.0	1,194
1833	Advances in Bioinformatics and Computational Biology. Lecture Notes in Computer Science, 2012, , .	1.0	1
1834	Genetic and Epigenomic Footprints of Folate. Progress in Molecular Biology and Translational Science, 2012, 108, 129-158.	0.9	50
1835	Cancer Epigenetics. Methods in Molecular Biology, 2012, , .	0.4	5
1836	Stem Cell Epigenetics and Human Disease. , 2012, , 481-501.		0
1839	BM-BC: a Bayesian method of base calling for Solexa sequence data. BMC Bioinformatics, 2012, 13, S6.	1.2	5
1840	Redistribution of H3K4me2 on neural tissue specific genes during mouse brain development. BMC Genomics, 2012, 13, S5.	1.2	25
1841	Integrative genome-wide chromatin signature analysis using finite mixture models. BMC Genomics, 2012, 13, S3.	1.2	5
1842	iASeq: integrative analysis of allele-specificity of protein-DNA interactions in multiple ChIP-seq datasets. BMC Genomics, 2012, 13, 681.	1.2	22
1843	A histone arginine methylation localizes to nucleosomes in satellite II and III DNA sequences in the human genome. BMC Genomics, 2012, 13, 630.	1.2	8
1844	Evidence for sequence biases associated with patterns of histone methylation. BMC Genomics, 2012, 13, 367.	1.2	12
1845	Epigenetics in Cardiovascular Biology. , 2012, , 331-340.		0
1846	Combinations of Histone Modifications Mark Exon Inclusion Levels. PLoS ONE, 2012, 7, e29911.	1.1	38
1847	Automated Workflow for Preparation of cDNA for Cap Analysis of Gene Expression on a Single Molecule Sequencer. PLoS ONE, 2012, 7, e30809.	1.1	22
1848	Probabilistic Inference for Nucleosome Positioning with MNase-Based or Sonicated Short-Read Data. PLoS ONE, 2012, 7, e32095.	1.1	20
1849	Integrated Epigenome Profiling of Repressive Histone Modifications, DNA Methylation and Gene Expression in Normal and Malignant Urothelial Cells. PLoS ONE, 2012, 7, e32750.	1.1	34
1850	Genome-Wide Evaluation of Histone Methylation Changes Associated with Leaf Senescence in Arabidopsis. PLoS ONE, 2012, 7, e33151.	1.1	83
1851	A Novel Human Polycomb Binding Site Acts As a Functional Polycomb Response Element in Drosophila. PLoS ONE, 2012, 7, e36365.	1.1	24

#	Article	IF	CITATIONS
1852	GPUmotif: An Ultra-Fast and Energy-Efficient Motif Analysis Program Using Graphics Processing Units. PLoS ONE, 2012, 7, e36865.	1.1	9
1853	Bivalent-Like Chromatin Markers Are Predictive for Transcription Start Site Distribution in Human. PLoS ONE, 2012, 7, e38112.	1.1	3
1854	Dissecting Epigenetic Silencing Complexity in the Mouse Lung Cancer Suppressor Gene Cadm1. PLoS ONE, 2012, 7, e38531.	1.1	3
1855	A Cell Cycle Role for the Epigenetic Factor CTCF-L/BORIS. PLoS ONE, 2012, 7, e39371.	1.1	37
1856	Functional and Molecular Characterization of the Role of CTCF in Human Embryonic Stem Cell Biology. PLoS ONE, 2012, 7, e42424.	1.1	20
1857	A Global Genome Segmentation Method for Exploration of Epigenetic Patterns. PLoS ONE, 2012, 7, e46811.	1.1	21
1858	Omeprazole Blocks STAT6 Binding to the Eotaxin-3 Promoter in Eosinophilic Esophagitis Cells. PLoS ONE, 2012, 7, e50037.	1.1	203
1859	The role of epigenetic mechanisms and processes in autoimmune disorders. Biologics: Targets and Therapy, 2012, 6, 307.	3.0	51
1860	Transcription factor binding at enhancers: shaping a genomic regulatory landscape in flux. Frontiers in Genetics, 2012, 3, 195.	1.1	40
1861	Chromatin loops, gene positioning, and gene expression. Frontiers in Genetics, 2012, 3, 217.	1.1	83
1862	Increased expression of stefin B in the nucleus of T98G astrocytoma cells delays caspase activation. Frontiers in Molecular Neuroscience, 2012, 5, 93.	1.4	15
1863	Genome-wide ChIP-DSL profiling of promoter methylation patterns associated with cancer and stem cell differentiation. , 0, , 210-222.		0
1864	Regulation of the stem cell epigenome by REST. , 0, , 146-162.		0
1865	Promoter and histone methylation and p16INK4A gene expression in colon cancer. Experimental and Therapeutic Medicine, 2012, 4, 865-870.	0.8	10
1866	The Tissue Specific Role of Estrogen and Progesterone in Human Endometrium and Mammary Gland. , 2012, , .		2
1867	DNA Methylation in Mammalian and Non-Mammalian Organisms. , 0, , .		2
1868	Novel Biomarkers in Pancreatic Cancer. , 2012, , .		0
1869	DNA Methylation, Stem Cells and Cancer. , 0, , .		2

#	Article	IF	Citations
1870	Structural Dynamics and Epigenetic Modifications of <i>Hoxc </i> Loci along the Anteroposterior Body Axis in Developing Mouse Embryos. International Journal of Biological Sciences, 2012, 8, 802-810.	2.6	10
1871	Effects of siRNA-mediated knockdown of jumonji domain containing 2A on proliferation, migration and invasion of the human breast cancer cell line MCF-7. Experimental and Therapeutic Medicine, 2012, 4, 755-761.	0.8	28
1872	Stem cell genomeâ€ŧoâ€systems biology. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2012, 4, 39-49.	6.6	4
1873	Linking genome to epigenome. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2012, 4, 297-309.	6.6	26
1874	Mapping physical interactions within chromatin by proteomic approaches. Proteomics, 2012, 12, 1609-1622.	1.3	16
1875	Epigenetics of Embryonic Stem Cells. Advances in Experimental Medicine and Biology, 2012, 741, 231-253.	0.8	9
1876	Inner workings and regulatory inputs that control Polycomb repressive complex 2. Chromosoma, 2012, 121, 221-234.	1.0	72
1877	DNA fragments binding CTCF in vitro and in vivo are capable of blocking enhancer activity. BMC Research Notes, 2012, 5, 178.	0.6	4
1878	Emerging functional and mechanistic paradigms of mammalian long non-coding RNAs. Nucleic Acids Research, 2012, 40, 6391-6400.	6.5	583
1879	Current Chemical Biology Approaches to Interrogate Protein Methyltransferases. ACS Chemical Biology, 2012, 7, 443-463.	1.6	121
1880	Distal Interleukin-1β (IL-1β) Response Element of Human Matrix Metalloproteinase-13 (MMP-13) Binds Activator Protein 1 (AP-1) Transcription Factors and Regulates Gene Expression. Journal of Biological Chemistry, 2012, 287, 1189-1197.	1.6	18
1881	Genome-wide assessment of oxidatively generated DNA damage. Free Radical Research, 2012, 46, 523-530.	1.5	19
1882	CTCF: insights into insulator function during development. Development (Cambridge), 2012, 139, 1045-1057.	1.2	143
1883	R-Loop Formation Is a Distinctive Characteristic of Unmethylated Human CpG Island Promoters. Molecular Cell, 2012, 45, 814-825.	4.5	673
1884	DNA–protein interactions: methods for detection and analysis. Molecular and Cellular Biochemistry, 2012, 365, 279-299.	1.4	131
1885	The macrosatellite DXZ4 mediates CTCF-dependent long-range intrachromosomal interactions on the human inactive X chromosome. Human Molecular Genetics, 2012, 21, 4367-4377.	1.4	70
1886	Chromatin organization is a major influence on regional mutation rates in human cancer cells. Nature, 2012, 488, 504-507.	13.7	602
1887	Histone Variant H2A.Bbd Is Associated with Active Transcription and mRNA Processing in Human Cells. Molecular Cell, 2012, 47, 596-607.	4.5	92

#	Article	IF	CITATIONS
1888	Tissue-specific analysis of chromatin state identifies temporal signatures of enhancer activity during embryonic development. Nature Genetics, 2012, 44, 148-156.	9.4	453
1889	Cfp1 integrates both CpG content and gene activity for accurate H3K4me3 deposition in embryonic stem cells. Genes and Development, 2012, 26, 1714-1728.	2.7	253
1890	Genome-Wide Approaches to Determining Nucleosome Occupancy in Metazoans Using MNase-Seq. Methods in Molecular Biology, 2012, 833, 413-419.	0.4	87
1891	Chemical and biochemical approaches in the study of histone methylation and demethylation. Medicinal Research Reviews, 2012, 32, 815-867.	5.0	51
1892	Chemical castration and antiâ€androgens induce differential gene expression in prostate cancer. Journal of Pathology, 2012, 227, 336-345.	2.1	29
1893	Epigenetics: Concepts and relevance to IBD pathogenesis. Inflammatory Bowel Diseases, 2012, 18, 1982-1996.	0.9	50
1894	Sequential ChIP-bisulfite sequencing enables direct genome-scale investigation of chromatin and DNA methylation cross-talk. Genome Research, 2012, 22, 1128-1138.	2.4	344
1895	Modular regulatory principles of large non-coding RNAs. Nature, 2012, 482, 339-346.	13.7	2,036
1896	Genetic inactivation of the polycomb repressive complex 2 in T cell acute lymphoblastic leukemia. Nature Medicine, 2012, 18, 298-302.	15.2	453
1897	Epigenetic regulation in RCC: opportunities for therapeutic intervention?. Nature Reviews Urology, 2012, 9, 147-155.	1.9	51
1898	Evidence for an intronic cis-regulatory element within CD69 gene. Genes and Immunity, 2012, 13, 356-362.	2.2	11
1899	Human tRNA genes function as chromatin insulators. EMBO Journal, 2012, 31, 330-350.	3.5	129
1900	Symmetric dimethylation of H3R2 is a newly identified histone mark that supports euchromatin maintenance. Nature Structural and Molecular Biology, 2012, 19, 136-144.	3.6	272
1901	Distinct DNA methylomes of newborns and centenarians. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 10522-10527.	3.3	687
1902	Integrated genome analysis suggests that most conserved non-coding sequences are regulatory factor binding sites. Nucleic Acids Research, 2012, 40, 7858-7869.	6.5	36
1903	Applications of High-Throughput Sequencing. , 2012, , 27-53.		1
1904	Small-molecule–induced DNA damage identifies alternative DNA structures in human genes. Nature Chemical Biology, 2012, 8, 301-310.	3.9	576
1905	Epigenetic reprogramming in mouse pre-implantation development and primordial germ cells. Development (Cambridge), 2012, 139, 15-31.	1.2	355

#	Article	IF	CITATIONS
1906	Transcription factors: from enhancer binding to developmental control. Nature Reviews Genetics, 2012, 13, 613-626.	7.7	1,726
1907	The Use of High-Throughput Technologies to Investigate Vascular Inflammation and Atherosclerosis. Arteriosclerosis, Thrombosis, and Vascular Biology, 2012, 32, 182-195.	1.1	31
1908	Genome Regulation by Long Noncoding RNAs. Annual Review of Biochemistry, 2012, 81, 145-166.	5.0	3,665
1909	ATAC-king the complexity of SAGA during evolution. Genes and Development, 2012, 26, 527-541.	2.7	160
1910	Global identification of transcriptional regulators of pluripotency and differentiation in embryonic stem cells. Nucleic Acids Research, 2012, 40, 8199-8209.	6.5	9
1911	Origins and Formation of Histone Methylation across the Human Cell Cycle. Molecular and Cellular Biology, 2012, 32, 2503-2514.	1.1	79
1912	DNA-binding factor CTCF and long-range gene interactions in V(D)J recombination and oncogene activation. Blood, 2012, 119, 6209-6218.	0.6	31
1913	A map of the cis-regulatory sequences in the mouse genome. Nature, 2012, 488, 116-120.	13.7	1,306
1914	Dynamic transitions in RNA polymerase II density profiles during transcription termination. Genome Research, 2012, 22, 1447-1456.	2.4	42
1915	Target genes of Topoisomerase $l\hat{l}^2$ regulate neuronal survival and are defined by their chromatin state.	0.0	142
	Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E934-43.	3.3	
1916	Chromatin Immunoprecipitation (ChIP) using Drosophila tissue. Journal of Visualized Experiments, 2012, .	0.2	8
1916 1917	Chromatin Immunoprecipitation (ChIP) using Drosophila tissue. Journal of Visualized		8
	Chromatin Immunoprecipitation (ChIP) using Drosophila tissue. Journal of Visualized Experiments, 2012, , . Organogenesis and functional genomics of the endocrine pancreas. Cellular and Molecular Life	0.2	
1917	Chromatin Immunoprecipitation (ChIP) using Drosophila tissue. Journal of Visualized Experiments, 2012, , . Organogenesis and functional genomics of the endocrine pancreas. Cellular and Molecular Life Sciences, 2012, 69, 2109-2123. Throwing transcription for a loop: expression of the genome in the 3D nucleus. Chromosoma, 2012,	0.2 2.4	10
1917 1918	Chromatin Immunoprecipitation (ChIP) using Drosophila tissue. Journal of Visualized Experiments, 2012, , . Organogenesis and functional genomics of the endocrine pancreas. Cellular and Molecular Life Sciences, 2012, 69, 2109-2123. Throwing transcription for a loop: expression of the genome in the 3D nucleus. Chromosoma, 2012, 121, 107-116. Expression of vernalization responsive genes in wheat is associated with histone H3 trimethylation.	0.2 2.4 1.0	10 23
1917 1918 1919	Chromatin Immunoprecipitation (ChIP) using Drosophila tissue. Journal of Visualized Experiments, 2012, , . Organogenesis and functional genomics of the endocrine pancreas. Cellular and Molecular Life Sciences, 2012, 69, 2109-2123. Throwing transcription for a loop: expression of the genome in the 3D nucleus. Chromosoma, 2012, 121, 107-116. Expression of vernalization responsive genes in wheat is associated with histone H3 trimethylation. Molecular Genetics and Genomics, 2012, 287, 575-590. Global histone H3 lysine 27 (H3K27) methylation levels and their prognostic relevance in renal cell	0.2 2.4 1.0 1.0	10 23 50
1917 1918 1919 1920	Chromatin Immunoprecipitation (ChIP) using Drosophila tissue. Journal of Visualized Experiments, 2012, , . Organogenesis and functional genomics of the endocrine pancreas. Cellular and Molecular Life Sciences, 2012, 69, 2109-2123. Throwing transcription for a loop: expression of the genome in the 3D nucleus. Chromosoma, 2012, 121, 107-116. Expression of vernalization responsive genes in wheat is associated with histone H3 trimethylation. Molecular Genetics and Genomics, 2012, 287, 575-590. Global histone H3 lysine 27 (H3K27) methylation levels and their prognostic relevance in renal cell carcinoma. BJU International, 2012, 109, 459-465. Nucleosome surface containing nucleosomal DNA entry/exit site regulates H3â€K36me3 <i>via</i>	0.2 2.4 1.0 1.3	10 23 50 58

ARTICLE IF CITATIONS # Bivalent histone modifications in early embryogenesis. Current Opinion in Cell Biology, 2012, 24, 1924 2.6 253 374-386. Redox signaling and histone acetylation in acute pancreatitis. Free Radical Biology and Medicine, 2012, 1.3 52, 819-837. Interrogating genomic and epigenomic data to understand prostate cancer. Biochimica Et Biophysica 1926 3.3 14 Acta: Reviews on Cancer, 2012, 1825, 186-196. Cortical spreading depression differentially affects lysine methylation of H3 histone at 1.1 neuroprotective genes and retrotransposón sequences. Brain Research, 2012, 1467, 113-119. NFâ€î₽B and chromatin: ten years on the path from basic mechanisms to candidate drugs. Immunological 1928 2.8 71 Reviews, 2012, 246, 183-192. Nucleosome positioning: bringing order to the eukaryotic genome. Trends in Cell Biology, 2012, 22, 1929 3.6 250-256. Non-coding RNAs: key regulators of mammalian transcription. Trends in Biochemical Sciences, 2012, 37, 1930 3.7 121 144-151. De novo DNA methylation: a germ cell perspective. Trends in Genetics, 2012, 28, 33-42. 2.9 Induction of the neural crest state: Control of stem cell attributes by gene regulatory, 1932 0.9 106 post-transcriptional and epigenetic interactions. Developmental Biology, 2012, 366, 10-21. The transcriptional programme controlled by Runx1 during early embryonic blood development. Developmental Biology, 2012, 366, 404-419 Mutations and epimutations in the origin of cancer. Experimental Cell Research, 2012, 318, 299-310. 1934 1.2 68 Histone modifications in herpesvirus infections. Biology of the Cell, 2012, 104, 139-164. 1935 Recent advances in <i>Schistosoma</i> genomics. Parasite Immunology, 2012, 34, 151-162. 1936 0.7 14 Disruption of CTCF at the miR-125b1 locus in gynecological cancers. BMC Cancer, 2012, 12, 40. 1.1 Effects of genetic variation in H3K79 methylation regulatory genes on clinical blood pressure and 1938 22 1.8 blood pressure response to hydrochlorothiazide. Journal of Translational Medicine, 2012, 10, 56. The epigenome in early vertebrate development. Genesis, 2012, 50, 192-206. 30 Hippocampal gene profiling: Toward a systems biology of the hippocampus. Hippocampus, 2012, 22, 1940 0.9 11 929-941. 1941 The tumor suppressor role of CTCF. Journal of Cellular Physiology, 2012, 227, 479-492. 44

#	Article	IF	CITATIONS
1942	The role of vitamin D in the FGF23, klotho, and phosphate bone-kidney endocrine axis. Reviews in Endocrine and Metabolic Disorders, 2012, 13, 57-69.	2.6	120
1943	CTCF and cohesin cooperatively mediate the cell-type specific interchromatin interaction between Bcl11b and Arhgap6 loci. Molecular and Cellular Biochemistry, 2012, 360, 243-251.	1.4	9
1944	Revealing epigenetic patterns in gene regulation through integrative analysis of epigenetic interaction network. Molecular Biology Reports, 2012, 39, 1701-1712.	1.0	9
1945	Polyamine analogs modulate gene expression by inhibiting lysine-specific demethylase 1 (LSD1) and altering chromatin structure in human breast cancer cells. Amino Acids, 2012, 42, 887-898.	1.2	78
1946	Epigenetic Regulation and Measurement of Epigenetic Changes. Biological Research for Nursing, 2013, 15, 373-381.	1.0	35
1947	Induction of human fetal hemoglobin expression by adenosine-2',3'-dialdehyde. Journal of Translational Medicine, 2013, 11, 14.	1.8	10
1948	Redistribution of H3K27me3 upon DNA hypomethylation results in de-repression of Polycomb target genes. Genome Biology, 2013, 14, R25.	13.9	200
1949	Nucleosomal DNA binding drives the recognition of H3K36-methylated nucleosomes by the PSIP1-PWWP domain. Epigenetics and Chromatin, 2013, 6, 12.	1.8	141
1950	Vertebrate GAGA factor associated insulator elements demarcate homeotic genes in the HOX clusters. Epigenetics and Chromatin, 2013, 6, 8.	1.8	25
1951	Epigenomic control of the innate immune response. Current Opinion in Pharmacology, 2013, 13, 582-587.	1.7	44
1952	Genome-wide distribution of histone H4 Lysine 16 acetylation sites and their relationship to gene expression. Genome Integrity, 2013, 4, 3.	1.0	46
1953	Transgene Site-Specific Integration: Problems and Solutions. Topics in Current Genetics, 2013, , 3-39.	0.7	3
1954	DNA unmethylome profiling by covalent capture of CpG sites. Nature Communications, 2013, 4, 2190.	5.8	53
1955	Chromatin-linked determinants of zygotic genome activation. Cellular and Molecular Life Sciences, 2013, 70, 1425-1437.	2.4	28
1958	New Perspectives in Regeneration. Current Topics in Microbiology and Immunology, 2013, 367, v-vii.	0.7	5
1959	Structure-function analysis reveals a novel mechanism for regulation of histone demethylase LSD2/AOF1/KDM1b. Cell Research, 2013, 23, 225-241.	5.7	61
1960	DNA replication-dependent binding of CTCF plays a critical role in adenovirus genome functions. Scientific Reports, 2013, 3, 2187.	1.6	14
1961	MicroRNA Cancer Regulation. Advances in Experimental Medicine and Biology, 2013, , .	0.8	17

#	Article	IF	CITATIONS
1962	Introduction to Next-Generation Nucleic Acid Sequencing in Cardiovascular Disease Research. Methods in Molecular Biology, 2013, 1027, 157-179.	0.4	1
1963	Mitochondrial DNA methylation as a next-generation biomarker and diagnostic tool. Molecular Genetics and Metabolism, 2013, 110, 25-34.	0.5	203
1964	Computational Reconstruction of Transcriptional Relationships from ChIP-Chip Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 300-307.	1.9	0
1965	Global Mapping of Transcription Factor Binding Sites by Sequencing Chromatin Surrogates: a Perspective on Experimental Design, Data Analysis, and Open Problems. Statistics in Biosciences, 2013, 5, 156-178.	0.6	4
1966	CpG islands under selective pressure are enriched with H3K4me3, H3K27ac and H3K36me3 histone modifications. BMC Evolutionary Biology, 2013, 13, 145.	3.2	5
1967	Dynamic regulation of epigenomic landscapes during hematopoiesis. BMC Genomics, 2013, 14, 193.	1.2	41
1968	Nuclear Factor I genomic binding associates with chromatin boundaries. BMC Genomics, 2013, 14, 99.	1.2	24
1969	An integrated approach to characterize transcription factor and microRNA regulatory networks involved in Schwann cell response to peripheral nerve injury. BMC Genomics, 2013, 14, 84.	1.2	35
1970	E-cadherin gene re-expression in chronic lymphocytic leukemia cells by HDAC inhibitors. BMC Cancer, 2013, 13, 88.	1.1	28
1971	Identification of regulatory regions of bidirectional genes in cervical cancer. BMC Medical Genomics, 2013, 6, S5.	0.7	16
1972	CpGIMethPred: computational model for predicting methylation status of CpG islands in human genome. BMC Medical Genomics, 2013, 6, S13.	0.7	41
1973	Signal transducer and activator of transcription (STAT)-3 regulates microRNA gene expression in chronic lymphocytic leukemia cells. Molecular Cancer, 2013, 12, 50.	7.9	56
1974	Pluripotent Stem Cells. Methods in Molecular Biology, 2013, , .	0.4	5
1975	Histone Variants in Development and Diseases. Journal of Genetics and Genomics, 2013, 40, 355-365.	1.7	23
1977	Computational methodology for ChIPâ€seq analysis. Quantitative Biology, 2013, 1, 54-70.	0.3	24
1978	Haploinsufficiency of KDM6A is associated with severe psychomotor retardation, global growth restriction, seizures and cleft palate. Human Genetics, 2013, 132, 537-552.	1.8	60
1979	Latent Regulatory Potential of Human-Specific Repetitive Elements. Molecular Cell, 2013, 49, 262-272.	4.5	62
1980	Arabidopsis histone methyltransferase SET DOMAIN GROUP2 is required for regulation of various hormone responsive genes. Journal of Plant Biology, 2013, 56, 39-48.	0.9	8

#	Article	IF	CITATIONS
1982	Transcription Factor Binding in Human Cells Occurs in Dense Clusters Formed around Cohesin Anchor Sites. Cell, 2013, 154, 801-813.	13.5	327
1983	Gene Regulation. Methods in Molecular Biology, 2013, , .	0.4	1
1984	Next Generation Sequencing in Cancer Research. , 2013, , .		5
1985	Impaired secretion of interferons by dendritic cells from aged subjects to influenza. Age, 2013, 35, 1785-1797.	3.0	68
1986	Understanding human diseases with high-throughput quantitative measurement and analysis of molecular signatures. Science China Life Sciences, 2013, 56, 213-219.	2.3	3
1987	Intragenic DNA methylation in transcriptional regulation, normal differentiation and cancer. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2013, 1829, 1161-1174.	0.9	188
1988	Differentiation and adaptation epigenetic networks: Translational research in gastric carcinogenesis. Science Bulletin, 2013, 58, 1-6.	1.7	18
1989	Combining genomic and proteomic approaches for epigenetics research. Epigenomics, 2013, 5, 439-452.	1.0	31
1990	Identification of functional modules of AKMT, a novel lysine methyltransferase regulating the motility of Toxoplasma gondii. Molecular and Biochemical Parasitology, 2013, 189, 43-53.	0.5	20
1991	Histone variants in pluripotency and disease. Development (Cambridge), 2013, 140, 2513-2524.	1.2	127
1992	Transcriptional Repression of Gata3 Is Essential for Early B Cell Commitment. Immunity, 2013, 38, 930-942.	6.6	58
1993	Early T helper cell programming of gene expression in human. Seminars in Immunology, 2013, 25, 282-290.	2.7	13
1994	Discovering common combinatorial histone modification patterns in the human genome. Gene, 2013, 518, 171-178.	1.0	14
1995	CAST-ChIP Maps Cell-Type-Specific Chromatin States in the Drosophila Central Nervous System. Cell Reports, 2013, 5, 271-282.	2.9	34
1996	Cellular Source and Mechanisms of High Transcriptome Complexity in the Mammalian Testis. Cell Reports, 2013, 3, 2179-2190.	2.9	497
1997	CTCF Regulates Kaposi's Sarcoma-Associated Herpesvirus Latency Transcription by Nucleosome Displacement and RNA Polymerase Programming. Journal of Virology, 2013, 87, 1789-1799.	1.5	34
1998	Boosting transcription by transcription: enhancer-associated transcripts. Chromosome Research, 2013, 21, 713-724.	1.0	26
1999	Predicting enhancer transcription and activity from chromatin modifications. Nucleic Acids Research, 2013, 41, 10032-10043.	6.5	128

#	Article	IF	CITATIONS
2000	The Histone Code of Toxoplasma gondii Comprises Conserved and Unique Posttranslational Modifications. MBio, 2013, 4, e00922-13.	1.8	85
2001	Genome-Wide Analysis of Histone Modifications: H3K4me2, H3K4me3, H3K9ac, and H3K27ac in Oryza sativa L. Japonica. Molecular Plant, 2013, 6, 1463-1472.	3.9	111
2002	Stress-Induced Mutagenesis. , 2013, , .		4
2003	RNAi screen identifies Jarid1b as a major regulator of mouse HSC activity. Blood, 2013, 122, 1545-1555.	0.6	57
2004	Macrophage Activation and Polarization as an Adaptive Component of Innate Immunity. Advances in Immunology, 2013, 120, 163-184.	1.1	352
2005	Transcriptional regulation by Polycomb group proteins. Nature Structural and Molecular Biology, 2013, 20, 1147-1155.	3.6	757
2006	Transcription-associated histone modifications and cryptic transcription. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2013, 1829, 84-97.	0.9	160
2007	Transposition of native chromatin for fast and sensitive epigenomic profiling of open chromatin, DNA-binding proteins and nucleosome position. Nature Methods, 2013, 10, 1213-1218.	9.0	5,209
2008	An epigenetic signature of developmental potential in neural stem cells and early neurons. Stem Cells, 2013, 31, 1868-1880.	1.4	41
2009	Positive and Negative Design for Nonconsensus Protein-DNA Binding Affinity in the Vicinity of Functional Binding Sites. Biophysical Journal, 2013, 105, 1653-1660.	0.2	20
2010	Mutations in regulators of the epigenome and their connections to global chromatin patterns in cancer. Nature Reviews Genetics, 2013, 14, 765-780.	7.7	373
2011	Classification of topological domains based on gene expression and regulation. Genome, 2013, 56, 415-423.	0.9	2
2012	Characterization of three loci for homologous gene targeting and transgene expression. Biotechnology and Bioengineering, 2013, 110, 2225-2235.	1.7	13
2013	Epigenetic Alterations in Acute Kidney Injury. Seminars in Nephrology, 2013, 33, 327-340.	0.6	47
2014	Meiotic recombination in mammals: localization and regulation. Nature Reviews Genetics, 2013, 14, 794-806.	7.7	506
2015	The nexus of chromatin regulation and intermediary metabolism. Nature, 2013, 502, 489-498.	13.7	341
2016	Epigenetics and Cancer. , 2013, , .		5
2017	Gene Silencing and Polycomb Group Proteins: An Overview of their Structure, Mechanisms and Phylogenetics. OMICS A Journal of Integrative Biology, 2013, 17, 283-296.	1.0	36

		CITATION R	EPORT	
#	Article		IF	CITATIONS
2018	Nutritional Control of Epigenetic Processes in Yeast and Human Cells. Genetics, 2013, 1	95, 831-844.	1.2	53
2019	Histone modifications for human epigenome analysis. Journal of Human Genetics, 2013	58, 439-445.	1.1	371
2020	Identification of Genetic Variants That Affect Histone Modifications in Human Cells. Scie 747-749.	nce, 2013, 342,	6.0	429
2021	Global DNA Methylation Remodeling Accompanies CD8 T Cell Effector Function. Journal Immunology, 2013, 191, 3419-3429.	of	0.4	167
2022	Mapping the HIF Transcription Factor in Cancer by ChIP-Seq Technology. , 2013, , 91-11	7.		0
2023	The MLL3/MLL4 Branches of the COMPASS Family Function as Major Histone H3K4 Mor Enhancers. Molecular and Cellular Biology, 2013, 33, 4745-4754.	nomethylases at	1.1	329
2024	Cell and Molecular Biology of Breast Cancer. , 2013, , .			10
2025	Human IL-31 is induced by IL-4 and promotes TH2-driven inflammation. Journal of Allergy Immunology, 2013, 132, 446-454.e5.	v and Clinical	1.5	147
2026	Epigenetics and Colorectal Cancer Pathogenesis. Cancers, 2013, 5, 676-713.		1.7	195
2027	Molecular Basis for the Regulation of the H3K4 Methyltransferase Activity of PRDM9. Co 2013, 5, 13-20.	ll Reports,	2.9	100
2028	Beyond GWASs: Illuminating the Dark Road from Association to Function. American Jou Genetics, 2013, 93, 779-797.	rnal of Human	2.6	688
2029	The Landscape of Microsatellite Instability in Colorectal and Endometrial Cancer Genom 155, 858-868.	es. Cell, 2013,	13.5	311
2030	Effect of natural genetic variation on enhancer selection and function. Nature, 2013, 50	3, 487-492.	13.7	294
2031	Extended Self-Renewal and Accelerated Reprogramming in the Absence of Kdm5b. Mole Cellular Biology, 2013, 33, 4793-4810.	cular and	1.1	58
2032	A Potential Suppressive Effect of Natural Antisense IL-1Î ² RNA on Lipopolysaccharide-Inc Expression. Journal of Immunology, 2013, 190, 6570-6578.	uced IL-1Î ²	0.4	28
2033	Long range epigenetic silencing is a transâ€species mechanism that results in cancer sp deregulation by overriding the chromatin domains of normal cells. Molecular Oncology, 1129-1141.		2.1	13
2034	Epigenetic Alterations in Oncogenesis. Advances in Experimental Medicine and Biology,	2013, 754, v-vii.	0.8	10
2035	CTCF: the protein, the binding partners, the binding sites and their chromatin loops. Phi Transactions of the Royal Society B: Biological Sciences, 2013, 368, 20120369.	osophical	1.8	191

#	Article	IF	CITATIONS
2036	Chromatin structure, pluripotency and differentiation. Experimental Biology and Medicine, 2013, 238, 259-270.	1.1	24
2037	Recombinant antibodies to histone post-translational modifications. Nature Methods, 2013, 10, 992-995.	9.0	58
2038	Nursing Genomics. Nursing Clinics of North America, 2013, 48, 523-556.	0.7	3
2039	Toward Breaking the Histone Code. Circulation: Cardiovascular Genetics, 2013, 6, 419-426.	5.1	0
2040	Epigenetics and Complex Traits. , 2013, , .		1
2041	An integrated transcriptome and epigenome analysis identifies a novel candidate gene for pancreatic cancer. BMC Medical Genomics, 2013, 6, 33.	0.7	31
2042	HIV latency and integration site placement in five cell-based models. Retrovirology, 2013, 10, 90.	0.9	104
2043	Experimental characterization of the human non-sequence-specific nucleic acid interactome. Genome Biology, 2013, 14, R81.	13.9	7
2044	LINEs of evidence: noncanonical DNA replication as an epigenetic determinant. Biology Direct, 2013, 8, 22.	1.9	17
2045	Epigenetic coordination of signaling pathways during the epithelial-mesenchymal transition. Epigenetics and Chromatin, 2013, 6, 28.	1.8	42
2046	Global differences in specific histone H3 methylation are associated with overweight and type 2 diabetes. Clinical Epigenetics, 2013, 5, 15.	1.8	38
2047	Epigenetic regulation of the ribosomal cistron seasonally modulates enrichment of H2A.Z and H2A.Zub in response to different environmental inputs in carp (Cyprinus carpio). Epigenetics and Chromatin, 2013, 6, 22.	1.8	22
2048	The nucleosome regulates the usage of polyadenylation sites in the human genome. BMC Genomics, 2013, 14, 912.	1.2	18
2049	Active enhancer positions can be accurately predicted from chromatin marks and collective sequence motif data. BMC Systems Biology, 2013, 7, S16.	3.0	15
2050	QChIPat: a quantitative method to identify distinct binding patterns for two biological ChIP-seq samples in different experimental conditions. BMC Genomics, 2013, 14, S3.	1.2	31
2051	Regulation of chromatin structure via histone post-translational modification and the link to carcinogenesis. Cancer and Metastasis Reviews, 2013, 32, 363-376.	2.7	50
2052	Histone H3 lysine 4 methyltransferases and demethylases in self-renewal and differentiation of stem cells. Cell and Bioscience, 2013, 3, 39.	2.1	84
2053	Cracking the ENCODE: From transcription to therapeutics. Hepatology, 2013, 57, 2532-2535.	3.6	12

#	Article	IF	Citations
2054	Nucleosome-free Region Dominates Histone Acetylation in Targeting SWR1 to Promoters for H2A.Z Replacement. Cell, 2013, 154, 1232-1245.	13.5	153
2055	Environmental Epigenomics in Health and Disease. Epigenetics and Human Health, 2013, , .	0.2	3
2056	Epigenetics of Pluripotency. Epigenetics and Human Health, 2013, , 207-223.	0.2	0
2057	Environmental Impact on Epigenetic Histone Language. Epigenetics and Human Health, 2013, , 163-187.	0.2	0
2058	Regulation of transcription by the MLL2 complex and MLL complex–associated AKAP95. Nature Structural and Molecular Biology, 2013, 20, 1156-1163.	3.6	51
2059	Environmental Epigenomics in Health and Disease. Epigenetics and Human Health, 2013, , .	0.2	3
2060	Microbiota impact on the epigenetic regulation of colorectal cancer. Trends in Molecular Medicine, 2013, 19, 714-725.	3.5	86
2061	Clinical and Pathologic Impact of Select Chromatin-modulating Tumor Suppressors in Clear Cell Renal Cell Carcinoma. European Urology, 2013, 63, 848-854.	0.9	198
2062	DNA methylation and differentiation: silencing, upregulation and modulation of gene expression. Epigenomics, 2013, 5, 553-568.	1.0	176
2063	The lysine specific demethylaseâ€1 (LSD1/KDM1A) regulates VEGFâ€A expression in prostate cancer. Molecular Oncology, 2013, 7, 555-566.	2.1	87
2064	Mapping Human Epigenomes. Cell, 2013, 155, 39-55.	13.5	481
2065	A Histone Acetylation Switch Regulates H2A.Z Deposition by the SWR-C Remodeling Enzyme. Science, 2013, 340, 195-199.	6.0	168
2066	Analysis for the Combinations of Histone Modifications inS.Cerevisiae. Biotechnology and Biotechnological Equipment, 2013, 27, 4026-4030.	0.5	1
2067	High-Resolution Mapping of In vivo Genomic Transcription Factor Binding Sites Using In situ DNase I Footprinting and ChIP-seq. DNA Research, 2013, 20, 325-338.	1.5	24
2068	Histone Deacetylase Inhibition Activates Transgene Expression from Integration-Defective Lentiviral Vectors in Dividing and Non-Dividing Cells. Human Gene Therapy, 2013, 24, 78-96.	1.4	50
2069	Differential analysis of rna methylation sequencing data. , 2013, , .		0
2070	From histones to RNA: role of methylation in cancer. Briefings in Functional Genomics, 2013, 12, 244-253.	1.3	20
2071	Complexity of the Alternative Splicing Landscape in Plants Â. Plant Cell, 2013, 25, 3657-3683.	3.1	731

#	Article	IF	CITATIONS
2072	Characterization of H3K9me3- and H4K20me3-associated circulating nucleosomal DNA by high-throughput sequencing in colorectal cancer. Tumor Biology, 2013, 34, 329-336.	0.8	57
2073	Epigenetic regulation of memory formation and maintenance. Learning and Memory, 2013, 20, 61-74.	0.5	294
2074	The Proteomic Investigation of Chromatin Functional Domains Reveals Novel Synergisms among Distinct Heterochromatin Components. Molecular and Cellular Proteomics, 2013, 12, 764-780.	2.5	54
2075	The epigenome of AML stem and progenitor cells. Epigenetics, 2013, 8, 92-104.	1.3	38
2076	Chromatin marks identify critical cell types for fine mapping complex trait variants. Nature Genetics, 2013, 45, 124-130.	9.4	553
2077	The methylation landscape of tumour metastasis. Biology of the Cell, 2013, 105, 73-90.	0.7	39
2078	Posttranscriptional Gene Regulation by Long Noncoding RNA. Journal of Molecular Biology, 2013, 425, 3723-3730.	2.0	517
2079	Intestinal Master Transcription Factor CDX2 Controls Chromatin Access for Partner Transcription Factor Binding. Molecular and Cellular Biology, 2013, 33, 281-292.	1.1	76
2080	BroadPeak: a novel algorithm for identifying broad peaks in diffuse ChIP-seq datasets. Bioinformatics, 2013, 29, 492-493.	1.8	33
2081	Genome-wide Chromatin State Transitions Associated with Developmental and Environmental Cues. Cell, 2013, 152, 642-654.	13.5	473
2082	Latent Enhancers Activated by Stimulation in Differentiated Cells. Cell, 2013, 152, 157-171.	13.5	693
2083	Embryonic stem cell and induced pluripotent stem cell: an epigenetic perspective. Cell Research, 2013, 23, 49-69.	5.7	152
2084	H2A.Z Facilitates Access of Active and Repressive Complexes to Chromatin in Embryonic Stem Cell Self-Renewal and Differentiation. Cell Stem Cell, 2013, 12, 180-192.	5.2	272
2085	Extensive histone post-translational modification in honey bees. Insect Biochemistry and Molecular Biology, 2013, 43, 125-137.	1.2	63
2086	Megabase Replication Domains Along the Human Genome: Relation to Chromatin Structure and Genome Organisation. Sub-Cellular Biochemistry, 2013, 61, 57-80.	1.0	15
2087	Epigenetic regulation in pluripotent stem cells: a key to breaking the epigenetic barrier. Philosophical Transactions of the Royal Society B: Biological Sciences, 2013, 368, 20120292.	1.8	107
2088	Minicircle DNA Vectors Achieve Sustained Expression Reflected by Active Chromatin and Transcriptional Level. Molecular Therapy, 2013, 21, 131-138.	3.7	103
2089	Methods for Cancer Epigenome Analysis. Advances in Experimental Medicine and Biology, 2013, 754, 313-338.	0.8	22

#	Article	IF	CITATIONS
2090	Genome-wide profiling of histone H3K4-tri-methylation and gene expression in rice under drought stress. Plant Molecular Biology, 2013, 81, 175-188.	2.0	164
2091	Regulation of Transcription through Acetylation of H3K122 on the Lateral Surface of the Histone Octamer. Cell, 2013, 152, 859-872.	13.5	209
2092	Genome-wide maps of polyadenylation reveal dynamic mRNA 3′-end formation in mammalian cell lineages. Rna, 2013, 19, 413-425.	1.6	46
2093	Connections between chromatin signatures and splicing. Wiley Interdisciplinary Reviews RNA, 2013, 4, 77-91.	3.2	46
2094	Doxorubicin Enhances Nucleosome Turnover around Promoters. Current Biology, 2013, 23, 782-787.	1.8	89
2095	InÂVivo T-Box Transcription Factor Profiling Reveals Joint Regulation of Embryonic Neuromesodermal Bipotency. Cell Reports, 2013, 4, 1185-1196.	2.9	97
2096	A Novel Mechanism for CTCF in the Epigenetic Regulation of Bax in Breast Cancer Cells. Neoplasia, 2013, 15, 898-IN14.	2.3	26
2097	Chemical genomics for studying parasite gene function and interaction. Trends in Parasitology, 2013, 29, 603-611.	1.5	4
2098	LinkNMF: Identification of histone modification modules in the human genome using nonnegative matrix factorization. Gene, 2013, 518, 215-221.	1.0	4
2099	SET for life: biochemical activities and biological functions of SET domain-containing proteins. Trends in Biochemical Sciences, 2013, 38, 621-639.	3.7	244
2100	Regulation of a Mammalian Gene Bearing a CpG Island Promoter and a Distal Enhancer. Cell Reports, 2013, 4, 445-453.	2.9	15
2102	Targeting DNA damage response: Threshold, chromatin landscape and beyond. , 2013, 138, 46-52.		5
2103	A tiered hidden Markov model characterizes multi-scale chromatin states. Genomics, 2013, 102, 1-7.	1.3	15
2104	Three promoters regulate the transcriptional activity of the human holocarboxylase synthetase gene. Journal of Nutritional Biochemistry, 2013, 24, 1963-1969.	1.9	4
2105	Complex genomic interactions in the dynamic regulation of transcription by the glucocorticoid receptor. Molecular and Cellular Endocrinology, 2013, 380, 16-24.	1.6	59
2106	Alternative splicing switching in stem cell lineages. Frontiers in Biology, 2013, 8, 50-59.	0.7	22
2107	Ethanol Induces Epigenetic Modulation of Prodynorphin and Pronociceptin Gene Expression in the Rat Amygdala Complex. Journal of Molecular Neuroscience, 2013, 49, 312-319.	1.1	71
2108	Dietary phytochemicals and cancer prevention: Nrf2 signaling, epigenetics, and cell death mechanisms in blocking cancer initiation and progression. , 2013, 137, 153-171.		210

#	Article	IF	CITATIONS
2109	High-throughput chromatin immunoprecipitation for genome-wide mapping of in vivo protein-DNA interactions and epigenomic states. Nature Protocols, 2013, 8, 539-554.	5.5	246
2110	Notch pathway activation targets AML-initiating cell homeostasis and differentiation. Journal of Experimental Medicine, 2013, 210, 301-319.	4.2	148
2111	Highâ€ŧhroughput sequencing for biology and medicine. Molecular Systems Biology, 2013, 9, 640.	3.2	251
2112	Genome-wide distribution of DNA methylation and DNA demethylation and related chromatin regulators in cancer. Biochimica Et Biophysica Acta: Reviews on Cancer, 2013, 1835, 155-163.	3.3	18
2113	Transcriptional and epigenetic regulation of human microRNAs. Cancer Letters, 2013, 331, 1-10.	3.2	111
2114	β-Estradiol-dependent activation of the JAK/STAT pathway requires p/CIP and CARM1. Biochimica Et Biophysica Acta - Molecular Cell Research, 2013, 1833, 1463-1475.	1.9	17
2115	Chromatin proteins captured by ChIP–mass spectrometry are linked to dosage compensation in Drosophila. Nature Structural and Molecular Biology, 2013, 20, 202-209.	3.6	100
2116	Histone Variants and Transcription Regulation. Sub-Cellular Biochemistry, 2013, 61, 319-341.	1.0	6
2117	Small-molecular modulators of cancer-associated epigenetic mechanisms. Molecular BioSystems, 2013, 9, 873.	2.9	42
2118	Web Resources for microRNA Research. Advances in Experimental Medicine and Biology, 2013, 774, 225-250.	0.8	16
2119	"Seq-ing―Insights into the Epigenetics of Neuronal Gene Regulation. Neuron, 2013, 77, 606-623.	3.8	73
2120	Epigenomics: Sequencing the Methylome. Methods in Molecular Biology, 2013, 973, 39-54.	0.4	3
2121	H2A.Z-dependent crosstalk between enhancer and promoter regulates Cyclin D1 expression. Oncogene, 2013, 32, 4243-4251.	2.6	44
2122	Pan-genomic binding of hypoxia-inducible transcription factors. Biological Chemistry, 2013, 394, 507-517.	1.2	90
2123	Transcription-dependent dynamic supercoiling is a short-range genomic force. Nature Structural and Molecular Biology, 2013, 20, 396-403.	3.6	270
2124	Signaling Pathways Differentially Affect RNA Polymerase II Initiation, Pausing, and Elongation Rate in Cells. Molecular Cell, 2013, 50, 212-222.	4.5	300
2125	Analysis of p300 Occupancy at the Early Stage of Stem Cell Differentiation by Chromatin Immunoprecipitation. Methods in Molecular Biology, 2013, 977, 315-321.	0.4	4
2126	Retinoic acid dependent histone 3 demethylation of the clustered <i>HOX</i> genes during neural differentiation of human embryonic stem cells. Biochemistry and Cell Biology, 2013, 91, 116-122.	0.9	26

ARTICLE IF CITATIONS Next-generation sequencing technologies for personalized medicine: promising but challenging. 2127 2.3 5 Science China Life Sciences, 2013, 56, 101-103. Cancer genome-sequencing study design. Nature Reviews Genetics, 2013, 14, 321-332. 2128 Epigenetic therapy: use of agents targeting deacetylation and methylation in cancer management. 2129 1.0 38 OncoTargets and Therapy, 2013, 6, 223. Mechanisms and Dynamics of Heterochromatin Formation During Mammalian Development. Current 2130 Topics in Developmental Biology, 2013, 104, 1-45. Genome-wide analysis reveals TET-and TDG-mediated 5-methylcytosine oxidation dynamics. Epigenetics 2131 1.8 0 and Chromatin, 2013, 6, . Modification of Enhancer Chromatin: What, How, and Why?. Molecular Cell, 2013, 49, 825-837. 1,200 4.5 The Role of DNA Methylation and Histone Modifications in Transcriptional Regulation in Humans. 2133 1.0 168 Sub-Cellular Biochemistry, 2013, 61, 289-317. Epigenetic Marking of the Zebrafish Developmental Program. Current Topics in Developmental Biology, 2134 1.0 2013, 104, 85-112 Genome-wide Analysis Reveals TET- and TDG-Dependent 5-Methylcytosine Oxidation Dynamics. Cell, 2013, 2135 13.5 440 153, 692-706. Predicting long non-coding RNAs using RNA sequencing. Methods, 2013, 63, 50-59. 1.9 DNA Methylation and Cancer Development: Molecular Mechanism. Cell Biochemistry and Biophysics, 2137 0.9 120 2013, 67, 501-513. Epigenetic Changes in Inflammatory and Autoimmune Diseases. Sub-Cellular Biochemistry, 2013, 61, 2138 1.0 24 455-478. Systems Proteomics of Healthy and Diseased Chromatin. Methods in Molecular Biology, 2013, 1005, 2139 0.4 1 77-93. Chromatin architecture defines the glucocorticoid response. Molecular and Cellular Endocrinology, 2140 1.6 2013, 380, 25-31. Epigenetic mechanisms in Alzheimer's disease: Implications for pathogenesis and therapy. Ageing 2141 5.0110 Research Reviews, 2013, 12, 1024-1041. Epigenetic changes in renal genes dysregulated in mouse and rat models of type 1 diabetes. Laboratory 2142 Investigation, 2013, 93, 543-552. Epigenetic Regulation of the Electrophysiological Phenotype of Human Embryonic Stem Cell-Derived 2143 Ventricular Cardiomyocytes: Insights for Driven Maturation and Hypertrophic Growth. Stem Cells 1.1 25 and Development, 2013, 22, 2678-2690. 2144 Multifaceted role of EZH2 in breast and prostate tumorigenesis. Epigenetics, 2013, 8, 464-476. 1.3

#	Article	IF	CITATIONS
2145	Computational Identification of Active Enhancers in Model Organisms. Genomics, Proteomics and Bioinformatics, 2013, 11, 142-150.	3.0	15
2146	BAF complexes facilitate decatenation of DNA by topoisomerase Ilα. Nature, 2013, 497, 624-627.	13.7	230
2147	Biology and Clinical Relevance of Estrogen Receptors in Prostate Cancer. , 2013, , 383-419.		0
2148	Epigenetic Control of Cytokine Gene Expression. Advances in Immunology, 2013, 118, 37-128.	1.1	60
2150	New Insights from Existing Sequence Data: Generating Breakthroughs without a Pipette. Molecular Cell, 2013, 49, 605-617.	4.5	12
2151	Chromatin Insulators: Linking Genome Organization to Cellular Function. Molecular Cell, 2013, 50, 461-474.	4.5	201
2152	Ectopic Activation of Germline and Placental Genes Identifies Aggressive Metastasis-Prone Lung Cancers. Science Translational Medicine, 2013, 5, 186ra66.	5.8	392
2153	Chd5 Requires PHD-Mediated Histone 3 Binding for Tumor Suppression. Cell Reports, 2013, 3, 92-102.	2.9	47
2154	Uniform, optimal signal processing of mapped deep-sequencing data. Nature Biotechnology, 2013, 31, 615-622.	9.4	145
2155	Epigenetics in the heart: the role of histone modifications in cardiac remodelling. Biochemical Society Transactions, 2013, 41, 789-796.	1.6	34
2156	Aberrant Epigenetic Gene Regulation in Lymphoid Malignancies. Seminars in Hematology, 2013, 50, 38-47.	1.8	17
2157	Browsing (Epi)genomes: A Guide to Data Resources and Epigenome Browsers for Stem Cell Researchers. Cell Stem Cell, 2013, 13, 14-21.	5.2	19
2158	PfSETvs methylation of histone H3K36 represses virulence genes in Plasmodium falciparum. Nature, 2013, 499, 223-227.	13.7	219
2159	Global H3K4me3 genome mapping reveals alterations of innate immunity signaling and overexpression of JMJD3 in human myelodysplastic syndrome CD34+ cells. Leukemia, 2013, 27, 2177-2186.	3.3	74
2160	On your histone mark, SET, methylate!. Epigenetics, 2013, 8, 457-463.	1.3	68
2161	Organizing the genome with H2A histone variants. Biochemical Journal, 2013, 449, 567-579.	1.7	34
2162	The correlation between histone modifications and gene expression. Epigenomics, 2013, 5, 113-116.	1.0	154
2163	Epigenome Analysis of Pluripotent Stem Cells. Methods in Molecular Biology, 2013, 997, 203-216.	0.4	2

#	Article	IF	CITATIONS
2165	The cancerâ€ŧestis antigen BORIS phenocopies the tumor suppressor CTCF in normal and neoplastic cells. International Journal of Cancer, 2013, 133, 1603-1613.	2.3	48
2166	A Method for Systematic Mapping of Protein Lysine Methylation Identifies Functions for HP1β in DNA Damage Response. Molecular Cell, 2013, 50, 723-735.	4.5	98
2167	Transcriptional regulation by the Set7 lysine methyltransferase. Epigenetics, 2013, 8, 361-372.	1.3	71
2168	Non-coding transcription at cis-regulatory elements: Computational and experimental approaches. Methods, 2013, 63, 66-75.	1.9	6
2169	The PARP inhibitor PJ34 modifies proliferation, NIS expression and epigenetic marks in thyroid cancer cell lines. Molecular and Cellular Endocrinology, 2013, 365, 1-10.	1.6	17
2170	Gene dysregulation by histone variant H2A.Z in bladder cancer. Epigenetics and Chromatin, 2013, 6, 34.	1.8	74
2171	Reduced C9orf72 gene expression in c9FTD/ALS is caused by histone trimethylation, an epigenetic event detectable in blood. Acta Neuropathologica, 2013, 126, 895-905.	3.9	263
2172	EPD and EPDnew, high-quality promoter resources in the next-generation sequencing era. Nucleic Acids Research, 2013, 41, D157-D164.	6.5	131
2173	A Bayesian Graphical Model for ChIP-Seq Data on Histone Modifications. Journal of the American Statistical Association, 2013, 108, 69-80.	1.8	23
2174	A Small-Molecule Inducer of PDX1 Expression Identified by High-Throughput Screening. Chemistry and Biology, 2013, 20, 1513-1522.	6.2	34
2175	Quantitative analysis reveals increased histone modifications and a broad nucleosome-free region bound by histone acetylases in highly expressed genes in human CD4+ T cells. Genomics, 2013, 101, 113-119.	1.3	7
2176	New opportunities for organ transplantation research: epigenetics is likely to be an important determinant of the host immune response. Epigenomics, 2013, 5, 243-246.	1.0	3
2177	A neural network based algorithm for gene expression prediction from chromatin structure. , 2013, , .		13
2178	H3.3 actively marks enhancers and primes gene transcription via opening higher-ordered chromatin. Genes and Development, 2013, 27, 2109-2124.	2.7	185
2179	Site-Specific and Regiospecific Installation of Methylarginine Analogues into Recombinant Histones and Insights into Effector Protein Binding. Journal of the American Chemical Society, 2013, 135, 2879-2882.	6.6	42
2180	Preferential localization of γH2AX foci in euchromatin of retina rod cells after DNA damage induction. Chromosome Research, 2013, 21, 789-803.	1.0	11
2181	Interplay between chromatin modifications and paused RNA polymerase II in dynamic transition between stalled and activated genes. Biological Reviews, 2013, 88, 40-48.	4.7	20
2182	Histone 3 Lysine 9 Trimethylation Is Differentially Associated With Isocitrate Dehydrogenase Mutations in Oligodendrogliomas and High-Grade Astrocytomas. Journal of Neuropathology and Experimental Neurology, 2013, 72, 298-306.	0.9	51

ARTICLE IF CITATIONS Mapping Yeast Transcriptional Networks. Genetics, 2013, 195, 9-36. 1.2 72 2183 The Role of Histone Demethylase GASC1 in Cancer and its Therapeutic Potential. Current Cancer 2184 0.2 Therapy Reviews, 2013, 9, 78-85. Discovery of cell-type specific regulatory elements in the human genome using differential chromatin 2185 6.5 19 modification analysis. Nucleic Acids Research, 2013, 41, 9230-9242. KDM5B histone demethylase controls epithelial-mesenchymal transition of cancer cells by regulating 2186 the expression of the microRNA-200 family. Cell Cycle, 2013, 12, 2100-2112. Integrating and mining the chromatin landscape of cell-type specificity using self-organizing maps. 2187 2.4 51 Genome Research, 2013, 23, 2136-2148. Systematic dissection of regulatory motifs in 2000 predicted human enhancers using a massively parallel reporter assay. Genome Research, 2013, 23, 800-811. 2188 2.4 298 Predicting the probability of H3K4me3 occupation at a base pair from the genome sequence context. 2189 1.8 5 Bioinformatics, 2013, 29, 1199-1205. Inferring chromatin-bound protein complexes from genome-wide binding assays. Genome Research, 2013, 23, 1295-1306. 2190 2.4 2191 Functional transcriptomics in the post-ENCODE era. Genome Research, 2013, 23, 1961-1973. 2.4 58 Chromatin and epigenetic features of long-range gene regulation. Nucleic Acids Research, 2013, 41, 6.5 7185-7199. Ash2 acts as an ecdysone receptor coactivator by stabilizing the histone methyltransferase Trr. 2193 0.9 18 Molecular Biology of the Cell, 2013, 24, 361-372. H2A.Z Acidic Patch Couples Chromatin Dynamics to Regulation of Gene Expression Programs during 2194 1.5 ESC Differentiation. PLo'S Genetics, 2013, 9, e1003725 Suv4-20h Histone Methyltransferases Promote Neuroectodermal Differentiation by Silencing the 2195 1.5 30 Pluripotency-Associated Oct-25 Gene. PLoS Genetics, 2013, 9, e1003188. Practical Guidelines for the Comprehensive Analysis of ChIP-seq Data. PLoS Computational Biology, 2196 1.5 221 2013, 9, e1003326. Estrogen receptor \hat{I} t can selectively repress dioxin receptor-mediated gene expression by targeting DNA 2197 6.5 75 methylation. Nucleic Acids Research, 2013, 41, 8094-8106. USF1 and hSET1A Mediated Epigenetic Modifications Regulate Lineage Differentiation and HoxB4 2198 Transcription. PLoS Genetics, 2013, 9, e1003524. HMCan: a method for detecting chromatin modifications in cancer samples using ChIP-seq data. 2199 1.8 39 Bioinformatics, 2013, 29, 2979-2986. 2200 Role of Polycomb Proteins in Regulating HSV-1 Latency. Viruses, 2013, 5, 1740-1757. 1.5

#	Article	IF	CITATIONS
2201	Finding Associations among Histone Modifications Using Sparse Partial Correlation Networks. PLoS Computational Biology, 2013, 9, e1003168.	1.5	39
2202	The Histone Demethylase Jarid1b Ensures Faithful Mouse Development by Protecting Developmental Genes from Aberrant H3K4me3. PLoS Genetics, 2013, 9, e1003461.	1.5	114
2203	Dynamic changes in genomic histone association and modification during activation of the <i>ASNS</i> and <i>ATF3</i> genes by amino acid limitation. Biochemical Journal, 2013, 449, 219-229.	1.7	8
2204	Sparsely correlated hidden Markov models with application to genome-wide location studies. Bioinformatics, 2013, 29, 533-541.	1.8	15
2205	Compound cis-regulatory elements with both boundary and enhancer sequences in the human genome. Bioinformatics, 2013, 29, 3109-3112.	1.8	2
2206	Major Histocompatibility Complex Class I Core Promoter Elements Are Not Essential for Transcription <i>in vivo</i> . Molecular and Cellular Biology, 2013, 33, 4395-4407.	1.1	9
2207	Understanding Variation in Transcription Factor Binding by Modeling Transcription Factor Genome-Epigenome Interactions. PLoS Computational Biology, 2013, 9, e1003367.	1.5	26
2208	Integrated Transcriptomic and Epigenomic Analysis of Primary Human Lung Epithelial Cell Differentiation. PLoS Genetics, 2013, 9, e1003513.	1.5	46
2209	Alpha-Interferon Suppresses Hepadnavirus Transcription by Altering Epigenetic Modification of cccDNA Minichromosomes. PLoS Pathogens, 2013, 9, e1003613.	2.1	135
2210	Navigating the transcriptional roadmap regulating plant secondary cell wall deposition. Frontiers in Plant Science, 2013, 4, 325.	1.7	124
2211	Human Genome Replication Proceeds through Four Chromatin States. PLoS Computational Biology, 2013, 9, e1003233.	1.5	54
2212	dPeak: High Resolution Identification of Transcription Factor Binding Sites from PET and SET ChIP-Seq Data. PLoS Computational Biology, 2013, 9, e1003246.	1.5	15
2213	A Newly Uncovered Group of Distantly Related Lysine Methyltransferases Preferentially Interact with Molecular Chaperones to Regulate Their Activity. PLoS Genetics, 2013, 9, e1003210.	1.5	138
2214	Binding of NF-κB to Nucleosomes: Effect of Translational Positioning, Nucleosome Remodeling and Linker Histone H1. PLoS Genetics, 2013, 9, e1003830.	1.5	50
2215	Dynamic Epigenetic Regulation of Gene Expression during the Life Cycle of Malaria Parasite Plasmodium falciparum. PLoS Pathogens, 2013, 9, e1003170.	2.1	90
2216	Mass Spectrometry-Based Proteomics for the Analysis of Chromatin Structure and Dynamics. International Journal of Molecular Sciences, 2013, 14, 5402-5431.	1.8	31
2217	Regulation of the Boundaries of Accessible Chromatin. PLoS Genetics, 2013, 9, e1003778.	1.5	16
2218	Silicon Era of Carbon-Based Life: Application of Genomics and Bioinformatics in Crop Stress Research. International Journal of Molecular Sciences, 2013, 14, 11444-11483.	1.8	8

#	Article	IF	CITATIONS
2219	Decoding a Signature-Based Model of Transcription Cofactor Recruitment Dictated by Cardinal Cis-Regulatory Elements in Proximal Promoter Regions. PLoS Genetics, 2013, 9, e1003906.	1.5	38
2220	EMdeCODE: a novel algorithm capable of reading words of epigenetic code to predict enhancers and retroviral integration sites and to identify H3R2me1 as a distinctive mark of coding versus non-coding genes. Nucleic Acids Research, 2013, 41, e48-e48.	6.5	9
2221	The histone H3.3K27M mutation in pediatric glioma reprograms H3K27 methylation and gene expression. Genes and Development, 2013, 27, 985-990.	2.7	570
2222	CTCF depletion alters chromatin structure and transcription of myeloid-specific factors. Journal of Molecular Cell Biology, 2013, 5, 308-322.	1.5	7
2223	Chromatin patterns associated with lung adenocarcinoma progression. Cell Cycle, 2013, 12, 1536-1543.	1.3	18
2224	Quantitative Proteomics Reveals That the Specific Methyltransferases Txr1p and Ezl2p Differentially Affect the Mono-, Di- and Trimethylation States of Histone H3 Lysine 27 (H3K27). Molecular and Cellular Proteomics, 2013, 12, 1678-1688.	2.5	16
2225	Effects of gene regulatory reprogramming on gene expression in human and mouse developing hearts. Philosophical Transactions of the Royal Society B: Biological Sciences, 2013, 368, 20120366.	1.8	6
2226	Deciphering cis -regulatory control in inflammatory cells. Philosophical Transactions of the Royal Society B: Biological Sciences, 2013, 368, 20120370.	1.8	17
2227	Control of Histone H3 Lysine 9 (H3K9) Methylation State via Cooperative Two-step Demethylation by Jumonji Domain Containing 1A (JMJD1A) Homodimer. Journal of Biological Chemistry, 2013, 288, 36948-36956.	1.6	25
2228	Segmenting the human genome based on states of neutral genetic divergence. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 14699-14704.	3.3	18
2229	Interplay between chromatin state, regulator binding, and regulatory motifs in six human cell types. Genome Research, 2013, 23, 1142-1154.	2.4	84
2230	Quantitative epigenetic co-variation in CpG islands and co-regulation of developmental genes. Scientific Reports, 2013, 3, 2576.	1.6	20
2231	Long non-coding RNA identification over mouse brain development by integrative modeling of chromatin and genomic features. Nucleic Acids Research, 2013, 41, 10044-10061.	6.5	65
2232	RNA polymerase II progression through H3K27me3-enriched gene bodies requires JMJD3 histone demethylase. Molecular Biology of the Cell, 2013, 24, 351-360.	0.9	48
2234	Integrated Analysis of Dysregulated IncRNA Expression in Fetal Cardiac Tissues with Ventricular Septal Defect. PLoS ONE, 2013, 8, e77492.	1.1	41
2235	Meeting the methodological challenges in molecular mapping of the embryonic epigenome. Molecular Human Reproduction, 2013, 19, 809-827.	1.3	11
2236	Immunology meets genomics. Briefings in Functional Genomics, 2013, 12, 469-470.	1.3	0
2237	DOT1L-Mediated H3K79 Methylation in Chromatin Is Dispensable for Wnt Pathway-Specific and Other Intestinal Epithelial Functions. Molecular and Cellular Biology, 2013, 33, 1735-1745.	1.1	31

#	Article	IF	CITATIONS
2238	Retroviral DNA Methylation and Epigenetic Repression Are Mediated by the Antiviral Host Protein Daxx. Journal of Virology, 2013, 87, 2137-2150.	1.5	47
2239	The Igf2/H19 muscle enhancer is an active transcriptional complex. Nucleic Acids Research, 2013, 41, 8126-8134.	6.5	19
2240	Epigenetic regulation of memory: implications in human cognitive disorders. Biomolecular Concepts, 2013, 4, 1-12.	1.0	20
2241	The emerging roles for histone demethylases in the modulation of signaling pathways. Biomolecular Concepts, 2013, 4, 13-27.	1.0	5
2242	Lamin B1 depletion in senescent cells triggers large-scale changes in gene expression and the chromatin landscape. Genes and Development, 2013, 27, 1787-1799.	2.7	440
2243	Mechanisms of in vivo binding site selection of the hematopoietic master transcription factor PU.1. Nucleic Acids Research, 2013, 41, 6391-6402.	6.5	76
2244	A general approach for discriminative de novo motif discovery from high-throughput data. Nucleic Acids Research, 2013, 41, e197-e197.	6.5	44
2245	Wellington: a novel method for the accurate identification of digital genomic footprints from DNase-seq data. Nucleic Acids Research, 2013, 41, e201-e201.	6.5	196
2246	Epigenomic plasticity enables human pancreatic $\hat{I}\pm$ to \hat{I}^2 cell reprogramming. Journal of Clinical Investigation, 2013, 123, 1275-1284.	3.9	365
2247	Detecting DNA–Protein Interactions in Living Cells—ChIP Approach. Advances in Protein Chemistry and Structural Biology, 2013, 91, 101-133.	1.0	6
2248	Purification of a specific native genomic locus for proteomic analysis. Nucleic Acids Research, 2013, 41, e195-e195.	6.5	49
2249	The mutational landscape of chromatin regulatory factors across 4,623 tumor samples. Genome Biology, 2013, 14, r106.	13.9	102
2250	Hallmarks of Aromatase Inhibitor Drug Resistance Revealed by Epigenetic Profiling in Breast Cancer. Cancer Research, 2013, 73, 6632-6641.	0.4	79
2251	Alteration of Histone H3 Lysine 4 Trimethylation on Putative Lytic Gene Promoters by Human Set1 Complex during Reactivation of Kaposi's Sarcoma-Associated Herpesvirus. Intervirology, 2013, 56, 91-103.	1.2	6
2252	Deciphering the transcriptional regulation of microRNA genes in humans with ACTLocater. Nucleic Acids Research, 2013, 41, e5-e5.	6.5	11
2253	Heterochromatinization induced by GAA-repeat hyperexpansion in Friedreich's ataxia can be reduced upon HDAC inhibition by vitamin B3. Human Molecular Genetics, 2013, 22, 2662-2675.	1.4	71
2254	Differential principal component analysis of ChIP-seq. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 6789-6794.	3.3	48
2255	Structural polymorphism in the L1 loop regions of human H2A.Z.1 and H2A.Z.2. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 2431-2439.	2.5	55

#	Article	IF	CITATIONS
2256	Unexplored Potentials of Epigenetic Mechanisms of Plants and Animals–-Theoretical Considerations. Genetics & Epigenetics, 2013, 5, GEG.S11752.	2.5	7
2257	The History of DNA Sequencing / ISTORIJAT SEKVENCIRANJA DNK. Journal of Medical Biochemistry, 2013, 32, 301-312.	0.7	21
2258	A lesson learned from the H3.3K27M mutation found in pediatric glioma. Cell Cycle, 2013, 12, 2546-2552.	1.3	50
2259	Regional chromatin decompaction in Cornelia de Lange syndrome associated with NIPBL disruption can be uncoupled from cohesin and CTCF. Human Molecular Genetics, 2013, 22, 4180-4193.	1.4	35
2260	Methylation of Histone H3 on Lysine 4 by the Lysine Methyltransferase SET1 Protein Is Needed for Normal Clock Gene Expression. Journal of Biological Chemistry, 2013, 288, 8380-8390.	1.6	49
2261	Unveiling the dynamics in RNA epigenetic regulations. , 2013, , .		6
2262	Gene regulation and epigenetics in Friedreich's ataxia. Journal of Neurochemistry, 2013, 126, 21-42.	2.1	49
2263	Epigenetic regulation of inducible gene expression in the immune system. Immunology, 2013, 139, 285-293.	2.0	52
2264	<scp>H2A.Z</scp> and <scp>H2B.Z</scp> doubleâ€variant nucleosomes define intergenic regions and dynamically occupy <scp><i>var</i></scp> gene promoters in the malaria parasite <i><scp>P</scp>lasmodium falciparum</i> . Molecular Microbiology, 2013, 87, 1167-1182.	1.2	67
2265	A double take on bivalent promoters. Genes and Development, 2013, 27, 1318-1338.	2.7	699
2266	Roles of histone methylâ€modifying enzymes in development and progression of cancer. Cancer Science, 2013, 104, 795-800.	1.7	25
2267	Nucleosome Distribution near the 3′ Ends of Genes in the Human Genome. Bioscience, Biotechnology and Biochemistry, 2013, 77, 2051-2055.	0.6	9
2268	Intragenic DNA methylation modulates alternative splicing by recruiting MeCP2 to promote exon recognition. Cell Research, 2013, 23, 1256-1269.	5.7	489
2269	RNA-sequencing analysis of high glucose-treated monocytes reveals novel transcriptome signatures and associated epigenetic profiles. Physiological Genomics, 2013, 45, 287-299.	1.0	28
2270	Defective DNA damage response and repair in liver cells expressing hepatitis B virus surface antigen. FASEB Journal, 2013, 27, 2316-2327.	0.2	17
2271	Histone H3 lysine methylation in cognition and intellectual disability disorders. Learning and Memory, 2013, 20, 570-579.	0.5	52
2272	Genome-Wide Analysis of Chromatin States Reveals Distinct Mechanisms of Sex-Dependent Gene Regulation in Male and Female Mouse Liver. Molecular and Cellular Biology, 2013, 33, 3594-3610.	1.1	140
2273	Histone variant selectivity at the transcription start site: H2A.Z or H2A.Lap1. Nucleus, 2013, 4, 431-437.	0.6	24

#	Article	IF	CITATIONS
2274	Conserved Chromosome 2q31 Conformations Are Associated with Transcriptional Regulation of GAD1 GABA Synthesis Enzyme and Altered in Prefrontal Cortex of Subjects with Schizophrenia. Journal of Neuroscience, 2013, 33, 11839-11851.	1.7	60
2275	The Malignant Brain Tumor (MBT) Domain Protein SFMBT1 Is an Integral Histone Reader Subunit of the LSD1 Demethylase Complex for Chromatin Association and Epithelial-to-mesenchymal Transition. Journal of Biological Chemistry, 2013, 288, 27680-27691.	1.6	42
2276	The Trithorax Group Protein Ash2l Is Essential for Pluripotency and Maintaining Open Chromatin in Embryonic Stem Cells. Journal of Biological Chemistry, 2013, 288, 5039-5048.	1.6	67
2277	Coordinate Changes in Histone Modifications, mRNA Levels, and Metabolite Profiles in Clonal INS-1 832/13 β-Cells Accompany Functional Adaptations to Lipotoxicity. Journal of Biological Chemistry, 2013, 288, 11973-11987.	1.6	66
2278	High Mobility Group Protein N5 (HMGN5) and Lamina-associated Polypeptide 2α (LAP2α) Interact and Reciprocally Affect Their Genome-wide Chromatin Organization. Journal of Biological Chemistry, 2013, 288, 18104-18109.	1.6	21
2279	Differential effects of cocaine on histone posttranslational modifications in identified populations of striatal neurons. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 9511-9516.	3.3	51
2280	Imprinting at the PLAGL1 domain is contained within a 70-kb CTCF/cohesin-mediated non-allelic chromatin loop. Nucleic Acids Research, 2013, 41, 2171-2179.	6.5	25
2281	Genome-Wide Prediction of Nucleosome Occupancy in Maize Reveals Plant Chromatin Structural Features at Genes and Other Elements at Multiple Scales Â. Plant Physiology, 2013, 162, 1127-1141.	2.3	24
2282	GWAS3D: detecting human regulatory variants by integrative analysis of genome-wide associations, chromosome interactions and histone modifications. Nucleic Acids Research, 2013, 41, W150-W158.	6.5	101
2283	Transient Expression of an LEDGF/p75 Chimera Retargets Lentivector Integration and Functionally Rescues in a Model for X-CGD. Molecular Therapy - Nucleic Acids, 2013, 2, e77.	2.3	13
2284	A novel Bayesian network inference algorithm for integrative analysis of heterogeneous deep sequencing data. Cell Research, 2013, 23, 440-443.	5.7	20
2285	Targeting genetic alterations in protein methyltransferases for personalized cancer therapeutics. Oncogene, 2013, 32, 939-946.	2.6	66
2286	Epigenetic regulation of the human genome: coherence between promoter activity and large-scale chromatin environment. Frontiers in Life Science: Frontiers of Interdisciplinary Research in the Life Sciences, 2013, 7, 44-62.	1.1	8
2287	A far downstream enhancer for murine Bcl11b controls its T-cell specific expression. Blood, 2013, 122, 902-911.	0.6	109
2288	Exploring genomes with a game engine. , 2013, , .		2
2289	Epigenetic Mechanisms in Learning and Memory. , 2013, , 121-170.		0
2290	Modulation of gene expression via overlapping binding sites exerted by ZNF143, Notch1 and THAP11. Nucleic Acids Research, 2013, 41, 4000-4014.	6.5	55
2291	Novel Long Noncoding RNAs Are Regulated by Angiotensin II in Vascular Smooth Muscle Cells. Circulation Research, 2013, 113, 266-278.	2.0	258

	CHATON	NREPORT	
#	Article	IF	CITATIONS
2292	The comprehensive epigenome map of piRNA clusters. Nucleic Acids Research, 2013, 41, 1581-1590.	6.5	29
2293	Genome-wide analysis of histone marks identifying an epigenetic signature of promoters and enhancers underlying cardiac hypertrophy. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 20164-20169.	3.3	210
2294	Establishing a hematopoietic genetic network through locus-specific integration of chromatin regulators. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E3398-407.	3.3	31
2295	SETD6 monomethylates H2AZ on lysine 7 and is required for the maintenance of embryonic stem cell self-renewal. Epigenetics, 2013, 8, 177-183.	1.3	63
2297	Nonparametric Bayesian Bi-Clustering for Next Generation Sequencing Count Data. Bayesian Analysis, 2013, 8, 759-780.	1.6	12
2298	The role of chromatin modifiers in normal and malignant hematopoiesis. Blood, 2013, 121, 3076-3084.	0.6	39
2299	Mechanisms of epigenetic deregulation in lymphoid neoplasms. Blood, 2013, 121, 4271-4279.	0.6	32
2300	Regulation of Translation as Response to Abiotic Stress. , 2013, , 127-147.		0
2301	AHT-ChIP-seq: a completely automated robotic protocol for high-throughput chromatin immunoprecipitation. Genome Biology, 2013, 14, R124.	13.9	28
2302	jMOSAiCS: joint analysis of multiple ChIP-seq datasets. Genome Biology, 2013, 14, R38.	13.9	50
2303	Genome-wide incorporation dynamics reveal distinct categories of turnover for the histone variant H3.3. Genome Biology, 2013, 14, R121.	13.9	123
2304	MMDiff: quantitative testing for shape changes in ChIP-Seq data sets. BMC Genomics, 2013, 14, 826.	1.2	30
2305	Regulation and Function of DNA and Histone Methylations. Current Pharmaceutical Design, 2013, 19, 719-733.	0.9	8
2306	Cytokine-induced Chromatin Modifications of the Type I Collagen Alpha 2 Gene during Intestinal Endothelial-to-Mesenchymal Transition. Inflammatory Bowel Diseases, 2013, 19, 1354-1364.	0.9	33
2307	From spots to beads— <scp>PTM</scp> â€peptide bead arrays for the characterization of antiâ€histone antibodies. Proteomics, 2013, 13, 1010-1015.	1.3	19
2308	Structural basis of a nucleosome containing histone H2A.B/H2A.Bbd that transiently associates with reorganized chromatin. Scientific Reports, 2013, 3, 3510.	1.6	61
2309	<i>Hoxc</i> Gene Collinear Expression and Epigenetic Modifications Established during Embryogenesis Are Maintained until after Birth. International Journal of Biological Sciences, 2013, 9, 960-965.	2.6	6
2310	The Epigenomics of Embryonic Stem Cell Differentiation. International Journal of Biological Sciences, 2013, 9, 1134-1144.	2.6	41

#	Article	IF	CITATIONS
2312	Transgenerational Inheritance in Mammals. , 2013, , 323-338.		4
2313	Epigenetic changes in colorectal cancer. Chinese Journal of Cancer, 2013, 32, 21-30.	4.9	53
2314	Epigenetic Modifications Unlock the Milk Protein Gene Loci during Mouse Mammary Gland Development and Differentiation. PLoS ONE, 2013, 8, e53270.	1.1	50
2315	Genome-Wide Alteration of Histone H3K9 Acetylation Pattern in Mouse Offspring Prenatally Exposed to Arsenic. PLoS ONE, 2013, 8, e53478.	1.1	85
2316	p63 Attenuates Epithelial to Mesenchymal Potential in an Experimental Prostate Cell Model. PLoS ONE, 2013, 8, e62547.	1.1	31
2317	Phenethylisothiocyanate Alters Site- and Promoter-Specific Histone Tail Modifications in Cancer Cells. PLoS ONE, 2013, 8, e64535.	1.1	27
2318	Posttranslational Modifications of the Histone 3 Tail and Their Impact on the Activity of Histone Lysine Demethylases In Vitro. PLoS ONE, 2013, 8, e67653.	1.1	23
2319	LOcating Non-Unique matched Tags (LONUT) to Improve the Detection of the Enriched Regions for ChIP-seq Data. PLoS ONE, 2013, 8, e67788.	1.1	12
2320	Distinct Mechanisms for Induction and Tolerance Regulate the Immediate Early Genes Encoding Interleukin 1β and Tumor Necrosis Factor α. PLoS ONE, 2013, 8, e70622.	1.1	33
2321	Multivalent Engagement of TFIID to Nucleosomes. PLoS ONE, 2013, 8, e73495.	1.1	19
2322	Synergistic Re-Activation of Epigenetically Silenced Genes by Combinatorial Inhibition of DNMTs and LSD1 in Cancer Cells. PLoS ONE, 2013, 8, e75136.	1.1	33
2323	A Silent Exonic SNP in Kdm3a Affects Nucleic Acids Structure but Does Not Regulate Experimental Autoimmune Encephalomyelitis. PLoS ONE, 2013, 8, e81912.	1.1	1
2324	RFECS: A Random-Forest Based Algorithm for Enhancer Identification from Chromatin State. PLoS Computational Biology, 2013, 9, e1002968.	1.5	205
2325	Molecular Characterization of a Human Matrix Attachment Region Epigenetic Regulator. PLoS ONE, 2013, 8, e79262.	1.1	34
2326	Potential of epigenetic mechanisms in AMD pathology. Frontiers in Bioscience - Scholar, 2013, S5, 412-425.	0.8	19
2327	T cell immunity as a tool for studying epigenetic regulation of cellular differentiation. Frontiers in Genetics, 2013, 4, 218.	1.1	43
2328	Insights into Chromatin Structure and Dynamics in Plants. Biology, 2013, 2, 1378-1410.	1.3	33
2329	Epigenetic conservation at gene regulatory elements revealed by non-methylated DNA profiling in seven vertebrates. ELife, 2013, 2, e00348.	2.8	192

#	Article	IF	CITATIONS
2330	Epigenetic biomarkers: a step forward for understanding periodontitis. Journal of Periodontal and Implant Science, 2013, 43, 111.	0.9	40
2331	Bayesian Model-Based Approaches for Solexa Sequencing Data. , 0, , 126-137.		0
2332	Statistical Aspects of ChIP-Seq Analysis. , 0, , 138-169.		1
2333	Bayesian Modeling of ChIP-Seq Data from Transcription Factor to Nucleosome Positioning. , 0, , 170-187.		0
2334	Epigenetic Reprogramming in Mist1â^'/â^' Mice Predicts the Molecular Response to Cerulein-Induced Pancreatitis. PLoS ONE, 2014, 9, e84182.	1.1	13
2335	Broad Shifts in Gene Expression during Early Postnatal Life Are Associated with Shifts in Histone Methylation Patterns. PLoS ONE, 2014, 9, e86957.	1.1	12
2336	FRA2 Is a STAT5 Target Gene Regulated by IL-2 in Human CD4 T Cells. PLoS ONE, 2014, 9, e90370.	1.1	12
2337	STEME: A Robust, Accurate Motif Finder for Large Data Sets. PLoS ONE, 2014, 9, e90735.	1.1	15
2338	Genome-Wide Analysis of the Chromatin Composition of Histone H2A and H3 Variants in Mouse Embryonic Stem Cells. PLoS ONE, 2014, 9, e92689.	1.1	18
2339	From Human Monocytes to Genome-Wide Binding Sites - A Protocol for Small Amounts of Blood: Monocyte Isolation/ChIP-Protocol/Library Amplification/Genome Wide Computational Data Analysis. PLoS ONE, 2014, 9, e94164.	1.1	4
2340	OccuPeak: ChIP-Seq Peak Calling Based on Internal Background Modelling. PLoS ONE, 2014, 9, e99844.	1.1	11
2341	Divergence and Selectivity of Expression-Coupled Histone Modifications in Budding Yeasts. PLoS ONE, 2014, 9, e101538.	1.1	7
2342	Gluco-Incretins Regulate Beta-Cell Glucose Competence by Epigenetic Silencing of Fxyd3 Expression. PLoS ONE, 2014, 9, e103277.	1.1	12
2343	Histone H3 Lysine 36 Methyltransferase Whsc1 Promotes the Association of Runx2 and p300 in the Activation of Bone-Related Genes. PLoS ONE, 2014, 9, e106661.	1.1	23
2344	Identification of Highly Conserved Putative Developmental Enhancers Bound by SOX3 in Neural Progenitors Using ChIP-Seq. PLoS ONE, 2014, 9, e113361.	1.1	27
2345	Epigenetics in T-cell Development and Function. Advances in Neuroimmune Biology, 2014, 5, 161-170.	0.7	1
2346	Bacterial SET domain proteins and their role in eukaryotic chromatin modification. Frontiers in Genetics, 2014, 5, 65.	1.1	39
2347	RNA-mediated pathogenic mechanisms in polyglutamine diseases and amyotrophic lateral sclerosis. Frontiers in Cellular Neuroscience, 2014, 8, 431.	1.8	25

#	Article	IF	CITATIONS
2348	Structure and Function of Human DNA Methyltransferases. , 2014, , .		0
2349	Genome-wide mapping of chromatin state of mouse forelimbs. Open Access Bioinformatics, 2014, 6, 1.	0.9	5
2350	A Tale of Effectors; Their Secretory Mechanisms and Computational Discovery in Pathogenic, Non-Pathogenic and Commensal Microbes. Molecular Biology (Los Angeles, Calif), 2014, 03, .	0.0	2
2351	Prediction of Gene Activity in Early B Cell Development Based on an Integrative Multi-Omics Analysis. Journal of Proteomics and Bioinformatics, 2014, 07, .	0.4	13
2352	Modelling complex features from histone modification signatures using genetic algorithm for the prediction of enhancer region. Bio-Medical Materials and Engineering, 2014, 24, 3807-3814.	0.4	4
2353	Emerging Role of the Peroxisome Proliferator-Activated Receptors in Hepatocellular Carcinoma. Journal of Carcinogenesis & Mutagenesis, 2014, 05, .	0.3	0
2357	A long non-coding RNA promotes full activation of adult gene expression in the chicken α-globin domain. Epigenetics, 2014, 9, 173-181.	1.3	50
2358	Quantifying ChIP-seq data: a spiking method providing an internal reference for sample-to-sample normalization. Genome Research, 2014, 24, 1157-1168.	2.4	143
2359	The DNA-binding factor Ctcf critically controls gene expression in macrophages. Cellular and Molecular Immunology, 2014, 11, 58-70.	4.8	34
2360	EZH2 as a potential target in cancer therapy. Epigenomics, 2014, 6, 341-351.	1.0	84
2361	Transcriptional analysis of endocrine disruption using zebrafish and massively parallel sequencing. Journal of Molecular Endocrinology, 2014, 52, R241-R256.	1.1	38
2362	Pathogenic Influenza Viruses and Coronaviruses Utilize Similar and Contrasting Approaches To Control Interferon-Stimulated Gene Responses. MBio, 2014, 5, e01174-14.	1.8	246
2363	Epigenetic regulation and heart failure. Expert Review of Cardiovascular Therapy, 2014, 12, 1087-1098.	0.6	8
2364	Chromosome boundary elements and regulation of heterochromatin spreading. Cellular and Molecular Life Sciences, 2014, 71, 4841-4852.	2.4	72
2365	The KDM5 family of histone demethylases as targets in oncology drug discovery. Epigenomics, 2014, 6, 277-286.	1.0	92
2366	Genome-wide analysis of H3.3 dissociation reveals high nucleosome turnover at distal regulatory regions of embryonic stem cells. Epigenetics and Chromatin, 2014, 7, 38.	1.8	38
2367	Functional chromatin features are associated with structural mutations in cancer. BMC Genomics, 2014, 15, 1013.	1.2	9
2368	Mechanistic stochastic model of histone modification pattern formation. Epigenetics and Chromatin, 2014, 7, 30.	1.8	18

щ.		IF	CITATIONS
# 2369	ARTICLE De novo prediction of cis-regulatory elements and modules through integrative analysis of a large number of ChIP datasets. BMC Genomics, 2014, 15, 1047.	ır 1.2	11
2370	Differential regulation of MAGE-A1 promoter activity by BORIS and Sp1, both interacting with the TATA binding protein. BMC Cancer, 2014, 14, 796.	1.1	14
2371	OncoCis: annotation of cis-regulatory mutations in cancer. Genome Biology, 2014, 15, 485.	3.8	22
2372	ChIP-Enrich: gene set enrichment testing for ChIP-seq data. Nucleic Acids Research, 2014, 42, e105-e105.	6.5	136
2373	Chromatin accessibility: a window into the genome. Epigenetics and Chromatin, 2014, 7, 33.	1.8	326
2374	Genome-wide Approaches Reveal Functional Vascular Endothelial Growth Factor (VEGF)-inducible Nuclear Factor of Activated T Cells (NFAT) c1 Binding to Angiogenesis-related Genes in the Endothelium. Journal of Biological Chemistry, 2014, 289, 29044-29059.	1.6	58
2375	Anp32e, a higher eukaryotic histone chaperone directs preferential recognition for H2A.Z. Cell Research, 2014, 24, 389-399.	5.7	110
2376	The role of epigenetics in the biology of multiple myeloma. Blood Cancer Journal, 2014, 4, e207-e207.	2.8	106
2377	BM-SNP: A Bayesian Model for SNP Calling Using High Throughput Sequencing Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2014, 11, 1038-1044.	1.9	3
2378	Stem Cell Transcriptional Networks. Methods in Molecular Biology, 2014, , .	0.4	6
2379	Methodologies in the Era of Cardiovascular "Omics― , 2014, , 15-55.		0
2380	Epigenetics and Cardiovascular Disease. , 2014, , 747-782.		0
2381	Histone Lysine Methylation in Diabetic Nephropathy. Journal of Diabetes Research, 2014, 2014, 1-9.	1.0	23
2382	Long-term genomic and epigenomic dysregulation as a consequence of prenatal alcohol exposure: a model for fetal alcohol spectrum disorders. Frontiers in Genetics, 2014, 5, 161.	1.1	57
2383	DNA methylation signatures link prenatal famine exposure to growth and metabolism. Nature Communications, 2014, 5, 5592.	5.8	494
2384	Relationships between DNA and Histone Modifications. , 2014, , .		0
2385	Histone Methyltransferase MMSET/NSD2 Alters EZH2 Binding and Reprograms the Myeloma Epigenome through Global and Focal Changes in H3K36 and H3K27 Methylation. PLoS Genetics, 2014, 10, e1004566.	1.5	178
2386	Imogene: identification of motifs and cis-regulatory modules underlying gene co-regulation. Nucleic Acids Research, 2014, 42, 6128-6145.	6.5	13

		15	0
#	Article	IF	CITATIONS
2387	Apoptotic Lymphocytes of H. sapiens Lose Nucleosomes in GC-Rich Promoters. PLoS Computational Biology, 2014, 10, e1003760.	1.5	4
2388	Epigenetic-based therapies for Friedreich ataxia. Frontiers in Genetics, 2014, 5, 165.	1.1	36
2389	Reconstruction of the Gene Regulatory Network Involved in the Sonic Hedgehog Pathway with a Potential Role in Early Development of the Mouse Brain. PLoS Computational Biology, 2014, 10, e1003884.	1.5	13
2391	Next-Generation Sequencing. , 2014, , 125-145.		4
2392	Epigenetic Regulation of Neural Crest Cells. , 2014, , 89-100.		1
2393	Genome-Wide Nucleosome Positioning Is Orchestrated by Genomic Regions Associated with DNase I Hypersensitivity in Rice. PLoS Genetics, 2014, 10, e1004378.	1.5	33
2394	Stage-Dependent and Locus-Specific Role of Histone Demethylase Jumonji D3 (JMJD3) in the Embryonic Stages of Lung Development. PLoS Genetics, 2014, 10, e1004524.	1.5	50
2395	Quantitative Genetics of CTCF Binding Reveal Local Sequence Effects and Different Modes of X-Chromosome Association. PLoS Genetics, 2014, 10, e1004798.	1.5	55
2396	Comparison of REST Cistromes across Human Cell Types Reveals Common and Context-Specific Functions. PLoS Computational Biology, 2014, 10, e1003671.	1.5	40
2397	LANA Binds to Multiple Active Viral and Cellular Promoters and Associates with the H3K4Methyltransferase hSET1 Complex. PLoS Pathogens, 2014, 10, e1004240.	2.1	68
2398	Epigenetic Involvement in Hutchinson-Gilford Progeria Syndrome: A Mini-Review. Gerontology, 2014, 60, 197-203.	1.4	71
2399	Epigenetic regulation of cardiac myocyte differentiationââ,¬Â. Frontiers in Genetics, 2014, 5, 375.	1.1	30
2400	Genome-wide mapping of DNase I hypersensitive sites and association analysis with gene expression in MSB1 cells. Frontiers in Genetics, 2014, 5, 308.	1.1	21
2401	Integrating Diverse Datasets Improves Developmental Enhancer Prediction. PLoS Computational Biology, 2014, 10, e1003677.	1.5	149
2402	H3K36 Histone Methyltransferase Setd2 Is Required for Murine Embryonic Stem Cell Differentiation toward Endoderm. Cell Reports, 2014, 8, 1989-2002.	2.9	67
2403	Epigenetic regulation and cancer (Review). Oncology Reports, 2014, 31, 523-532.	1.2	114
2404	Genomic Characterization of the Mouse Ribosomal DNA Locus. G3: Genes, Genomes, Genetics, 2014, 4, 243-254.	0.8	39
2405	Reconfiguration of nucleosome-depleted regions at distal regulatory elements accompanies DNA methylation of enhancers and insulators in cancer. Genome Research, 2014, 24, 1421-1432.	2.4	174

#	Article	IF	CITATIONS
2406	The histone methyltransferase Dot1/DOT1L as a critical regulator of the cell cycle. Cell Cycle, 2014, 13, 726-738.	1.3	91
2407	Children are not just little adults: recent advances in understanding of diffuse intrinsic pontine glioma biology. Pediatric Research, 2014, 75, 205-209.	1.1	70
2408	Transcription factor binding predicts histone modifications in human cell lines. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 13367-13372.	3.3	109
2409	Noncoding <scp>RNAs</scp> and the borders of heterochromatin. Wiley Interdisciplinary Reviews RNA, 2014, 5, 835-847.	3.2	21
2410	Large Scale Analysis of Co-existing Post-translational Modifications in Histone Tails Reveals Global Fine Structure of Cross-talk. Molecular and Cellular Proteomics, 2014, 13, 1855-1865.	2.5	65
2411	Nonâ€radioactive Protein Lysine Methyltransferase Microplate Assay Based on Reading Domains. ChemMedChem, 2014, 9, 554-559.	1.6	7
2412	Targeted Chromatin Profiling Reveals Novel Enhancers in Ig H and Ig L Chain Loci. Journal of Immunology, 2014, 192, 1064-1070.	0.4	23
2413	Epigenomics $\hat{a} \in $ Understanding the Epigenetic Landscape of Cells. , 2014, , .		0
2414	Application of histone modification-specific interaction domains as an alternative to antibodies. Genome Research, 2014, 24, 1842-1853.	2.4	52
2415	Epigenetic Therapy of Cancer. , 2014, , .		1
2416	A Model-based approach to transcription regulatory network reconstruction from time-course gene expression data. , 2014, 2014, 4767-70.		3
2417	Activation of Muscle Enhancers by MyoD and epigenetic modifiers. Journal of Cellular Biochemistry, 2014, 115, n/a-n/a.	1.2	15
2418	Chemical agents for binding post-translationally methylated lysines and arginines. Supramolecular		
	Chemistry, 2014, 26, 583-590.	1.5	9
2419		1.5 1.3	9 30
2419 2420	Chemistry, 2014, 26, 583-590. Siteâ€specific human histone H3 methylation stability: fast K4me3 turnover. Proteomics, 2014, 14,		
	 Chemistry, 2014, 26, 583-590. Siteâ€specific human histone H3 methylation stability: fast K4me3 turnover. Proteomics, 2014, 14, 2190-2199. Integrating omics into the cardiac differentiation of human pluripotent stem cells. Wiley 	1.3	30
2420	Chemistry, 2014, 26, 583-590. Siteâ€specific human histone H3 methylation stability: fast K4me3 turnover. Proteomics, 2014, 14, 2190-2199. Integrating omics into the cardiac differentiation of human pluripotent stem cells. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2014, 6, 311-328.	1.3 6.6	30 4

#	Article	IF	CITATIONS
2425	Determinants of G quadruplexâ€induced epigenetic instability in <scp>REV</scp> 1â€deficient cells. EMBO Journal, 2014, 33, 2507-2520.	3.5	111
2426	Assessing quality standards for ChIP-seq and related massive parallel sequencing-generated datasets: When rating goes beyond avoiding the crisis. Genomics Data, 2014, 2, 268-273.	1.3	7
2427	The worm has turned. BioEssays, 2014, 36, 157-162.	1.2	0
2428	Fine-tuning of epigenetic regulation with respect to promoter CpG content in a cell type-specific manner. Epigenetics, 2014, 9, 747-759.	1.3	11
2429	How the proteome packages the genome for cardiovascular development. Proteomics, 2014, 14, 2115-2126.	1.3	3
2430	Altered Histone Mark Deposition and DNA Methylation at Homeobox Genes in Human Oral Squamous Cell Carcinoma. Journal of Cellular Physiology, 2014, 229, 1405-1416.	2.0	34
2431	A 3D Map of the Human Genome at Kilobase Resolution Reveals Principles of Chromatin Looping. Cell, 2014, 159, 1665-1680.	13.5	6,520
2432	Minireview: Conversing With Chromatin: The Language of Nuclear Receptors. Molecular Endocrinology, 2014, 28, 3-15.	3.7	16
2433	The epigenomic tool kit. Drug Discovery Today: Disease Models, 2014, 12, 27-33.	1.2	0
2434	Dynamics of genomic <scp>H</scp> 3 <scp>K</scp> 27me3 domains and role of <scp>EZH</scp> 2 during pancreatic endocrine specification. EMBO Journal, 2014, 33, 2157-2170.	3.5	70
2435	Chromatin Properties of Regulatory DNA Probed by Manipulation of Transcription Factors. Journal of Computational Biology, 2014, 21, 569-577.	0.8	4
2436	Critical role of histone demethylase Jmjd3 in the regulation of CD4+ T-cell differentiation. Nature Communications, 2014, 5, 5780.	5.8	136
2437	Epigenetics in the hematologic malignancies. Haematologica, 2014, 99, 1772-1783.	1.7	60
2438	Cfp1 is required for gene expression-dependent H3K4 trimethylation and H3K9 acetylation in embryonic stem cells. Genome Biology, 2014, 15, 451.	3.8	77
2439	Epigenetic regulation of thyroid hormone-induced adult intestinal stem cell development during anuran metamorphosis. Cell and Bioscience, 2014, 4, 73.	2.1	27
2440	Chronic cocaine-regulated epigenomic changes in mouse nucleus accumbens. Genome Biology, 2014, 15, R65.	13.9	151
2441	Impact of sequencing depth in ChIP-seq experiments. Nucleic Acids Research, 2014, 42, e74-e74.	6.5	69
2443	Histone Methyltransferases: Opportunities in Cancer Drug Discovery. , 2014, , 189-226.		1

#	Article	IF	CITATIONS
2444	Molecular and Cellular Oncology. Molecular and Cellular Oncology, 2014, 1, e29052.	0.3	0
2445	Inference of interactions between chromatin modifiers and histone modifications: from ChIP-Seq data to chromatin-signaling. Nucleic Acids Research, 2014, 42, 13689-13695.	6.5	23
2446	Mapping of six somatic linker histone H1 variants in human breast cancer cells uncovers specific features of H1.2. Nucleic Acids Research, 2014, 42, 4474-4493.	6.5	87
2447	Gene regulatory elements of the cardiac conduction system. Briefings in Functional Genomics, 2014, 13, 28-38.	1.3	6
2448	Histone modifications involved in cassette exon inclusions: a quantitative and interpretable analysis. BMC Genomics, 2014, 15, 1148.	1.2	13
2449	Chromatin structure is distinct between coding and non-coding single nucleotide polymorphisms. BMC Molecular Biology, 2014, 15, 22.	3.0	3
2450	The DEK oncoprotein binds to highly and ubiquitously expressed genes with a dual role in their transcriptional regulation. Molecular Cancer, 2014, 13, 215.	7.9	29
2451	Metabolic control of the epigenome in systemic Lupus erythematosus. Autoimmunity, 2014, 47, 256-264.	1.2	60
2452	Interrogation of allelic chromatin states in human cells by high-density ChIP-genotyping. Epigenetics, 2014, 9, 1238-1251.	1.3	9
2453	A687V EZH2 Is a Driver of Histone H3 Lysine 27 (H3K27) Hypertrimethylation. Molecular Cancer Therapeutics, 2014, 13, 3062-3073.	1.9	44
2454	Epigenetic dysregulation by nickel through repressive chromatin domain disruption. Proceedings of the United States of America, 2014, 111, 14631-14636.	3.3	39
2455	Genome-wide analysis of histone modifications in latently HIV-1 infected T cells. Aids, 2014, 28, 1719-1728.	1.0	27
2456	Promoter-proximal transcription factor binding is transcriptionally active when coupled with nucleosome repositioning in immediate vicinity. Nucleic Acids Research, 2014, 42, 9602-9611.	6.5	13
2457	Dynamics of histone variant H3.3 and its coregulation with H2A.Z at enhancers and promoters. Nucleus, 2014, 5, 21-27.	0.6	26
2458	Epigenetic remodelling and dysregulation of DLGAP4 is linked with early-onset cerebellar ataxia. Human Molecular Genetics, 2014, 23, 6163-6176.	1.4	19
2459	Transcriptional Repression of Histone Deacetylase 3 by the Histone Demethylase KDM2A Is Coupled to Tumorigenicity of Lung Cancer Cells. Journal of Biological Chemistry, 2014, 289, 7483-7496.	1.6	60
2460	Correlating Histone Modification Patterns with Gene Expression Data During Hematopoiesis. Methods in Molecular Biology, 2014, 1150, 175-187.	0.4	6
2461	Histone Modifications Are Associated with Δ9-Tetrahydrocannabinol-mediated Alterations in Antigen-specific T Cell Responses. Journal of Biological Chemistry, 2014, 289, 18707-18718.	1.6	73

#	Article	IF	CITATIONS
2462	Mass spectrometry analysis of histone post translational modifications. Drug Discovery Today: Disease Models, 2014, 12, 41-48.	1.2	6
2463	HTZ-1/H2A.z and MYS-1/MYST HAT act redundantly to maintain cell fates in somatic gonadal cells through repression of <i>ceh-22</i> in <i>C. elegans</i> . Development (Cambridge), 2014, 141, 209-218.	1.2	13
2464	Endogenous Stem Cell-Based Brain Remodeling in Mammals. Pancreatic Islet Biology, 2014, , .	0.1	0
2466	Exploring genomes with a game engine. Faraday Discussions, 2014, 169, 443-453.	1.6	7
2467	Quantitative ChIP-Seq Normalization Reveals Global Modulation of the Epigenome. Cell Reports, 2014, 9, 1163-1170.	2.9	442
2468	Transcriptional Regulation of the Albumin Gene Depends on the Removal of Histone Methylation Marks by the FAD-Dependent Monoamine Oxidase Lysine-Specific Demethylase 1 in HepG2 Human Hepatocarcinoma Cells. Journal of Nutrition, 2014, 144, 997-1001.	1.3	10
2469	Transcription Restores DNA Repair to Heterochromatin, Determining Regional Mutation Rates in Cancer Genomes. Cell Reports, 2014, 9, 1228-1234.	2.9	104
2470	Omics Approaches in Breast Cancer. , 2014, , .		10
2471	Breast Cancer Genomics. , 2014, , 53-103.		0
2472	Th1/Th2 Cell Differentiation and Molecular Signals. Advances in Experimental Medicine and Biology, 2014, 841, 15-44.	0.8	161
2473	The methyltransferase G9a regulates HoxA9-dependent transcription in AML. Genes and Development, 2014, 28, 317-327.	2.7	121
2475	Nucleosome regulatory dynamics in response to TGFÂ. Nucleic Acids Research, 2014, 42, 6921-6934.	6.5	6
2476	Enriched domain detector: a program for detection of wide genomic enrichment domains robust against local variations. Nucleic Acids Research, 2014, 42, e92-e92.	6.5	111
2477	MLL fusion proteins link transcriptional coactivators to previously active CpG-rich promoters. Nucleic Acids Research, 2014, 42, 4241-4256.	6.5	43
2478	Overexpression of Cancer-Associated Genes via Epigenetic Derepression Mechanisms in Gynecologic Cancer. Frontiers in Oncology, 2014, 4, 12.	1.3	27
2479	AGO2 and SETDB1 cooperate in promoter-targeted transcriptional silencing of the androgen receptor gene. Nucleic Acids Research, 2014, 42, 13545-13556.	6.5	47
2480	Links Between Injury-Induced Brain Remodeling and Oncogenesis. Pancreatic Islet Biology, 2014, , 199-226.	0.1	0
2481	The TCF C-clamp DNA binding domain expands the Wnt transcriptome via alternative target recognition. Nucleic Acids Research, 2014, 42, 13615-13632.	6.5	34

#	Article	IF	CITATIONS
2482	Histones and Their Modifications in Ovarian Cancer ââ,¬â€œ Drivers of Disease and Therapeutic Targets. Frontiers in Oncology, 2014, 4, 144.	1.3	46
2483	Transcription factor CTCF and mammalian genome organization. Biopolymers and Cell, 2014, 30, 260-272.	0.1	2
2484	CTCF induces histone variant incorporation, erases the H3K27me3 histone mark and opens chromatin. Nucleic Acids Research, 2014, 42, 11941-11951.	6.5	41
2485	Large-Scale Quality Analysis of Published ChIP-seq Data. G3: Genes, Genomes, Genetics, 2014, 4, 209-223.	0.8	125
2486	Genome-Wide Analysis of Histone Modifications in Human Endometrial Stromal Cells. Molecular Endocrinology, 2014, 28, 1656-1669.	3.7	72
2487	Distinct and Predictive Histone Lysine Acetylation Patterns at Promoters, Enhancers, and Gene Bodies. G3: Genes, Genomes, Genetics, 2014, 4, 2051-2063.	0.8	39
2488	Localized, non-random differences in chromatin accessibility between homologous metaphase chromosomes. Molecular Cytogenetics, 2014, 7, 70.	0.4	8
2489	Epigenetic modifications are associated with inter-species gene expression variation in primates. Genome Biology, 2014, 15, 547.	3.8	72
2490	Current and potential epigenetic targets in multiple myeloma. Epigenomics, 2014, 6, 215-228.	1.0	11
2491	Determinants of expression variability. Nucleic Acids Research, 2014, 42, 3503-3514.	6.5	68
2492	The genome-wide molecular signature of transcription factors in leukemia. Experimental Hematology, 2014, 42, 637-650.	0.2	13
		0.2	
2493	Evolution of Alu Elements toward Enhancers. Cell Reports, 2014, 7, 376-385.	2.9	134
2493 2494	Evolution of Alu Elements toward Enhancers. Cell Reports, 2014, 7, 376-385. Flightless I (Drosophila) homolog facilitates chromatin accessibility of the estrogen receptor α target genes in MCF-7 breast cancer cells. Biochemical and Biophysical Research Communications, 2014, 446, 608-613.		134 15
	Flightless I (Drosophila) homolog facilitates chromatin accessibility of the estrogen receptor α target genes in MCF-7 breast cancer cells. Biochemical and Biophysical Research Communications, 2014, 446,	2.9	
2494	Flightless I (Drosophila) homolog facilitates chromatin accessibility of the estrogen receptor α target genes in MCF-7 breast cancer cells. Biochemical and Biophysical Research Communications, 2014, 446, 608-613. The promise and failures of epigenetic therapies for cancer treatment. Cancer Treatment Reviews, 2014,	2.9 1.0	15
2494 2495	 Flightless I (Drosophila) homolog facilitates chromatin accessibility of the estrogen receptor α target genes in MCF-7 breast cancer cells. Biochemical and Biophysical Research Communications, 2014, 446, 608-613. The promise and failures of epigenetic therapies for cancer treatment. Cancer Treatment Reviews, 2014, 40, 153-169. DNA promoter and histone H3 methylation downregulate NGX6 in gastric cancer cells. Medical 	2.9 1.0 3.4	15 76
2494 2495 2496	 Flightless I (Drosophila) homolog facilitates chromatin accessibility of the estrogen receptor α target genes in MCF-7 breast cancer cells. Biochemical and Biophysical Research Communications, 2014, 446, 608-613. The promise and failures of epigenetic therapies for cancer treatment. Cancer Treatment Reviews, 2014, 40, 153-169. DNA promoter and histone H3 methylation downregulate NGX6 in gastric cancer cells. Medical Oncology, 2014, 31, 817. Histone H2A.Z deregulation in prostate cancer. Cause or effect?. Cancer and Metastasis Reviews, 2014, 	2.9 1.0 3.4 1.2	15 76 9

#	Article	IF	CITATIONS
2500	Small but sturdy: small RNAs in cellular memory and epigenetics. Genes and Development, 2014, 28, 423-431.	2.7	59
2501	Mature miR-183, negatively regulated by transcription factor GATA3, promotes 3T3-L1 adipogenesis through inhibition of the canonical Wnt/β-catenin signaling pathway by targeting LRP6. Cellular Signalling, 2014, 26, 1155-1165.	1.7	49
2502	Two independent transcription initiation codes overlap on vertebrate core promoters. Nature, 2014, 507, 381-385.	13.7	182
2503	The epigenome in pluripotency and differentiation. Epigenomics, 2014, 6, 121-137.	1.0	20
2504	The chromatin architectural proteins HMGD1 and H1 bind reciprocally and have opposite effects on chromatin structure and gene regulation. BMC Genomics, 2014, 15, 92.	1.2	35
2505	Histone Modification Patterns and Their Responses to Environment. Current Environmental Health Reports, 2014, 1, 11-21.	3.2	36
2506	A nucleosomal approach to inferring causal relationships of histone modifications. BMC Genomics, 2014, 15, S7.	1.2	3
2507	Computational prediction of transcription factor binding sites based on an integrative approach incorporating genomic and epigenomic features. Genes and Genomics, 2014, 36, 25-30.	0.5	0
2508	Synonymous Mutations Frequently Act as Driver Mutations in Human Cancers. Cell, 2014, 156, 1324-1335.	13.5	482
2509	Enhancer RNAs and regulated transcriptional programs. Trends in Biochemical Sciences, 2014, 39, 170-182.	3.7	442
2510	CTCF: an architectural protein bridging genome topology and function. Nature Reviews Genetics, 2014, 15, 234-246.	7.7	892
2511	Comparative Proteomic Analysis of Histone Post-translational Modifications upon Ischemia/Reperfusion-Induced Retinal Injury. Journal of Proteome Research, 2014, 13, 2175-2186.	1.8	16
2512	Histone methylation mediates plasticity of human <scp>FOXP</scp> 3 ⁺ regulatory T cells by modulating signature gene expressions. Immunology, 2014, 141, 362-376.	2.0	17
2514	A New Bump in the Epigenetic Landscape. Molecular Cell, 2014, 53, 857-858.	4.5	5
2515	A Role for H3K4 Monomethylation in Gene Repression and Partitioning of Chromatin Readers. Molecular Cell, 2014, 53, 979-992.	4.5	191
2516	B Cell Differentiation Is Associated with Reprogramming the CCCTC Binding Factor–Dependent Chromatin Architecture of the Murine MHC Class II Locus. Journal of Immunology, 2014, 192, 3925-3935.	0.4	25
2517	Neurotrophins: Transcription and Translation. Handbook of Experimental Pharmacology, 2014, 220, 67-100.	0.9	90
2518	An unexpected journey: Lysine methylation across the proteome. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2014, 1839, 1395-1403.	0.9	83

	CITATION RE	PORT	
#	Article	IF	CITATIONS
2519	Domains of genome-wide gene expression dysregulation in Down's syndrome. Nature, 2014, 508, 345-350.	13.7	298
2520	The Role of Chromatin Modifications in Progression through Mouse Meiotic Prophase. Journal of Genetics and Genomics, 2014, 41, 97-106.	1.7	40
2521	Differential Effects of RUNX2 on the Androgen Receptor in Prostate Cancer: Synergistic Stimulation of a Gene Set Exemplified by SNAI2 and Subsequent Invasiveness. Cancer Research, 2014, 74, 2857-2868.	0.4	30
2522	Alterations of Global Histone H3K9 and H3K27 Methylation Levels in Bladder Cancer. Urologia Internationalis, 2014, 93, 113-118.	0.6	31
2523	Histone variants at the transcription start-site. Trends in Genetics, 2014, 30, 199-209.	2.9	55
2524	Biochemical systems approaches for the analysis of histone modification readout. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2014, 1839, 657-668.	0.9	17
2525	Techniques and Methodological Approaches in Breast Cancer Research. , 2014, , .		12
2526	Broadly permissive intestinal chromatin underlies lateral inhibition and cell plasticity. Nature, 2014, 506, 511-515.	13.7	207
2527	rSNPBase: a database for curated regulatory SNPs. Nucleic Acids Research, 2014, 42, D1033-D1039.	6.5	107
2528	Reduced Euchromatin histone methyltransferase 1 causes developmental delay, hypotonia, and cranial abnormalities associated with increased bone gene expression in Kleefstra syndrome mice. Developmental Biology, 2014, 386, 395-407.	0.9	65
2529	Mammalian epigenetic mechanisms. IUBMB Life, 2014, 66, 240-256.	1.5	98
2530	Comparative epigenetic analyses reveal distinct patterns of oncogenic pathways activation in breast cancer subtypes. Human Molecular Genetics, 2014, 23, 5378-5393.	1.4	31
2532	Aberrant TAL1 activation is mediated by an interchromosomal interaction in human T-cell acute lymphoblastic leukemia. Leukemia, 2014, 28, 349-361.	3.3	50
2533	Coupling transcription factor occupancy to nucleosome architecture with DNase-FLASH. Nature Methods, 2014, 11, 66-72.	9.0	58
2534	Variation in chromatin accessibility in human kidney cancer links H3K36 methyltransferase loss with widespread RNA processing defects. Genome Research, 2014, 24, 241-250.	2.4	160
2535	Losartan reverses permissive epigenetic changes in renal glomeruli of diabetic db/db mice. Kidney International, 2014, 85, 362-373.	2.6	110
2536	Applications of alignment-free methods in epigenomics. Briefings in Bioinformatics, 2014, 15, 419-430.	3.2	40
2537	ANP32E is a histone chaperone that removes H2A.Z from chromatin. Nature, 2014, 505, 648-653.	13.7	217

#	Article	IF	Citations
2538	Plant Epigenetics and Epigenomics. Methods in Molecular Biology, 2014, , .	0.4	5
2539	Polycomb-Dependent H3K27me1 and H3K27me2 Regulate Active Transcription and Enhancer Fidelity. Molecular Cell, 2014, 53, 49-62.	4.5	403
2540	Long Noncoding RNAs Expression Profile of the Developing Mouse Heart. Journal of Cellular Biochemistry, 2014, 115, 910-918.	1.2	34
2541	Distal enhancers: new insights into heart development and disease. Trends in Cell Biology, 2014, 24, 294-302.	3.6	42
2542	Gene transcription in the zebrafish embryo: regulators and networks. Briefings in Functional Genomics, 2014, 13, 131-143.	1.3	14
2543	Message control in developmental transitions; deciphering chromatin's role using zebrafish genomics. Briefings in Functional Genomics, 2014, 13, 106-120.	1.3	0
2544	Protein Deimination in Human Health and Disease. , 2014, , .		10
2545	Development of strategies for integrated breeding, genetics and applied genomics for genetic improvement of aquatic organisms. Aquaculture, 2014, 420-421, S121-S123.	1.7	8
2546	Familial and Somatic Mutations of Histone-Modifying Enzymes in Cancer. , 2014, , 65-85.		0
2547	Genome-wide approaches reveal EGR1-controlled regulatory networks associated with neurodegeneration. Neurobiology of Disease, 2014, 63, 107-114.	2.1	70
2548	Large replication skew domains delimit GC-poor gene deserts in human. Computational Biology and Chemistry, 2014, 53, 153-165.	1.1	5
2549	Telbivudine treatment corrects HBV-induced epigenetic alterations in liver cells of patients with chronic hepatitis B. Carcinogenesis, 2014, 35, 53-61.	1.3	13
2550	Epigenetic Control of <i>Ccr7</i> Expression in Distinct Lineages of Lung Dendritic Cells. Journal of Immunology, 2014, 193, 4904-4913.	0.4	40
2551	Exon skipping event prediction based on histone modifications. Interdisciplinary Sciences, Computational Life Sciences, 2014, 6, 241-249.	2.2	10
2552	Identification of 2,4-diamino-6,7-dimethoxyquinoline derivatives as G9a inhibitors. MedChemComm, 2014, 5, 1821-1828.	3.5	34
2553	Histone-Mediated Epigenetics in Addiction. Progress in Molecular Biology and Translational Science, 2014, 128, 51-87.	0.9	17
2554	Nuclear <scp>ARRB</scp> 1 induces pseudohypoxia and cellular metabolism reprogramming in prostate cancer. EMBO Journal, 2014, 33, 1365-1382.	3.5	57
2555	The relationship between lysine 4 on histone H 3 methylation levels of alcohol tolerance genes and changes of ethanol tolerance in S accharomyces cerevisiae. Microbial Biotechnology, 2014, 7, 307-314.	2.0	6

ARTICLE IF CITATIONS Enhancer alterations in cancer: a source for a cell identity crisis. Genome Medicine, 2014, 6, 77. 47 2556 3.6 Macrophages: Biology and Role in the Pathology of Diseases., 2014, , . CTCF Controls <i>HOXA</i> Cluster Silencing and Mediates PRC2-Repressive Higher-Order Chromatin 2558 1.1 31 Structure in NT2/D1 Cells. Molecular and Cellular Biology, 2014, 34, 3867-3879. Transcriptional Control of Inflammatory Responses. Cold Spring Harbor Perspectives in Biology, 2014, 95 6, a016261-a016261. Structure and function of the nucleosome-binding PWWP domain. Trends in Biochemical Sciences, 2560 3.7 154 2014, 39, 536-547. Adeno-Associated Virus Type 2 Wild-Type and Vector-Mediated Genomic Integration Profiles of Human Diploid Fibroblasts Analyzed by Third-Generation PacBio DNA Sequencing. Journal of Virology, 2014, 1.5 88, 11253-11263. Decoding neural transcriptomes and epigenomes via high-throughput sequencing. Nature 2562 7.1 49 Neuroscience, 2014, 17, 1463-1475. Enhancer Interaction Networks as a Means for Singular Olfactory Receptor Expression. Cell, 2014, 159, 2563 13.5 543-557. Expanded Genetic Code Technologies for Incorporating Modified Lysine at Multiple Sites. 2564 29 1.3 ChemBioChem, 2014, 15, 2181-2187. Unravelling the genomic targets of small molecules using high-throughput sequencing. Nature Reviews Genetics, 2014, 15, 783-796. Enhancers Are Major Targets for Murine Leukemia Virus Vector Integration. Journal of Virology, 2014, 2566 1.5 88 88, 4504-4513. BET-independent MLV-based Vectors Target Away From Promoters and Regulatory Elements. Molecular 2.3 2567 Therapy - Nucleic Acids, 2014, 3, e179. Long-range interaction and correlation between <i>MYC</i> enhancer and oncogenic long noncoding 2568 RNA <i>CARLo-5</i>. Proceedings of the National Academy of Sciences of the United States of America, 3.3 174 2014, 111, 4173-4178. Role of NSD1 in H2O2-induced GSTM3 suppression. Cellular Signalling, 2014, 26, 2757-2764. 2570 1.7 Mutations in <i>SETD2 </i> cause a novel overgrowth condition. Journal of Medical Genetics, 2014, 51, 2571 1.5 96 512-517. Histone Deacetylation Critically Determines T Cell Subset Radiosensitivity. Journal of Immunology, 2572 0.4 2014, 193, 1451-1458. A regulatory element affects the activity and chromatin structure of the chicken \hat{I} +globin $3\hat{e}^2$ enhancer. 2574 0.9 4 Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2014, 1839, 1233-1241. 2576 GATA-3 Function in Innate and Adaptive Immunity. Immunity, 2014, 41, 191-206. 6.6

#	Article	IF	CITATIONS
2577	Functional interplay between MyoD and CTCF in regulating long-range chromatin interactions during differentiation. Journal of Cell Science, 2014, 127, 3757-67.	1.2	31
2578	Pathogenic Histone Modifications in Schizophrenia are Targets for Therapy. , 2014, , 241-251.		5
2579	Gene Expression in the Addicted Brain. International Review of Neurobiology, 2014, 116, 251-273.	0.9	46
2580	Regulation of histone H3K4 methylation in brain development and disease. Philosophical Transactions of the Royal Society B: Biological Sciences, 2014, 369, 20130514.	1.8	113
2581	A Macrohistone Variant Links Dynamic Chromatin Compaction to BRCA1-Dependent Genome Maintenance. Cell Reports, 2014, 8, 1049-1062.	2.9	179
2582	The Path to Personalized Cardiovascular Medicine. , 2014, , 837-871.		0
2583	Epigenetic reprogramming of cortical neurons through alteration of dopaminergic circuits. Molecular Psychiatry, 2014, 19, 1193-1200.	4.1	14
2584	The role of long non-coding RNAs in neurodevelopment, brain function and neurological disease. Philosophical Transactions of the Royal Society B: Biological Sciences, 2014, 369, 20130507.	1.8	164
2585	Importance of C/EBPÎ ² Binding and Histone Acetylation Status in the Promoter Regions for Induction of IGFBP-1, PRL, and Mn-SOD by cAMP in Human Endometrial Stromal Cells. Endocrinology, 2014, 155, 275-286.	1.4	41
2586	The role of H3K4me3 and H3K9/14ac in the induction by dexamethasone of Per1 and Sgk1, two glucococorticoid early response genes that mediate the effects of acute stress in mammals. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2014, 1839, 866-872.	0.9	8
2587	High-throughput functional testing of ENCODE segmentation predictions. Genome Research, 2014, 24, 1595-1602.	2.4	232
2588	Active enhancers are delineated de novo during hematopoiesis, with limited lineage fidelity among specified primary blood cells. Genes and Development, 2014, 28, 1827-1839.	2.7	38
2589	Evolutionary conservation of the eumetazoan gene regulatory landscape. Genome Research, 2014, 24, 639-650.	2.4	143
2590	Hierarchical Bayesian Models for ChIP-seq Data. , 2014, , 297-314.		0
2591	LEVERAGING BIOLOGICAL REPLICATES TO IMPROVE ANALYSIS IN CHIP-SEQ EXPERIMENTS. Computational and Structural Biotechnology Journal, 2014, 9, e201401002.	1.9	57
2592	Complex interactions of transcription factors in mediating cytokine biology in T cells. Immunological Reviews, 2014, 261, 141-156.	2.8	95
2593	H3K4me3 Breadth Is Linked to Cell Identity and Transcriptional Consistency. Cell, 2014, 158, 673-688.	13.5	404
2594	Improved bottomâ€up strategy to efficiently separate hypermodified histone peptides through ultraâ€HPLC separation on a bench top Orbitrap instrument. Proteomics, 2014, 14, 2212-2225.	1.3	28

#	Article	IF	CITATIONS
2595	Mechanism governing a stem cell-generating <i>cis</i> -regulatory element. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E1091-100.	3.3	40
2596	hSETD1A Regulates Wnt Target Genes and Controls Tumor Growth of Colorectal Cancer Cells. Cancer Research, 2014, 74, 775-786.	0.4	63
2597	Histone methylation and V(D)J recombination. International Journal of Hematology, 2014, 100, 230-237.	0.7	13
2598	The role of chromatin dynamics in immune cell development. Immunological Reviews, 2014, 261, 9-22.	2.8	57
2599	Deciphering the epigenetic code of T lymphocytes. Immunological Reviews, 2014, 261, 50-61.	2.8	15
2600	Oncometabolitesâ€driven tumorigenesis: From genetics to targeted therapy. International Journal of Cancer, 2014, 135, 2237-2248.	2.3	119
2601	High-resolution digital profiling of the epigenome. Nature Reviews Genetics, 2014, 15, 814-827.	7.7	112
2602	New insights into the maternal to zygotic transition. Development (Cambridge), 2014, 141, 3834-3841.	1.2	109
2603	Low activity of LSD1 elicits a pro-inflammatory gene expression profile in riboflavin-deficient human T Lymphoma Jurkat cells. Genes and Nutrition, 2014, 9, 422.	1.2	23
2604	Study of cell differentiation by phylogenetic analysis using histone modification data. BMC Bioinformatics, 2014, 15, 269.	1.2	12
2605	Transcriptional regulation and spatial interactions of head-to-head genes. BMC Genomics, 2014, 15, 519.	1.2	17
2606	Differences among brain tumor stem cell types and fetal neural stem cells in focal regions of histone modifications and DNA methylation, broad regions of modifications, and bivalent promoters. BMC Genomics, 2014, 15, 724.	1.2	14
2607	piRNA clusters and open chromatin structure. Mobile DNA, 2014, 5, 22.	1.3	86
2608	Genetic factors underlying discordance in chromatin accessibility between monozygotic twins. Genome Biology, 2014, 15, R72.	13.9	6
2609	Cotranscriptional histone H2B monoubiquitylation is tightly coupled with RNA polymerase II elongation rate. Genome Research, 2014, 24, 1572-1583.	2.4	74
2610	Toxicogenomic effect of nickel and beyond. Archives of Toxicology, 2014, 88, 1645-1650.	1.9	27
2611	Chromatin dynamics: H3K4 methylation and H3 variant replacement during development and in cancer. Cellular and Molecular Life Sciences, 2014, 71, 3439-3463.	2.4	37
2612	Deep sequencing reveals novel Set7 networks. Cellular and Molecular Life Sciences, 2014, 71, 4471-4486.	2.4	26

#	Article	IF	CITATIONS
2613	Dynamics of DOT1L localization and H3K79 methylation during meiotic prophase I in mouse spermatocytes. Chromosoma, 2014, 123, 147-164.	1.0	48
2614	Getting down to the core of histone modifications. Chromosoma, 2014, 123, 355-371.	1.0	12
2615	Cancer genomics identifies disrupted epigenetic genes. Human Genetics, 2014, 133, 713-725.	1.8	47
2616	Decoding ChIP-seq with a double-binding signal refines binding peaks to single-nucleotides and predicts cooperative interaction. Genome Research, 2014, 24, 1686-1697.	2.4	21
2617	The BAF60 Subunit of the SWI/SNF Chromatin-Remodeling Complex Directly Controls the Formation of a Gene Loop at <i>FLOWERING LOCUS C</i> in <i>Arabidopsis</i> Â. Plant Cell, 2014, 26, 538-551.	3.1	82
2618	The genomic landscape of mantle cell lymphoma is related to the epigenetically determined chromatin state of normal B cells. Blood, 2014, 123, 2988-2996.	0.6	224
2619	The PEG13-DMR and brain-specific enhancers dictate imprinted expression within the 8q24 intellectual disability risk locus. Epigenetics and Chromatin, 2014, 7, 5.	1.8	46
2620	ChIP-less analysis of chromatin states. Epigenetics and Chromatin, 2014, 7, 7.	1.8	26
2621	Transcriptional and epigenetic regulation of PPARÎ ³ expression during adipogenesis. Cell and Bioscience, 2014, 4, 29.	2.1	182
2622	KDM5B focuses H3K4 methylation near promoters and enhancers during embryonic stem cell self-renewal and differentiation. Genome Biology, 2014, 15, R32.	13.9	120
2623	Cross-enhancement of ANGPTL4 transcription by HIF1 alpha and PPAR beta/delta is the result of the conformational proximity of two response elements. Genome Biology, 2014, 15, R63.	13.9	58
2624	Genome-Wide Profiling of Transcription Factor Binding and Epigenetic Marks in Adipocytes by ChIP-seq. Methods in Enzymology, 2014, 537, 261-279.	0.4	23
2625	Role of epigenetic mechanisms in the development of chronic complications of diabetes. Diabetes Research and Clinical Practice, 2014, 105, 164-175.	1.1	60
2626	EZH2: Not EZHY (Easy) to Deal. Molecular Cancer Research, 2014, 12, 639-653.	1.5	92
2627	Epigenetic Regulation of Epidermal Differentiation. Cold Spring Harbor Perspectives in Medicine, 2014, 4, a015263-a015263.	2.9	42
2628	The Impact of Next-Generation Sequencing Technology on Bacterial Genomics. , 2014, , 31-58.		2
2629	Insulators recruit histone methyltransferase d <scp>M</scp> es4 to regulate chromatin of flanking genes. EMBO Journal, 2014, 33, 1599-1613.	3.5	34
2630	Statistical Analysis of Next Generation Sequencing Data. , 2014, , .		20

#	Article	IF	CITATIONS
2631	A Systems Theoretic Approach to Systems and Synthetic Biology II: Analysis and Design of Cellular Systems. , 2014, , .		0
2632	Some Statistical Strategies for DAE-seq Data Analysis: Variable Selection and Modeling Dependencies Among Observations. Journal of the American Statistical Association, 2014, 109, 78-94.	1.8	6
2633	UTX and MLL4 Coordinately Regulate Transcriptional Programs for Cell Proliferation and Invasiveness in Breast Cancer Cells. Cancer Research, 2014, 74, 1705-1717.	0.4	198
2634	Dynamic patterns of histone H3 lysine 4 methyltransferases and demethylases during mouse preimplantation development. In Vitro Cellular and Developmental Biology - Animal, 2014, 50, 603-613.	0.7	46
2635	Chromatin states reveal functional associations for globally defined transcription start sites in four human cell lines. BMC Genomics, 2014, 15, 120.	1.2	17
2636	The phenotypic predisposition of the parent in F1 hybrid is correlated with transcriptome preference of the positive general combining ability parent. BMC Genomics, 2014, 15, 297.	1.2	12
2637	EXPRSS: an Illumina based high-throughput expression-profiling method to reveal transcriptional dynamics. BMC Genomics, 2014, 15, 341.	1.2	36
2638	Software for pre-processing Illumina next-generation sequencing short read sequences. Source Code for Biology and Medicine, 2014, 9, 8.	1.7	196
2639	Multiscale representation of genomic signals. Nature Methods, 2014, 11, 689-694.	9.0	31
2640	Dynamic GATA4 enhancers shape the chromatin landscape central to heart development and disease. Nature Communications, 2014, 5, 4907.	5.8	142
2641	Maternal Epigenetic Inheritance and Stress During Gestation. , 2014, , 197-219.		3
2642	SETD6 controls the expression of estrogen-responsive genes and proliferation of breast carcinoma cells. Epigenetics, 2014, 9, 942-950.	1.3	30
2643	Photoreceptor partner FHY1 has an independent role in gene modulation and plant development under far-red light. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 11888-11893.	3.3	14
2644	Probabilistic partitioning methods to find significant patterns in ChIP-Seq data. Bioinformatics, 2014, 30, 2406-2413.	1.8	14
2645	Computational discovery of feature patterns in nucleosomal DNA sequences. Genomics, 2014, 104, 87-95.	1.3	1
2646	Identifying and mitigating bias in next-generation sequencing methods for chromatin biology. Nature Reviews Genetics, 2014, 15, 709-721.	7.7	295
2647	Broad-Enrich: functional interpretation of large sets of broad genomic regions. Bioinformatics, 2014, 30, i393-i400.	1.8	21
2648	Improved nucleosome-positioning algorithm iNPS for accurate nucleosome positioning from sequencing data. Nature Communications, 2014, 5, 4909.	5.8	55

#	Article	IF	CITATIONS
2649	Epigenetic mechanisms in epilepsy. Progress in Brain Research, 2014, 213, 279-316.	0.9	54
2650	The Osteoblast to Osteocyte Transition: Epigenetic Changes and Response to the Vitamin D ₃ Hormone. Molecular Endocrinology, 2014, 28, 1150-1165.	3.7	113
2651	Histone post-translational modifications induced by histone deacetylase inhibition in transcriptional control units of NIS gene. Molecular Biology Reports, 2014, 41, 5257-5265.	1.0	8
2652	Epigenetic perspectives on cancer chemotherapy response. Pharmacogenomics, 2014, 15, 699-715.	0.6	11
2653	Natural variation of histone modification and its impact on gene expression in the rat genome. Genome Research, 2014, 24, 942-953.	2.4	53
2654	Posttranslational modifications of histone deacetylases: Implications for cardiovascular diseases. , 2014, 143, 168-180.		75
2655	Towards understanding methyllysine readout. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2014, 1839, 686-693.	0.9	51
2656	A Histone Methylation Network Regulates Transgenerational Epigenetic Memory in C.Âelegans. Cell Reports, 2014, 7, 113-126.	2.9	146
2657	Deciphering histone code of transcriptional regulation in malaria parasites by large-scale data mining. Computational Biology and Chemistry, 2014, 50, 3-10.	1.1	5
2658	Nuclear architecture as an epigenetic regulator of neural development and function. Neuroscience, 2014, 264, 39-50.	1.1	23
2659	<i>Arabidopsis</i> Phytochrome A Directly Targets Numerous Promoters for Individualized Modulation of Genes in a Wide Range of Pathways. Plant Cell, 2014, 26, 1949-1966.	3.1	73
2660	Epigenetic Silencing of the Human <i>NOS2</i> Gene: Rethinking the Role of Nitric Oxide in Human Macrophage Inflammatory Responses. Journal of Immunology, 2014, 192, 2326-2338.	0.4	107
2661	Switching on sex: transcriptional regulation of the testis-determining gene <i>Sry</i> . Development (Cambridge), 2014, 141, 2195-2205.	1.2	113
2662	The 3D Genome in Transcriptional Regulation and Pluripotency. Cell Stem Cell, 2014, 14, 762-775.	5.2	353
2663	Repressive histone methylation: A case study in deterministic versus stochastic gene regulation. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2014, 1839, 1373-1384.	0.9	18
2664	Targeting histone lysine demethylases — Progress, challenges, and the future. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2014, 1839, 1416-1432.	0.9	170
2665	Epigenetic regulation of Progesterone Receptor isoforms: From classical models to the sexual brain. Molecular and Cellular Endocrinology, 2014, 392, 115-124.	1.6	9
2666	Promoter-specific relevance of histone modifications induced by dexamethasone during the regulation of pro-inflammatory mediators. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2014, 1839, 571-578.	0.9	3

#	Article	IF	CITATIONS
2667	Functional interactions among microRNAs and long noncoding RNAs. Seminars in Cell and Developmental Biology, 2014, 34, 9-14.	2.3	561
2668	piRNA pathway targets active LINE1 elements to establish the repressive H3K9me3 mark in germ cells. Genes and Development, 2014, 28, 1410-1428.	2.7	184
2669	A Dual Role for the Histone Methyltransferase PR-SET7/SETD8 and Histone H4 Lysine 20 Monomethylation in the Local Regulation of RNA Polymerase II Pausing. Journal of Biological Chemistry, 2014, 289, 7425-7437.	1.6	33
2670	Integrating genetics and epigenetics in myelodysplastic syndromes: advances in pathogenesis and disease evolution. British Journal of Haematology, 2014, 166, 646-659.	1.2	26
2671	Hunting for Darwin's gemmules and Lamarck's fluid: Transgenerational signaling and histone methylation. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2014, 1839, 1440-1453.	0.9	12
2672	Physicochemical modifications of histones and their impact on epigenomics. Drug Discovery Today, 2014, 19, 1372-1379.	3.2	16
2673	H3K4me2 reliably defines transcription factor binding regions in different cells. Genomics, 2014, 103, 222-228.	1.3	85
2674	Histone variants: emerging players in cancer biology. Cellular and Molecular Life Sciences, 2014, 71, 379-404.	2.4	141
2675	Impact of artifact removal on ChIP quality metrics in ChIP-seq and ChIP-exo data. Frontiers in Genetics, 2014, 5, 75.	1.1	222
2676	Structures and functions in the crowded nucleus: new biophysical insights. Frontiers in Physics, 2014, 2, .	1.0	17
2677	Extensive regulation of the non oding transcriptome by hypoxia: role of <scp>HIF</scp> in releasing paused <scp>RNA</scp> pol2. EMBO Reports, 2014, 15, 70-76.	2.0	146
2678	Characteristic bimodal profiles of RNA polymerase II at thousands of active mammalian promoters. Genome Biology, 2014, 15, R85.	13.9	33
2679	Toxicopanomics: Applications of Genomics, Transcriptomics, Proteomics, and Lipidomics in Predictive Mechanistic Toxicology. , 2014, , 295-332.		3
2680	The role of HTLV-1 clonality, proviral structure, and genomic integration site in adult T-cell leukemia/lymphoma. Blood, 2014, 123, 3925-3931.	0.6	112
2681	Loss of Asxl1 leads to myelodysplastic syndrome–like disease in mice. Blood, 2014, 123, 541-553.	0.6	145
2682	Modelling epigenetic regulation of gene expression in 12 human cell types reveals combinatorial patterns of cellâ€typeâ€specific genes. IET Systems Biology, 2014, 8, 104-115.	0.8	3
2683	The ChroP Approach Combines ChIP and Mass Spectrometry to Dissect Locus-specific Proteomic Landscapes of Chromatin. Journal of Visualized Experiments, 2014, , .	0.2	21
2684	Dynamics of enhancers in myeloid antigen presenting cells upon LPS stimulation. BMC Genomics, 2014, 15, S4.	1.2	2

		CITATION REPORT		
#	Article		IF	CITATIONS
2685	Post-ovulatory ageing of mouse oocytes affects the distribution of specific spindle-asso proteins and Akt expression levels. Reproduction, Fertility and Development, 2014, 26,		0.1	12
2686	Aging alters histone H3 lysine 4 methylation in mouse germinal vesicle stage oocytes. I Fertility and Development, 2015, 27, 419.	Reproduction,	0.1	28
2687	Global mapping of the regulatory interactions of histone residues. FEBS Letters, 2015,	589, 4061-4070.	1.3	8
2688	Chromatin structure analysis enables detection of DNA insertions into the mammalian genome. Biochemistry and Biophysics Reports, 2015, 2, 143-152.	nuclear	0.7	2
2689	Glycogen synthase kinaseâ€3 controls ILâ€10 expression in CD4 ⁺ effecto through epigenetic modification of the ILâ€10 promoter. European Journal of Immunol 1103-1115.		1.6	44
2690	Molecular components of the circadian clock in mammals. Diabetes, Obesity and Meta 6-11.	bolism, 2015, 17,	2.2	170
2691	Genome-wide DNA methylation map of human neutrophils reveals widespread inter-ince epigenetic variation. Scientific Reports, 2015, 5, 17328.	lividual	1.6	59
2692	Integrated analysis of DNA methylation and microRNA regulation of the lung adenocar transcriptome. Oncology Reports, 2015, 34, 585-594.	cinoma	1.2	22
2693	The right place at the right time: chaperoning core histone variants. EMBO Reports, 20	15, 16, 1454-1466.	2.0	55
2694	High-throughput profiling of influenza A virus hemagglutinin gene at single-nucleotide Scientific Reports, 2014, 4, 4942.	resolution.	1.6	147
2695	Wavelet-based genetic association analysis of functional phenotypes arising from high sequencing assays. Annals of Applied Statistics, 2015, 9, 655-686.	-throughput	0.5	22
2696	EHMT1 and EHMT2 inhibition induces fetal hemoglobin expression. Blood, 2015, 126,	1930-1939.	0.6	76
2697	Functional analysis of the 11q23.3 glioma susceptibility locus implicates PHLDB1 and I susceptibility. Scientific Reports, 2015, 5, 17367.	DDX6 in glioma	1.6	27
2698	AF4 uses the SL1 components of RNAP1 machinery to initiate MLL fusion- and AEP-dep transcription. Nature Communications, 2015, 6, 8869.	endent	5.8	44
2699	The interplay of histone modifications $\hat{a} \in \mathbb{C}$ writers that read. EMBO Reports, 2015, 16,	1467-1481.	2.0	604
2700	Characteristics of Long Non-coding RNAs in the Brown Norway Rat and Alterations in t Salt-Sensitive Rat. Scientific Reports, 2014, 4, 7146.	he Dahl	1.6	41
2701	Chromatin remodeling and bivalent histone modifications in embryonic stem cells. EMI 2015, 16, 1609-1619.	30 Reports,	2.0	196
2702	Integrative Analysis of Multiple ChIP-X Data Sets Using Correlation Motifs. , 0, , 110-13	2.		0

# 2703	ARTICLE Epigenetics of Suicidal Behaviour. Advances in Biological Psychiatry, 0, , 75-87.	IF 0.2	CITATIONS 2
2704	Fully automated high-throughput chromatin immunoprecipitation for ChIP-seq: Identifying ChIP-quality p300 monoclonal antibodies. Scientific Reports, 2014, 4, 5152.	1.6	34
2705	Carcinogenesis. , 2015, , 1135-1172.		0
2706	An NGS Workflow Blueprint for DNA Sequencing Data and Its Application in Individualized Molecular Oncology. Cancer Informatics, 2015, 14s5, CIN.S30793.	0.9	10
2707	A Statistical Framework to Predict Functional Non-Coding Regions in the Human Genome Through Integrated Analysis of Annotation Data. Scientific Reports, 2015, 5, 10576.	1.6	144
2708	Identification of novel trans-crosstalk between histone modifications via genome-wide analysis of maximal deletion effect. Genes and Genomics, 2015, 37, 693-701.	0.5	1
2709	BIDCHIPS: bias decomposition and removal from ChIP-seq data clarifies true binding signal and its functional correlates. Epigenetics and Chromatin, 2015, 8, 33.	1.8	17
2710	Differences in histone modifications between slow- and fast-twitch muscle of adult rats and following overload, denervation, or valproic acid administration. Journal of Applied Physiology, 2015, 119, 1042-1052.	1.2	22
2711	Promoter-like epigenetic signatures in exons displaying cell type-specific splicing. Genome Biology, 2015, 16, 236.	3.8	32
2712	Affinity-seq detects genome-wide PRDM9 binding sites and reveals the impact of prior chromatin modifications on mammalian recombination hotspot usage. Epigenetics and Chromatin, 2015, 8, 31.	1.8	77
2713	Progressive Chromatin Condensation and H3K9 Methylation Regulate the Differentiation of Embryonic and Hematopoietic Stem Cells. Stem Cell Reports, 2015, 5, 728-740.	2.3	106
2714	Direct ChIP-Seq significance analysis improves target prediction. BMC Genomics, 2015, 16, S4.	1.2	8
2715	cChIP-seq: a robust small-scale method for investigation of histone modifications. BMC Genomics, 2015, 16, 1083.	1.2	14
2716	Characterization of genome-wide H3K27ac profiles reveals a distinct PM2.5-associated histone modification signature. Environmental Health, 2015, 14, 65.	1.7	37
2717	Tip60 complex binds to active Pol II promoters and a subset of enhancers and co-regulates the c-Myc network in mouse embryonic stem cells. Epigenetics and Chromatin, 2015, 8, 45.	1.8	48
2718	Functionally distinct patterns of nucleosome remodeling at enhancers in glucocorticoid-treated acute lymphoblastic leukemia. Epigenetics and Chromatin, 2015, 8, 53.	1.8	22
2719	Epigenetic States of Nephron Progenitors and Epithelial Differentiation. Journal of Cellular Biochemistry, 2015, 116, 893-902.	1.2	15
2720	Nonparametric Tests for Differential Histone Enrichment with ChIP-Seq Data. Cancer Informatics, 2015, 14s1, CIN.S13972.	0.9	2

#	Article	IF	CITATIONS
2721	Histone Demethylase Utx Regulates Differentiation and Mineralization in Osteoblasts. Journal of Cellular Biochemistry, 2015, 116, 2628-2636.	1.2	17
2722	H2A.Z mediates different aspects of chromatin function and modulates flowering responses in Arabidopsis. Plant Journal, 2015, 83, 96-109.	2.8	59
2723	Interplay between transcriptional control and chromatin regulation in the oligodendrocyte lineage. Glia, 2015, 63, 1357-1375.	2.5	33
2724	A multiscale approach to simulating the conformational properties of unbound multiâ€ <scp>C</scp> ₂ <scp>H</scp> ₂ zinc finger proteins. Proteins: Structure, Function and Bioinformatics, 2015, 83, 1604-1615.	1.5	3
2725	Partners in crime: The role of tandem modules in gene transcription. Protein Science, 2015, 24, 1347-1359.	3.1	11
2726	A resource for characterizing genomeâ€wide binding and putative target genes of transcription factors expressed during secondary growth and wood formation in <i>Populus</i> . Plant Journal, 2015, 82, 887-898.	2.8	51
2727	Genome-wide Massive Sequencing in Embryonic Stem Cell Biology:Recent Insights and Challenges. Journal of Stem Cell Research & Therapy, 2015, 05, .	0.3	0
2728	Clobal histone post-translational modifications and cancer: Biomarkers for diagnosis, prognosis and treatment?. World Journal of Biological Chemistry, 2015, 6, 333.	1.7	92
2729	The Histone H3K9 Demethylase Kdm3b Is Required for Somatic Growth and Female Reproductive Function. International Journal of Biological Sciences, 2015, 11, 494-507.	2.6	33
2730	Long Noncoding RNA: its partners and their roles in cancer. Neoplasma, 2015, 62, 846-854.	0.7	12
2731	Epigenetic and Posttranslational Modifications in Light Signal Transduction and the Circadian Clock in Neurospora crassa. International Journal of Molecular Sciences, 2015, 16, 15347-15383.	1.8	19
2732	Transcriptional Activation of Inflammatory Genes: Mechanistic Insight into Selectivity and Diversity. Biomolecules, 2015, 5, 3087-3111.	1.8	46
2733	The Structural Determinants behind the Epigenetic Role of Histone Variants. Genes, 2015, 6, 685-713.	1.0	30
2734	Histone Methylation Marks on Circulating Nucleosomes as Novel Blood-Based Biomarker in Colorectal Cancer. International Journal of Molecular Sciences, 2015, 16, 29654-29662.	1.8	66
2735	Functional Role of G9a Histone Methyltransferase in Cancer. Frontiers in Immunology, 2015, 6, 487.	2.2	192
2736	Epigenetic modulation of brain gene networks for cocaine and alcohol abuse. Frontiers in Neuroscience, 2015, 9, 176.	1.4	69
2737	Nutriepigenomics. , 2015, , 313-347.		4
2738	ClusTrack: Feature Extraction and Similarity Measures for Clustering of Genome-Wide Data Sets. PLoS ONE, 2015, 10, e0123261.	1.1	3

#	Article	IF	CITATIONS
2739	One Size Doesn't Fit All - RefEditor: Building Personalized Diploid Reference Genome to Improve Read Mapping and Genotype Calling in Next Generation Sequencing Studies. PLoS Computational Biology, 2015, 11, e1004448.	1.5	11
2740	MoSET1 (Histone H3K4 Methyltransferase in Magnaporthe oryzae) Regulates Global Gene Expression during Infection-Related Morphogenesis. PLoS Genetics, 2015, 11, e1005385.	1.5	69
2741	Multiplexing of ChIP-Seq Samples in an Optimized Experimental Condition Has Minimal Impact on Peak Detection. PLoS ONE, 2015, 10, e0129350.	1.1	0
2742	The Histone Methyltransferase Inhibitor A-366 Uncovers a Role for G9a/GLP in the Epigenetics of Leukemia. PLoS ONE, 2015, 10, e0131716.	1.1	65
2743	A Quantitative Profiling Tool for Diverse Genomic Data Types Reveals Potential Associations between Chromatin and Pre-mRNA Processing. PLoS ONE, 2015, 10, e0132448.	1.1	5
2744	A Multidisciplinary Biospecimen Bank of Renal Cell Carcinomas Compatible with Discovery Platforms at Mayo Clinic, Scottsdale, Arizona. PLoS ONE, 2015, 10, e0132831.	1.1	9
2745	c-Myb Binding Sites in Haematopoietic Chromatin Landscapes. PLoS ONE, 2015, 10, e0133280.	1.1	20
2746	Reporter Gene Silencing in Targeted Mouse Mutants Is Associated with Promoter CpG Island Methylation. PLoS ONE, 2015, 10, e0134155.	1.1	3
2747	The TrxG Complex Mediates Cytokine Induced De Novo Enhancer Formation in Islets. PLoS ONE, 2015, 10, e0141470.	1.1	9
2748	Dynamic Trk and G Protein Signalings Regulate Dopaminergic Neurodifferentiation in Human Trophoblast Stem Cells. PLoS ONE, 2015, 10, e0143852.	1.1	10
2749	Immunosuppressant MPA Modulates Tight Junction through Epigenetic Activation of MLCK/MLC-2 Pathway via p38MAPK. Frontiers in Physiology, 2015, 6, 381.	1.3	13
2750	Epigenetics: general characteristics and implications for oral health. Restorative Dentistry & Endodontics, 2015, 40, 14.	0.6	37
2751	MicroRNA Promoter Identification in <i>Arabidopsis</i> Using Multiple Histone Markers. BioMed Research International, 2015, 2015, 1-10.	0.9	57
2752	Genome-Wide Expression of MicroRNAs Is Regulated by DNA Methylation in Hepatocarcinogenesis. Gastroenterology Research and Practice, 2015, 2015, 1-12.	0.7	20
2753	HIV Tat controls RNA Polymerase II and the epigenetic landscape to transcriptionally reprogram target immune cells. ELife, 2015, 4, .	2.8	47
2754	Epigenetic Changes in Endothelial Progenitors as a Possible Cellular Basis for Glycemic Memory in Diabetic Vascular Complications. Journal of Diabetes Research, 2015, 2015, 1-17.	1.0	55
2755	Genomic instability and carcinogenesis. , 0, , 93-112.		0
2756	Involvement of histone H2B monoubiquitination in the regulation of mouse preimplantation development. Journal of Reproduction and Development, 2015, 61, 179-184.	0.5	12

		CITATION REPORT		
#	Article		IF	CITATIONS
2757	New insights into the epigenetic control of satellite cells. World Journal of Stem Cells, 2	2015, 7, 945.	1.3	26
2758	Genetic Determinants of Epigenetic Patterns: Providing Insight into Disease. Molecular 21, 400-409.	Medicine, 2015,	1.9	10
2759	Histone demethylase RBP2 decreases miR-21 in blast crisis of chronic myeloid leukemia 2015, 6, 1249-1261.	a. Oncotarget,	0.8	33
2760	Base-resolution methylation patterns accurately predict transcription factor bindings ir Nucleic Acids Research, 2015, 43, 2757-2766.	ι νίνο.	6.5	46
2761	Regulation of DNA methylation dictates Cd4 expression during the development of hel cytotoxic T cell lineages. Nature Immunology, 2015, 16, 746-754.	per and	7.0	72
2762	DNA immunoprecipitation semiconductor sequencing (DIP-SC-seq) as a rapid method t genome wide epigenetic signatures. Scientific Reports, 2015, 5, 9778.	to generate	1.6	16
2764	Introduction to Data Types in Epigenomics. Translational Bioinformatics, 2015, , 3-34.		0.0	2
2765	Expression of Non-acetylatable H2A.Z in Myoblast Cells Blocks Myoblast Differentiation Disruption of MyoD Expression. Journal of Biological Chemistry, 2015, 290, 13234-132		1.6	26
2766	Calibrating ChIP-Seq with Nucleosomal Internal Standards to Measure Histone Modific Genome Wide. Molecular Cell, 2015, 58, 886-899.	ation Density	4.5	69
2767	Personalized Epigenetics. , 2015, , 123-150.			0
2768	Identification of Jumonji AT-Rich Interactive Domain 1A Inhibitors and Their Effect on C Medicinal Chemistry Letters, 2015, 6, 665-670.	ancer Cells. ACS	1.3	46
2769	Pannexin-1 Up-regulation in the Dorsal Root Ganglion Contributes to Neuropathic Pain Journal of Biological Chemistry, 2015, 290, 14647-14655.	Development.	1.6	83
2770	The State of the Art of Epigenetic Technologies. , 2015, , 1-18.			1
2771	Enzymatic Assays of Histone Methyltransferase Enzymes. , 2015, , 333-361.			5
2772	A Genome-Wide Perspective on Metabolism. Handbook of Experimental Pharmacology	, 2015, 233, 1-28.	0.9	3
2773	Pitfalls in ecological research – transgenerational effects. Folia Geobotanica, 2015, 5	0, 75-85.	0.4	25
2774	Acetylation of intragenic histones on HPV16 correlates with enhanced HPV16 gene exp Virology, 2015, 482, 244-259.	pression.	1.1	21
2775	Methyllysine Recognition by the Royal Family Modules: Chromo, Tudor, MBT, Chromo B PWWP Domains. , 2015, , 49-82.	Barrel, and		3

#	Article	IF	CITATIONS
2776	Histone Variant H2A.Z.2 Mediates Proliferation and Drug Sensitivity of Malignant Melanoma. Molecular Cell, 2015, 59, 75-88.	4.5	166
2777	The Human Genome Project: Where Are We Now and Where Are We Going?. , 2015, , 7-31.		0
2780	Epigenomic Biomarkers for the Advance of Personalized Medicine. Translational Bioinformatics, 2015, , 187-217.	0.0	0
2781	T helper 2 (Th2) cell differentiation, type 2 innate lymphoid cell (ILC2) development and regulation of interleukin-4 (IL-4) and IL-13 production. Cytokine, 2015, 75, 14-24.	1.4	307
2782	Enhancer-associated RNAs as therapeutic targets. Expert Opinion on Biological Therapy, 2015, 15, 723-734.	1.4	28
2783	Regulation of Peripheral Nerve Myelin Maintenance by Gene Repression through Polycomb Repressive Complex 2. Journal of Neuroscience, 2015, 35, 8640-8652.	1.7	48
2784	Elevated expression of histone demethylase PHF8 associates with adverse prognosis in patients of laryngeal and hypopharyngeal squamous cell carcinoma. Epigenomics, 2015, 7, 143-153.	1.0	22
2785	The Epigenome and Aging. Molecular and Integrative Toxicology, 2015, , 155-195.	0.5	0
2787	Epigenetics of Personalized Toxicology. , 2015, , 245-282.		1
2788	Enhancer modeling uncovers transcriptional signatures of individual cardiac cell states in <i>Drosophila</i> . Nucleic Acids Research, 2015, 43, 1726-1739.	6.5	12
2789	Epigenome Engineering in Cancer: Fairytale or a Realistic Path to the Clinic?. Frontiers in Oncology, 2015, 5, 22.	1.3	63
2790	Protein–DNA binding in high-resolution. Critical Reviews in Biochemistry and Molecular Biology, 2015, 50, 269-283.	2.3	41
2791	Enhancing our understanding of enhancers in Tâ€helper cells. European Journal of Immunology, 2015, 45, 2998-3001.	1.6	2
2792	Translocation of forkhead box O1 to the nuclear periphery induces histone modifications that regulate transcriptional repression of <i><scp>PCK</scp>1</i> in HepG2 cells. Genes To Cells, 2015, 20, 340-357.	0.5	21
2793	H3K36 Trimethylation-Mediated Epigenetic Regulation is Activated by Bam and Promotes Germ Cell Differentiation During Early Oogenesis in <i>Drosophila</i> . Biology Open, 2015, 4, 119-124.	0.6	11
2794	In the loop: promoter–enhancer interactions and bioinformatics. Briefings in Bioinformatics, 2016, 17, bbv097.	3.2	115
2795	Uncoupling histone turnover from transcription-associated histone H3 modifications. Nucleic Acids Research, 2015, 43, 3972-3985.	6.5	28
2796	Biological chromodynamics: a general method for measuring protein occupancy across the genome by calibrating ChIP-seq. Nucleic Acids Research, 2015, 43, gkv670.	6.5	131

#	Article	IF	CITATIONS
2797	High-resolution mapping of H4K16 and H3K23 acetylation reveals conserved and unique distribution patterns in <i>Arabidopsis</i> and rice. Epigenetics, 2015, 10, 1044-1053.	1.3	48
2798	Dynamic Control of Long-Range Genomic Interactions at the Immunoglobulin κ Light-Chain Locus. Advances in Immunology, 2015, 128, 183-271.	1.1	26
2799	"ldentification Card― Sites on Histone Modification of Cancer Cell. Chinese Medical Sciences Journal, 2015, 30, 203-209.	0.2	2
2800	ChromClust: A semi-supervised chromatin clustering toolkit for mining histone modifications interplay. Genomics, 2015, 106, 355-359.	1.3	5
2801	Embryonic transcription is controlled by maternally defined chromatin state. Nature Communications, 2015, 6, 10148.	5.8	103
2802	Genome-Wide Epigenetic Studies in Human Disease: A Primer on -Omic Technologies. American Journal of Epidemiology, 2016, 183, kwv187.	1.6	23
2803	Set1 and MLL1/2 Target Distinct Sets of Functionally Different Genomic Loci InÂVivo. Cell Reports, 2015, 13, 2741-2755.	2.9	56
2804	Developmentally arrested <i>Austrofundulus limnaeus</i> embryos have changes in post-translational modifications of histone H3. Journal of Experimental Biology, 2015, 219, 544-52.	0.8	18
2805	Predicting chromatin organization using histone marks. Genome Biology, 2015, 16, 162.	3.8	98
2806	Disrupted intricacy of histone H3K4 methylation in neurodevelopmental disorders. Epigenomics, 2015, 7, 503-519.	1.0	143
2807	The histone methyltransferase SDG8 mediates the epigenetic modification of light and carbon responsive genes in plants. Genome Biology, 2015, 16, 79.	3.8	91
2808	Generation of an anti-EpCAM antibody and epigenetic regulation of EpCAM in colorectal cancer. International Journal of Oncology, 2015, 46, 1788-1800.	1.4	12
2809	Epigenetic bivalent marking is permissive to the synergy of HDAC and PARP inhibitors on TXNIP expression in breast cancer cells. Oncology Reports, 2015, 33, 2199-2206.	1.2	16
2810	Transcriptional Enhancers: Bridging the Genome and Phenome. Cold Spring Harbor Symposia on Quantitative Biology, 2015, 80, 17-26.	2.0	28
2811	Common and distinct DNA-binding and regulatory activities of the BEN-solo transcription factor family. Genes and Development, 2015, 29, 48-62.	2.7	41
2812	Identification and Computational Analysis of Gene Regulatory Elements. Cold Spring Harbor Protocols, 2015, 2015, pdb.top083642.	0.2	7
2813	Histone Variants and Epigenetics. Cold Spring Harbor Perspectives in Biology, 2015, 7, a019364.	2.3	275
2815	Dependence of radiation-induced H2AX phosphorylation on histone methylation: Evidence from the chromatin immunoprecipitation assay. International Journal of Radiation Biology, 2015, 91, 346-353.	1.0	6

#	Article	IF	CITATIONS
2816	Multiple dimensions of epigenetic gene regulation in the malaria parasite <i>Plasmodium falciparum</i> . BioEssays, 2015, 37, 182-194.	1.2	54
2817	What are super-enhancers?. Nature Genetics, 2015, 47, 8-12.	9.4	598
2818	Neuroepigenomics: resources, obstacles, and opportunities. Neuroepigenetics, 2015, 1, 2-13.	2.8	16
2819	Gonadotropin gene transcription is activated by menin-mediated effects on the chromatin. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2015, 1849, 328-341.	0.9	15
2820	The PRMT5 arginine methyltransferase: many roles in development, cancer and beyond. Cellular and Molecular Life Sciences, 2015, 72, 2041-2059.	2.4	364
2821	Vision from next generation sequencing: Multi-dimensional genome-wide analysis for producing gene regulatory networks underlying retinal development, aging and disease. Progress in Retinal and Eye Research, 2015, 46, 1-30.	7.3	50
2822	Targeting histone lysine methylation in cancer. , 2015, 150, 1-22.		164
2823	Chromatin-wide Profiling of DYRK1A Reveals a Role as a Gene-Specific RNA Polymerase II CTD Kinase. Molecular Cell, 2015, 57, 506-520.	4.5	103
2824	Infection and Autoimmune Thyroid Diseases. , 2015, , 891-918.		5
2825	Androgens regulate SMAD ubiquitination regulatory factorâ€1 expression and prostate cancer cell invasion. Prostate, 2015, 75, 561-572.	1.2	17
2826	Stem cell activation in skeletal muscle regeneration. Cellular and Molecular Life Sciences, 2015, 72, 1663-1677.	2.4	114
2827	DNA double strand break repair pathway choice: a chromatin based decision?. Nucleus, 2015, 6, 107-113.	0.6	87
2828	Epigenetic Heterogeneity in HIV-1 Latency Establishment. Scientific Reports, 2015, 5, 7701.	1.6	54
2829	ChIPping Away at the Drosophila Clock. Methods in Enzymology, 2015, 551, 323-347.	0.4	6
2831	Large-scale imputation of epigenomic datasets for systematic annotation of diverse human tissues. Nature Biotechnology, 2015, 33, 364-376.	9.4	354
2832	Polycomb group protein-mediated histone modifications during cell differentiation. Epigenomics, 2015, 7, 75-84.	1.0	28
2833	Quantitative Proteomic Analysis of Histone Modifications. Chemical Reviews, 2015, 115, 2376-2418.	23.0	306
2834	Integrative analysis of 111 reference human epigenomes. Nature, 2015, 518, 317-330.	13.7	5,653

#	Article	IF	CITATIONS
2835	Regulation of CD4 Tâ€cell differentiation and inflammation by repressive histone methylation. Immunology and Cell Biology, 2015, 93, 245-252.	1.0	18
2836	From trans to cis: transcriptional regulatory networks in neocortical development. Trends in Genetics, 2015, 31, 77-87.	2.9	55
2837	Lysine-Specific Demethylase 2 Suppresses Lipid Influx and Metabolism in Hepatic Cells. Molecular and Cellular Biology, 2015, 35, 1068-1080.	1.1	28
2838	Intrauterine growth restriction disrupts developmental epigenetics around distal growth hormone response elements on the rat hepatic IGFâ€l gene. FASEB Journal, 2015, 29, 1176-1184.	0.2	30
2839	ZNF143 provides sequence specificity to secure chromatin interactions at gene promoters. Nature Communications, 2015, 6, 6186.	5.8	173
2840	SMYD1 and G6PD modulation are critical events for miR-206-mediated differentiation of rhabdomyosarcoma. Cell Cycle, 2015, 14, 1389-1402.	1.3	41
2841	An Alternative Retinoic Acid-responsive Stra6 Promoter Regulated in Response to Retinol Deficiency. Journal of Biological Chemistry, 2015, 290, 4356-4366.	1.6	23
2842	A Sensitive Approach to Map Genome-wide 5-Hydroxymethylcytosine and 5-Formylcytosine at Single-Base Resolution. Molecular Cell, 2015, 57, 750-761.	4.5	77
2843	Epigenetic studies of suicidal behavior. Neurocase, 2015, 21, 134-143.	0.2	19
2844	Sequence and regulation of the porcine FSHR gene promoter. Animal Reproduction Science, 2015, 154, 95-104.	0.5	8
2845	Induction of histone H3K4 methylation at the promoter, enhancer, and transcribed regions of the Si and Sglt1 genes in rat jejunum in response to a high-starch/low-fat diet. Nutrition, 2015, 31, 366-372.	1.1	24
2846	Novel CTCF binding at a site in exon1A of BCL6 is associated with active histone marks and a transcriptionally active locus. Oncogene, 2015, 34, 246-256.	2.6	15
2847	Selective Inhibitors of Protein Methyltransferases. Journal of Medicinal Chemistry, 2015, 58, 1596-1629.	2.9	112
2848	Epigenetic and metabolic regulation of breast cancer stem cells. Journal of Zhejiang University: Science B, 2015, 16, 10-17.	1.3	23
2849	Histone methyltransferase Dot1L plays a role in postembryonic development in <i>Xenopus tropicalis</i> . FASEB Journal, 2015, 29, 385-393.	0.2	25
2850	ZmGRF, a GA regulatory factor from maize, promotes flowering and plant growth in Arabidopsis. Plant Molecular Biology, 2015, 87, 157-167.	2.0	11
2851	An ultra-low-input native ChIP-seq protocol for genome-wide profiling of rare cell populations. Nature Communications, 2015, 6, 6033.	5.8	322
2852	Fetal iron deficiency induces chromatin remodeling at the <i>Bdnf</i> locus in adult rat hippocampus. American Journal of Physiology - Regulatory Integrative and Comparative Physiology, 2015, 308, R276-R282.	0.9	64

#	Article	IF	Citations
2853	Chromatin Changes at the <i>PPAR-γ2</i> Promoter During Bone Marrow-Derived Multipotent Stromal Cell Culture Correlate With Loss of Gene Activation Potential. Stem Cells, 2015, 33, 2169-2181.	1.4	15
2854	Eukaryotic enhancers: common features, regulation, and participation in diseases. Cellular and Molecular Life Sciences, 2015, 72, 2361-2375.	2.4	39
2855	Histone variants: the artists of eukaryotic chromatin. Science China Life Sciences, 2015, 58, 232-239.	2.3	15
2856	A survey of computational methods in transcriptome-wide alternative splicing analysis. Biomolecular Concepts, 2015, 6, 59-66.	1.0	18
2857	Transcription factor interaction with COMPASS-like complex regulates histone H3K4 trimethylation for specific gene expression in plants. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 2900-2905.	3.3	106
2858	Differential DNA mismatch repair underlies mutation rate variation across the human genome. Nature, 2015, 521, 81-84.	13.7	310
2859	Nuclear architecture dictates HIV-1 integration site selection. Nature, 2015, 521, 227-231.	13.7	277
2860	Repression of Hox genes by LMP1 in nasopharyngeal carcinoma and modulation of glycolytic pathway genes by HoxC8. Oncogene, 2015, 34, 6079-6091.	2.6	50
2861	An Integrative Breakage Model of genome architecture, reshuffling and evolution. BioEssays, 2015, 37, 479-488.	1.2	54
2862	The epigenetics of aging and neurodegeneration. Progress in Neurobiology, 2015, 131, 21-64.	2.8	334
2863	Polycomb genes, miRNA, and their deregulation in B-cell malignancies. Blood, 2015, 125, 1217-1225.	0.6	37
2865	LSD1n is an H4K20 demethylase regulating memory formation via transcriptional elongation control. Nature Neuroscience, 2015, 18, 1256-1264.	7.1	131
2866	MIR retrotransposon sequences provide insulators to the human genome. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E4428-37.	3.3	104
2867	Epigenetic regulation of the intestinal epithelium. Cellular and Molecular Life Sciences, 2015, 72, 4139-4156.	2.4	35
2868	The thermogenic circuit: Regulators of thermogenic competency and differentiation. Genes and Diseases, 2015, 2, 164-172.	1.5	13
2869	Coordinated action of histone modification and microRNA regulations in human genome. Gene, 2015, 570, 277-281.	1.0	15
2870	Systematic Screening of Promoter Regions Pinpoints Functional <i>Cis</i> -Regulatory Mutations in a Cutaneous Melanoma Genome. Molecular Cancer Research, 2015, 13, 1218-1226.	1.5	29
2871	Applications of Deep Sequencing to Developmental Systems. , 2015, , 37-48.		1

ARTICLE IF CITATIONS Pontin functions as an essential coactivator for Oct4-dependent lincRNA expression in mouse 2872 5.8 24 embryonic stem cells. Nature Communications, 2015, 6, 6810. Sculpting the Transcriptome During the Oocyte-to-Embryo Transition in Mouse. Current Topics in 1.0 Developmental Biology, 2015, 113, 305-349. Inverted-Repeat RNAs Targeting <i>FT </i>Intronic Regions Promote <i>FT </i>Expression in Arabidopsis. 2874 1.5 16 Plant and Cell Physiology, 2015, 56, 1667-1678. Determinants of Receptor- and Tissue-Specific Actions in Androgen Signaling. Endocrine Reviews, 2015, 8.9 93 36, 357-384. Extracting biomarkers of commitment to cancer development: potential role of vibrational 2876 1.5 17 spectroscopy in systems biology. Expert Review of Molecular Diagnostics, 2015, 15, 693-713. Inhibitors of Jumonji C-Domain Histone Demethylases., 2015, , 439-469. Epigenetic aberrations in acute myeloid leukemia: Early key events during leukemogenesis. Experimental 2878 0.2 47 Hematology, 2015, 43, 609-624. The role of DNA methylation in directing the functional organization of the cancer epigenome. 2879 2.4 90 Genome Research, 2015, 25, 467-477. Regulation of Oxidative Stress in Pulmonary Artery Endothelium. Modulation of Extracellular 2880 Superoxide Dismutase and NOX4 Expression Using Histone Deacetylase Class I Inhibitors. American 1.4 30 Journal of Respiratory Cell and Molecular Biology, 2015, 53, 513-524. An update on the epigenetics of psychotic diseases and autism. Epigenomics, 2015, 7, 427-449. 1.0 RNA Exosome Regulates AID DNA Mutator Activity in the B Cell Genome. Advances in Immunology, 2015, 2882 1.1 29 127, 257-308. IKAROS: a multifunctional regulator of the polymerase II transcription cycle. Trends in Genetics, 2015, 2883 2.9 31, 500-508. Integrative epigenomic and genomic filtering for methylation markers in hepatocellular carcinomas. 2884 0.7 24 BMC Medical Genomics, 2015, 8, 28. Peptidyl
prolyl Isomerase Pin1 Directly Enhances the DNA Binding Functions of Estrogen Receptor
α. Journal of Biological Chemistry, 2015, 290, 13749-13762. 2885 1.6 JMJD3 as an epigenetic regulator in development and disease. International Journal of Biochemistry and 2886 1.2 111 Cell Biology, 2015, 67, 148-157. An Interactive Database for the Assessment of Histone Antibody Specificity. Molecular Cell, 2015, 59, 2887 139 502-511. Simple and inexpensive ribosome profiling analysis of mRNA translation. Methods, 2015, 91, 69-74. 2888 1.9 45 Sound of silence: the properties and functions of repressive Lys methyltransferases. Nature Reviews 2889 16.1 161 Molecular Cell Biology, 2015, 16, 499-513.

#	Article	IF	CITATIONS
2890	Reproduction and nutriment–nurture crosstalk: epigenetic perspectives. Journal of Reproductive Health and Medicine, 2015, 1, 50-59.	0.3	3
2891	TPO-Induced Metabolic Reprogramming Drives Liver Metastasis of Colorectal Cancer CD110+ Tumor-Initiating Cells. Cell Stem Cell, 2015, 17, 47-59.	5.2	115
2892	The Drosophila histone demethylase dKDM5/LID regulates hematopoietic development. Developmental Biology, 2015, 405, 260-268.	0.9	12
2893	The Epigenetic Regulator G9a Mediates Tolerance to RNA Virus Infection in Drosophila. PLoS Pathogens, 2015, 11, e1004692.	2.1	106
2894	Targeting EZH2 and PRC2 dependence as novel anticancer therapy. Experimental Hematology, 2015, 43, 698-712.	0.2	101
2895	Identification of peculiar and common effects of histone modifications on transcription. Journal of Theoretical Biology, 2015, 380, 24-39.	0.8	1
2896	A unified architecture of transcriptional regulatory elements. Trends in Genetics, 2015, 31, 426-433.	2.9	173
2897	Confluence-Induced Squamous Differentiation Is Not Accompanied by Changes in H3K27me3 Repressive Epigenetic Mark. Journal of Investigative Dermatology, 2015, 135, 2446-2454.	0.3	1
2898	Histone Demethylases KDM4A and KDM4C Regulate Differentiation of Embryonic Stem Cells to Endothelial Cells. Stem Cell Reports, 2015, 5, 10-21.	2.3	40
2899	SET7/9 Enzyme Regulates Cytokine-induced Expression of Inducible Nitric-oxide Synthase through Methylation of Lysine 4 at Histone 3 in the Islet β Cell. Journal of Biological Chemistry, 2015, 290, 16607-16618.	1.6	21
2900	Computational Methods Used in Systems Biology. , 2015, , 85-115.		3
2901	Targeting DOT1L and HOX gene expression in MLL-rearranged leukemia and beyond. Experimental Hematology, 2015, 43, 673-684.	0.2	97
2902	Multiplex Eukaryotic Transcription (In)activation: Timing, Bursting and Cycling of a Ratchet Clock Mechanism. PLoS Computational Biology, 2015, 11, e1004236.	1.5	25
2903	KMT1E-mediated chromatin modifications at the FcÎ ³ RIIb promoter regulate thymocyte development. Genes and Immunity, 2015, 16, 162-169.	2.2	14
2904	Embryonic Stem Cell Specific "Master―Replication Origins at the Heart of the Loss of Pluripotency. PLoS Computational Biology, 2015, 11, e1003969.	1.5	22
2905	The altered fate of aging satellite cells is determined by signaling and epigenetic changes. Frontiers in Genetics, 2015, 6, 59.	1.1	20
2906	You are never alone: crosstalk among epigenetic players. Science Bulletin, 2015, 60, 899-904.	4.3	3
2907	Epigenetics of T cells regulated by Polycomb/Trithorax molecules. Trends in Molecular Medicine, 2015, 21, 330-340.	3.5	25

#	Article	IF	CITATIONS
2908	Epigenetic Determinants of Erythropoiesis: Role of the Histone Methyltransferase SetD8 in Promoting Erythroid Cell Maturation and Survival. Molecular and Cellular Biology, 2015, 35, 2073-2087.	1.1	30
2909	Chromatin changes in response to drought, salinity, heat, and cold stresses in plants. Frontiers in Plant Science, 2015, 6, 114.	1.7	367
2910	Regulation of stimulus-inducible gene expression in myeloid cells. Seminars in Immunology, 2015, 27, 33-43.	2.7	5
2911	Next Generation Sequencing-based analysis of RNA polymerase functions. Methods, 2015, 86, 37-44.	1.9	5
2912	Opposite expression of <i>CYP51A1</i> and its natural antisense transcript <i>AluCYP51A1</i> in adenovirus type 37 infected retinal pigmented epithelial cells. FEBS Letters, 2015, 589, 1383-1388.	1.3	6
2913	Overexpression of JMJD3 may contribute to demethylation of H3K27me3 in CD4 + T cells from patients with systemic sclerosis. Clinical Immunology, 2015, 161, 396-399.	1.4	27
2914	High-throughput and quantitative assessment of enhancer activity in mammals by CapStarr-seq. Nature Communications, 2015, 6, 6905.	5.8	138
2915	Flow-induced protein kinase A–CREB pathway acts via BMP signaling to promote HSC emergence. Journal of Experimental Medicine, 2015, 212, 633-648.	4.2	47
2916	Transcription-Dependent Generation of a Specialized Chromatin Structure at the TCRÎ ² Locus. Journal of Immunology, 2015, 194, 3432-3443.	0.4	10
2917	Epigenetics of the failing heart. Heart Failure Reviews, 2015, 20, 435-459.	1.7	16
2918	Molecular mechanisms of MLL-associated leukemia. International Journal of Hematology, 2015, 101, 352-361.	0.7	34
2919	Polycomb repressive complex 2 epigenomic signature defines age-associated hypermethylation and gene expression changes. Epigenetics, 2015, 10, 484-495.	1.3	60
2920	histoneHMM: Differential analysis of histone modifications with broad genomic footprints. BMC Bioinformatics, 2015, 16, 60.	1.2	28
2921	Global epigenomic analysis indicates that Epialleles contribute to Allele-specific expression via Allele-specific histone modifications in hybrid rice. BMC Genomics, 2015, 16, 232.	1.2	23
2922	Proteogenomics analysis reveals specific genomic orientations of distal regulatory regions composed by non-canonical histone variants. Epigenetics and Chromatin, 2015, 8, 13.	1.8	10
2923	Pharmacological manipulation of transcription factor protein-protein interactions: opportunities and obstacles. Cell Regeneration, 2015, 4, 4:2.	1.1	52
2924	The Eukaryotic Promoter Database: expansion of EPDnew and new promoter analysis tools. Nucleic Acids Research, 2015, 43, D92-D96.	6.5	238
2925	Structural organization of human replication timing domains. FEBS Letters, 2015, 589, 2944-2957.	1.3	28

#	Article	IF	CITATIONS
2926	Computer-aided Molecular Design of Compounds Targeting Histone Modifying Enzymes. Computational and Structural Biotechnology Journal, 2015, 13, 358-365.	1.9	19
2927	p53-dependent expression of CXCR5 chemokine receptor in MCF-7 breast cancer cells. Scientific Reports, 2015, 5, 9330.	1.6	43
2928	Multi-layered epigenetic mechanisms contribute to transcriptional memory in T lymphocytes. BMC Immunology, 2015, 16, 27.	0.9	17
2929	The Ensembl Regulatory Build. Genome Biology, 2015, 16, 56.	3.8	382
2931	Long noncoding RNA turnover. Biochimie, 2015, 117, 15-21.	1.3	55
2932	The roles of chromatin-remodelers and epigenetic modifiers in kidney cancer. Cancer Genetics, 2015, 208, 206-214.	0.2	48
2933	Histone Methyltransferase SET1 Mediates Angiotensin II–Induced Endothelin-1 Transcription and Cardiac Hypertrophy in Mice. Arteriosclerosis, Thrombosis, and Vascular Biology, 2015, 35, 1207-1217.	1.1	47
2934	Combinatorial Roles of DNA Methylation and Histone Modifications on Gene Expression. Advances in Intelligent Systems and Computing, 2015, , 123-135.	0.5	6
2935	The NSD family of protein methyltransferases in human cancer. Epigenomics, 2015, 7, 863-874.	1.0	76
2936	Epigenetic regulation by histone demethylases in hypoxia. Epigenomics, 2015, 7, 791-811.	1.0	124
2937	Chemical profiling of the genome with anti-cancer drugs defines target specificities. Nature Chemical Biology, 2015, 11, 472-480.	3.9	62
2938	Epigenetic modifications and noncoding RNAs in cardiac hypertrophy and failure. Nature Reviews Cardiology, 2015, 12, 488-497.	6.1	117
2939	The DREAM complex promotes gene body H2A.Z for target repression. Genes and Development, 2015, 29, 495-500.	2.7	53
2940	FEATnotator: A tool for integrated annotation of sequence features and variation, facilitating interpretation in genomics experiments. Methods, 2015, 79-80, 11-17.	1.9	7
2941	Nucleosome-specific, Time-dependent Changes in Histone Modifications during Activation of the Early Growth Response 1 (Egr1) Gene. Journal of Biological Chemistry, 2015, 290, 197-208.	1.6	21
2942	Trimethylation of Lys36 on H3 restricts gene expression change during aging and impacts life span. Genes and Development, 2015, 29, 718-731.	2.7	121
2943	Epigenetic regulation of drug metabolism and transport. Acta Pharmaceutica Sinica B, 2015, 5, 106-112.	5.7	62
2944	Pluripotency Activity of Nanog Requires Biochemical Stabilization by Variant Histone Protein H2A.Z. Stem Cells, 2015, 33, 2126-2134.	1.4	10

#	Article	IF	CITATIONS
2945	PLZF Regulates <i>CCR6</i> and Is Critical for the Acquisition and Maintenance of the Th17 Phenotype in Human Cells. Journal of Immunology, 2015, 194, 4350-4361.	0.4	33
2946	The histone H3 lysine-27 demethylase Jmjd3 plays a critical role in specific regulation of Th17 cell differentiation. Journal of Molecular Cell Biology, 2015, 7, 505-516.	1.5	90
2947	DOT1L inhibits SIRT1-mediated epigenetic silencing to maintain leukemic gene expression in MLL-rearranged leukemia. Nature Medicine, 2015, 21, 335-343.	15.2	200
2948	Mass Spectrometric Quantification of Histone Post-translational Modifications by a Hybrid Chemical Labeling Method. Molecular and Cellular Proteomics, 2015, 14, 1148-1158.	2.5	82
2949	Depletion of REF/Aly alters gene expression and reduces RNA polymerase II occupancy. Nucleic Acids Research, 2015, 43, 504-519.	6.5	30
2950	Long-lasting pro-inflammatory suppression of microglia by LPS-preconditioning is mediated by RelB-dependent epigenetic silencing. Brain, Behavior, and Immunity, 2015, 48, 205-221.	2.0	131
2951	Histone H2B monoubiquitination: roles to play in human malignancy. Endocrine-Related Cancer, 2015, 22, T19-T33.	1.6	108
2952	Histone Methyltransferase Setd8 Represses Gata2 Expression and Regulates Erythroid Maturation. Molecular and Cellular Biology, 2015, 35, 2059-2072.	1.1	21
2953	Polycomb Repressive Complex 2 Confers BRG1 Dependency on the <i>CIITA</i> Locus. Journal of Immunology, 2015, 194, 5007-5013.	0.4	17
2954	Comprehensive discovery of DNA motifs in 349 human cells and tissues reveals new features of motifs. Nucleic Acids Research, 2015, 43, 74-83.	6.5	13
2955	The autism-associated chromatin modifier CHD8 regulates other autism risk genes during human neurodevelopment. Nature Communications, 2015, 6, 6404.	5.8	316
2956	Heregulin Co-opts PR Transcriptional Action Via Stat3 Role As a Coregulator to Drive Cancer Growth. Molecular Endocrinology, 2015, 29, 1468-1485.	3.7	12
2957	Stress-activated Dendritic Cells (DC) Induce Dual Interleukin (IL)-15- and IL1β-mediated Pathways, Which May Elicit CD4+ Memory T Cells and Interferon (IFN)-stimulated Genes. Journal of Biological Chemistry, 2015, 290, 15595-15609.	1.6	11
2958	Epigenetics in the Vascular Endothelium. Arteriosclerosis, Thrombosis, and Vascular Biology, 2015, 35, 2297-2306.	1.1	48
2959	A Stochastic Segmentation Model for the Indentification of Histone Modification and DNase I Hypersensitive Sites in Chromatin. ICSA Book Series in Statistics, 2015, , 469-493.	0.0	0
2960	Different distribution of histone modifications in genes with unidirectional and bidirectional transcription and a role of CTCF and cohesin in directing transcription. BMC Genomics, 2015, 16, 300.	1.2	25
2961	Is this the right normalization? A diagnostic tool for ChIP-seq normalization. BMC Bioinformatics, 2015, 16, 150.	1.2	10
2962	hVGAT-mCherry: A novel molecular tool for analysis of GABAergic neurons derived from human pluripotent stem cells. Molecular and Cellular Neurosciences, 2015, 68, 244-257.	1.0	22

#	Article	IF	CITATIONS
2963	Long-Range Transcriptional Control of the <i>ll2</i> Gene by an Intergenic Enhancer. Molecular and Cellular Biology, 2015, 35, 3880-3891.	1.1	13
2964	The oncogenic role of GASC1 in chemically induced mouse skin cancer. Mammalian Genome, 2015, 26, 591-597.	1.0	10
2965	Chromatin Interactions in the Control of Immunoglobulin Heavy Chain Gene Assembly. Advances in Immunology, 2015, 128, 41-92.	1.1	35
2966	Development of novel cellular histone-binding and chromatin-displacement assays for bromodomain drug discovery. Epigenetics and Chromatin, 2015, 8, 37.	1.8	32
2967	Exposure to coplanar PCBs induces endothelial cell inflammation through epigenetic regulation of NF-κB subunit p65. Toxicology and Applied Pharmacology, 2015, 289, 457-465.	1.3	51
2968	Targeting epigenetic regulations in cancer. Acta Biochimica Et Biophysica Sinica, 2016, 48, 97-109.	0.9	60
2969	Stepping inside the realm of epigenetic modifiers. Biomolecular Concepts, 2015, 6, 119-136.	1.0	10
2970	BioWardrobe: an integrated platform for analysis of epigenomics and transcriptomics data. Genome Biology, 2015, 16, 158.	3.8	74
2971	The impact of read length on quantification of differentially expressed genes and splice junction detection. Genome Biology, 2015, 16, 131.	3.8	98
2972	An Overview of Genome Organization and How We Got There: from FISH to Hi-C. Microbiology and Molecular Biology Reviews, 2015, 79, 347-372.	2.9	190
2973	Silver nanoparticle-induced hemoglobin decrease involves alteration of histone 3 methylation status. Biomaterials, 2015, 70, 12-22.	5.7	87
2974	Making the case for chromatin profiling: a new tool to investigate the immune-regulatory landscape. Nature Reviews Immunology, 2015, 15, 585-594.	10.6	32
2975	Epigenetic mechanisms and boundaries in the regulation of mammalian Hox clusters. Mechanisms of Development, 2015, 138, 160-169.	1.7	9
2976	Identification of chromatin marks at TERRA promoter and encoding region. Biochemical and Biophysical Research Communications, 2015, 467, 1052-1057.	1.0	17
2977	CTCF Recruits Centromeric Protein CENP-E to the Pericentromeric/Centromeric Regions of Chromosomes through Unusual CTCF-Binding Sites. Cell Reports, 2015, 12, 1704-1714.	2.9	25
2978	H3K23me2 is a new heterochromatic mark in <i>Caenorhabditis elegans</i> . Nucleic Acids Research, 2015, 43, gkv1063.	6.5	37
2979	Genome-wide mapping of histone H3 lysine 4 trimethylation in Eucalyptus grandis developing xylem. BMC Plant Biology, 2015, 15, 117.	1.6	26
2980	Chromatin states and nuclear organization in development — a view from the nuclear lamina. Genome Biology, 2015, 16, 174.	3.8	67

#	Article	IF	CITATIONS
2981	Dynamic enhancer–gene body contacts during transcription elongation. Genes and Development, 2015, 29, 1992-1997.	2.7	72
2982	Histone ubiquitylation and its roles in transcription and DNA damage response. DNA Repair, 2015, 36, 36-42.	1.3	60
2983	p75NTR-dependent activation of NF-κB regulates microRNA-503 transcription and pericyte–endothelial crosstalk in diabetes after limb ischaemia. Nature Communications, 2015, 6, 8024.	5.8	119
2984	Highâ€wire act: the poised genome and cellular memory. FEBS Journal, 2015, 282, 1675-1691.	2.2	19
2986	Mapping of histone modifications in episomal HBV cccDNA uncovers an unusual chromatin organization amenable to epigenetic manipulation. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E5715-24.	3.3	191
2987	Nucleosome compaction facilitates HP1 \hat{I}^3 binding to methylated H3K9. Nucleic Acids Research, 2015, 43, gkv841.	6.5	30
2988	Spatial Interplay between Polycomb and Trithorax Complexes Controls Transcriptional Activity in T Lymphocytes. Molecular and Cellular Biology, 2015, 35, 3841-3853.	1.1	18
2989	Nucleosome competition reveals processive acetylation by the SAGA HAT module. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E5461-70.	3.3	55
2990	Interaction of the Jhd2 Histone H3 Lys-4 Demethylase with Chromatin Is Controlled by Histone H2A Surfaces and Restricted by H2B Ubiquitination. Journal of Biological Chemistry, 2015, 290, 28760-28777.	1.6	10
2991	Cell-specific gene promoters are marked by broader spans of H3K4me3 and are associated with robust gene expression patterns. Epigenomics, 2015, 7, 129-131.	1.0	4
2992	The Application of Next Generation Sequencing Techniques to Plant Epigenomics. , 2015, , 13-31.		0
2994	Systematic chromatin state comparison of epigenomes associated with diverse properties including sex and tissue type. Nature Communications, 2015, 6, 7973.	5.8	57
2995	Broad H3K4me3 is associated with increased transcription elongation and enhancer activity at tumor-suppressor genes. Nature Genetics, 2015, 47, 1149-1157.	9.4	276
2996	Exploiting genomics and natural genetic variation to decode macrophage enhancers. Trends in Immunology, 2015, 36, 507-518.	2.9	32
2997	Thyroid hormone signaling controls hair follicle stem cell function. Molecular Biology of the Cell, 2015, 26, 1263-1272.	0.9	36
2998	Identify Critical Genes in Development with Consistent H3K4me2 Patterns across Multiple Tissues. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 1104-1111.	1.9	1
2999	Transcription Factor Repertoire of Homeostatic Eosinophilopoiesis. Journal of Immunology, 2015, 195, 2683-2695.	0.4	43
3000	Super-enhancers: Asset management in immune cell genomes. Trends in Immunology, 2015, 36, 519-526.	2.9	36

#	Article	IF	CITATIONS
3001	Absence of canonical marks of active chromatin in developmentally regulated genes. Nature Genetics, 2015, 47, 1158-1167.	9.4	75
3002	Transcriptional Regulation of the Pancreatic Islet: Implications for Islet Function. Current Diabetes Reports, 2015, 15, 66.	1.7	11
3003	Chromatin perturbations during the DNA damage response in higher eukaryotes. DNA Repair, 2015, 36, 8-12.	1.3	51
3004	Development and Use of Assay Conditions Suited to Screening for and Profiling of SET-Domain-Targeted Inhibitors of the MLL/SET1 Family of Lysine Methyltransferases. Assay and Drug Development Technologies, 2015, 13, 221-234.	0.6	7
3005	ChIP-Seq to Analyze the Binding of Replication Proteins to Chromatin. Methods in Molecular Biology, 2015, 1300, 155-168.	0.4	13
3006	Comparative Analysis of Gene Regulatory Networks: From Network Reconstruction to Evolution. Annual Review of Cell and Developmental Biology, 2015, 31, 399-428.	4.0	170
3007	Lineage relationship of CD8+ T cell subsets is revealed by progressive changes in the epigenetic landscape. Cellular and Molecular Immunology, 0, , .	4.8	7
3008	Histone H3 Lysine 27 demethylases Jmjd3 and Utx are required for T-cell differentiation. Nature Communications, 2015, 6, 8152.	5.8	105
3009	Comparative analyses of CTCF and BORIS occupancies uncover two distinct classes of CTCF binding genomic regions. Genome Biology, 2015, 16, 161.	3.8	83
3010	The histone variant H2A.Z is an important regulator of enhancer activity. Nucleic Acids Research, 2015, 43, gkv825.	6.5	80
3011	Epigenetic gene regulation and stem cell function. , 2015, , 149-181.		0
3012	Identification of intergenic long noncoding RNA by deep sequencing. , 2015, , 223-235.		0
3013	Genetically altered cancer epigenome. , 2015, , 265-289.		1
3014	A novel apoptosis-inducing mechanism of 5-aza-2′-deoxycitidine in melanoma cells: Demethylation of TNF-α and activation of FOXO1. Cancer Letters, 2015, 369, 344-353.	3.2	13
3015	H3K4/H3K9me3 Bivalent Chromatin Domains Targeted by Lineage-Specific DNA Methylation Pauses Adipocyte Differentiation. Molecular Cell, 2015, 60, 584-596.	4.5	180
3016	Inferring Selective Constraint from Population Genomic Data Suggests Recent Regulatory Turnover in the Human Brain. Genome Biology and Evolution, 2015, 7, 3511-3528.	1.1	25
3017	Extranucleosomal DNA enhances the activity of the LSD1/CoREST histone demethylase complex. Nucleic Acids Research, 2015, 43, 4868-4880.	6.5	35
3018	Perinuclear Anchoring of H3K9-Methylated Chromatin Stabilizes Induced Cell Fate in C.Âelegans Embryos. Cell, 2015, 163, 1333-1347.	13.5	169

#	Article	IF	CITATIONS
3019	Affinity reagents for studying histone modifications & guidelines for their quality control. Epigenomics, 2015, 7, 1185-1196.	1.0	12
3020	Aberrant intracellular localization of H3k4me3 demonstrates anÂearly epigenetic phenomenon in Alzheimer's disease. Neurobiology of Aging, 2015, 36, 3121-3129.	1.5	54
3021	Genomic Analysis Through High-Throughput Sequencing. , 2015, , 297-311.		0
3022	Serine/arginine-rich splicing factor 3 (SRSF3) regulates homologous recombination-mediated DNA repair. Molecular Cancer, 2015, 14, 158.	7.9	40
3023	Functional Crosstalk Between Lysine Methyltransferases on Histone Substrates: The Case of G9A/GLP and Polycomb Repressive Complex 2. Antioxidants and Redox Signaling, 2015, 22, 1365-1381.	2.5	26
3024	Age-dependent clinical prognostic value of histone modifications in colorectal cancer. Translational Research, 2015, 165, 578-588.	2.2	12
3025	KDM4 histone demethylase inhibitors for anti-cancer agents: a patent review. Expert Opinion on Therapeutic Patents, 2015, 25, 135-144.	2.4	28
3026	Promoter or enhancer, what's the difference? Deconstruction of established distinctions and presentation of a unifying model. BioEssays, 2015, 37, 314-323.	1.2	92
3027	ATRX promotes gene expression by facilitating transcriptional elongation through guanine-rich coding regions. Human Molecular Genetics, 2015, 24, 1824-1835.	1.4	71
3028	Differential IncRNA expression profiles in brown and white adipose tissues. Molecular Genetics and Genomics, 2015, 290, 699-707.	1.0	31
3029	Non-histone protein methylation as a regulator of cellular signalling and function. Nature Reviews Molecular Cell Biology, 2015, 16, 5-17.	16.1	403
3030	A Stationary Wavelet Entropy-Based Clustering Approach Accurately Predicts Gene Expression. Journal of Computational Biology, 2015, 22, 236-249.	0.8	7
3031	Regulation of Pancreatic Islet Formation. , 2015, , 109-128.		3
3032	Mapping active promoters by Ch <scp>IP</scp> â€seq profiling of H3K4me3 in cichlid fish – a first step to uncover cisâ€regulatory elements in ecological model teleosts. Molecular Ecology Resources, 2015, 15, 761-771.	2.2	22
3033	Reversible Inhibitors of LSD1 as Therapeutic Agents in Acute Myeloid Leukemia: Clinical Significance and Progress to Date. Medicinal Research Reviews, 2015, 35, 586-618.	5.0	120
3034	A stress-induced early innate response causes multidrug tolerance in melanoma. Oncogene, 2015, 34, 4448-4459.	2.6	125
3035	Histone Methyltransferase hSETD1A Is a Novel Regulator of Metastasis in Breast Cancer. Molecular Cancer Research, 2015, 13, 461-469.	1.5	53
3036	O-GlcNAc signaling in cancer metabolism and epigenetics. Cancer Letters, 2015, 356, 244-250.	3.2	122

			-
#	Article	IF	CITATIONS
3037	Early-Life Experience, Epigenetics, and the Developing Brain. Neuropsychopharmacology, 2015, 40, 141-153.	2.8	232
3038	Prostate cancer epigenetic biomarkers: next-generation technologies. Oncogene, 2015, 34, 1609-1618.	2.6	44
3039	Molecular dynamics for computational proteomics of methylated histone H3. Biochimica Et Biophysica Acta - General Subjects, 2015, 1850, 1026-1040.	1.1	6
3040	Signaling Pathways and Epigenetic Regulations in the Control of <i>RORγt</i> Expression in T Helper 17 Cells. International Reviews of Immunology, 2015, 34, 305-317.	1.5	2
3041	Parasite Genomics Protocols. Methods in Molecular Biology, 2015, 1201, v-vi.	0.4	2
3042	Ash2L enables P53-dependent apoptosis by favoring stable transcription pre-initiation complex formation on its pro-apoptotic target promoters. Oncogene, 2015, 34, 2461-2470.	2.6	22
3043	Histones: At the Crossroads of Peptide and Protein Chemistry. Chemical Reviews, 2015, 115, 2296-2349.	23.0	188
3044	Single molecule and single cell epigenomics. Methods, 2015, 72, 41-50.	1.9	35
3045	Epigenetic approaches to regeneration of bone and cartilage from stem cells. Expert Opinion on Biological Therapy, 2015, 15, 181-193.	1.4	15
3046	Targeting the histone orthography of cancer: drugs for writers, erasers and readers. British Journal of Pharmacology, 2015, 172, 2716-2732.	2.7	95
3047	Comparative analysis of methods for genome-wide nucleosome cartography. Briefings in Bioinformatics, 2015, 16, 576-587.	3.2	26
3048	Predictive modelling of gene expression from transcriptional regulatory elements. Briefings in Bioinformatics, 2015, 16, 616-628.	3.2	33
3049	Protein arginine methyltransferases (PRMTs): Role in chromatin organization. Advances in Biological Regulation, 2015, 57, 173-184.	1.4	67
3050	<scp>EZH</scp> 2: an emerging role in melanoma biology and strategies for targeted therapy. Pigment Cell and Melanoma Research, 2015, 28, 21-30.	1.5	47
3051	Genome-wide profiling of the cardiac transcriptome after myocardial infarction identifies novel heart-specific long non-coding RNAs. European Heart Journal, 2015, 36, 353-368.	1.0	244
3054	DNA Methylation Biomarkers in Lung Cancer. , 2016, , 259-273.		1
3055	The Histone Code and Disease. , 2016, , 417-445.		1
3056	The transposable element environment of human genes is associated with histone and expression changes in cancer. BMC Genomics, 2016, 17, 588.	1.2	8

\sim			<u> </u>	
CIT.	ΔΤΙ	ON	REP	JBT
\sim			IVEL V	

#	Article	IF	CITATIONS
3057	Histone Posttranslational Modifications in Breast Cancer and Their Use in Clinical Diagnosis and Prognosis. , 2016, , 467-477.		0
3058	Epigenetic Alterations in Endocrine-Dependent Cancers: Implications of Endocrine Dysfunctions. , 2016, , 351-374.		0
3059	Histone Methylation Modifiers in Medical Therapeutics. , 2016, , 705-729.		1
3060	The Role of PHD Fingers in Chromatin Signaling. , 2016, , 127-147.		6
3061	Orchestrating epigenetic roles targeting ocular tumors. OncoTargets and Therapy, 2016, 9, 1001.	1.0	3
3062	Chromatin Dynamics and Epigenetics of Stem Cells and Stem-Like Cancer Cells. , 2016, , 311-327.		0
3063	Identification of Nedd9 as a TGF-β-Smad2/3 Target Gene Involved in RANKL-Induced Osteoclastogenesis by Comprehensive Analysis. PLoS ONE, 2016, 11, e0157992.	1.1	11
3064	PeakXus: comprehensive transcription factor binding site discovery from ChIP-Nexus and ChIP-Exo experiments. Bioinformatics, 2016, 32, i629-i638.	1.8	10
3065	Epigenetic Regulations of GABAergic Neurotransmission: Relevance for Neurological Disorders and Epigenetic Therapy. Medical Epigenetics, 2016, 4, 1-19.	262.3	6,201
3066	EZH2 in normal hematopoiesis and hematological malignancies. Oncotarget, 2016, 7, 2284-2296.	0.8	77
3066 3067	EZH2 in normal hematopoiesis and hematological malignancies. Oncotarget, 2016, 7, 2284-2296. Chromatin Signaling in Aging and Cellular Senescence. , 2016, , 287-309.	0.8	77
		0.8	
3067	Chromatin Signaling in Aging and Cellular Senescence. , 2016, , 287-309. Effects of Wutou Decoction on DNA Methylation and Histone Modifications in Rats with		0
3067 3068	Chromatin Signaling in Aging and Cellular Senescence. , 2016, , 287-309. Effects of Wutou Decoction on DNA Methylation and Histone Modifications in Rats with Collagen-Induced Arthritis. Evidence-based Complementary and Alternative Medicine, 2016, 2016, 1-9. Dynamic Changes in Occupancy of Histone Variant H2A.Z during Induced Somatic Cell Reprogramming.	0.5	0 8
3067 3068 3069	Chromatin Signaling in Aging and Cellular Senescence. , 2016, , 287-309. Effects of Wutou Decoction on DNA Methylation and Histone Modifications in Rats with Collagen-Induced Arthritis. Evidence-based Complementary and Alternative Medicine, 2016, 2016, 1-9. Dynamic Changes in Occupancy of Histone Variant H2A.Z during Induced Somatic Cell Reprogramming. Stem Cells International, 2016, 2016, 1-10.	0.5	0 8 5
3067 3068 3069 3070	Chromatin Signaling in Aging and Cellular Senescence. , 2016, , 287-309. Effects of Wutou Decoction on DNA Methylation and Histone Modifications in Rats with Collagen-Induced Arthritis. Evidence-based Complementary and Alternative Medicine, 2016, 2016, 1-9. Dynamic Changes in Occupancy of Histone Variant H2A.Z during Induced Somatic Cell Reprogramming. Stem Cells International, 2016, 2016, 1-10. Networks and Consortia for Epigenetic Drug Discovery. , 2016, , 143-166.	0.5	0 8 5 1
3067 3068 3069 3070 3071	Chromatin Signaling in Aging and Cellular Senescence. , 2016, , 287-309. Effects of Wutou Decoction on DNA Methylation and Histone Modifications in Rats with Collagen-Induced Arthritis. Evidence-based Complementary and Alternative Medicine, 2016, 2016, 1-9. Dynamic Changes in Occupancy of Histone Variant H2A.Z during Induced Somatic Cell Reprogramming. Stem Cells International, 2016, 2016, 1-10. Networks and Consortia for Epigenetic Drug Discovery. , 2016, , 143-166. Zebrafish offer aquaculture research their services. , 2016, , 165-194.	0.5	0 8 5 1 5

\sim	T A T I	ON	Repo	DT
			REDU	
	/		ILLI U	- C - L

#	Article	IF	CITATIONS
3075	Histone modifications facilitate the coexpression of bidirectional promoters in rice. BMC Genomics, 2016, 17, 768.	1.2	10
3076	Mapping H4K20me3 onto the chromatin landscape of senescent cells indicates a function in control of cell senescence and tumor suppression through preservation of genetic and epigenetic stability. Genome Biology, 2016, 17, 158.	3.8	65
3077	Temperature Shift Alters DNA Methylation and Histone Modification Patterns in Gonadal Aromatase (cyp19a1) Gene in Species with Temperature-Dependent Sex Determination. PLoS ONE, 2016, 11, e0167362.	1.1	48
3078	Linking Core Promoter Classes to Circadian Transcription. PLoS Genetics, 2016, 12, e1006231.	1.5	7
3079	The Arginine Methyltransferase PRMT6 Cooperates with Polycomb Proteins in Regulating HOXA Gene Expression. PLoS ONE, 2016, 11, e0148892.	1.1	21
3080	Towards a Safer, More Randomized Lentiviral Vector Integration Profile Exploring Artificial LEDGF Chimeras. PLoS ONE, 2016, 11, e0164167.	1.1	24
3081	The Evolution of New Technologies and Methods in Clinical Epigenetics Research. , 2016, , 67-89.		1
3082	Cancer Epigenetics. , 2016, , 41-59.		2
3083	Epigenetic regulation of long noncoding RNA UCA1 by SATB1 in breast cancer. BMB Reports, 2016, 49, 578-583.	1.1	39
3084	Impacts of Histone Lysine Methylation onÂChromatin. , 2016, , 25-53.		0
3085	Methylome Analysis of Complex Diseases. , 2016, , 441-456.		0
3086	Epigenetic determinants of cardiovascular gene expression: vascular endothelium. Epigenomics, 2016, 8, 959-979.	1.0	13
3087	<scp>CRISPR</scp> /Cas9 genome editing throws descriptive 3â€D genome folding studies for a loop. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2016, 8, 286-299.	6.6	3
3088	Discovery of novel small molecule inhibitors of lysine methyltransferase G9a and their mechanism in leukemia cell lines. European Journal of Medicinal Chemistry, 2016, 122, 382-393.	2.6	37
3089	Every transcription factor deserves its map: Scaling up epitope tagging of proteins to bypass antibody problems. BioEssays, 2016, 38, 801-811.	1.2	13
3090	Nuclear Factor κB1/RelA Mediates Inflammation in Human Lung Epithelial Cells at Atmospheric Oxygen Levels. Journal of Cellular Physiology, 2016, 231, 1611-1620.	2.0	9
3091	Roles for the Histone Modifying and Exchange Complex NuA4 in Cell Cycle Progression in <i>Drosophila melanogaster</i> . Genetics, 2016, 203, 1265-1281.	1.2	18
3092	Divergent transcription and epigenetic directionality of human promoters. FEBS Journal, 2016, 283, 4214-4222.	2.2	22

#	Article	IF	CITATIONS
3093	Ensembl regulation resources. Database: the Journal of Biological Databases and Curation, 2016, 2016, bav119.	1.4	45
3094	Epigenetic Mechanisms Regulating the Transition from Embryonic Stem Cells Towards a Differentiated Neural Progeny. , 2016, , 151-173.		0
3095	Genetic variants in <scp><i>ABCG</i></scp> <i>1</i> are associated with survival of nonsmall ell lung cancer patients. International Journal of Cancer, 2016, 138, 2592-2601.	2.3	41
3096	GnRH agonist with low-dose hCG (dual trigger) is associated with higher risk of severe ovarian hyperstimulation syndrome compared to GnRH agonist alone. Journal of Assisted Reproduction and Genetics, 2016, 33, 1175-1184.	1.2	35
3097	Dynamic Histone Acetylation of H3K4me3 Nucleosome Regulates <i>MCL1</i> Preâ€mRNA Splicing. Journal of Cellular Physiology, 2016, 231, 2196-2204.	2.0	13
3098	Reusable, extensible, and modifiable R scripts and Kepler workflows for comprehensive single set ChIP-seq analysis. BMC Bioinformatics, 2016, 17, 270.	1.2	4
3099	Genome-Wide Identification of Regulatory Sequences Undergoing Accelerated Evolution in the Human Genome. Molecular Biology and Evolution, 2016, 33, 2565-2575.	3.5	64
3100	Global intron retention mediated gene regulation during CD4 ⁺ T cell activation. Nucleic Acids Research, 2016, 44, 6817-6829.	6.5	96
3101	Nuclear PKC-Î, facilitates rapid transcriptional responses in human memory CD4+ T cells <i>via</i> p65 and H2B phosphorylation. Journal of Cell Science, 2016, 129, 2448-61.	1.2	11
3102	Continual removal of H3K9 promoter methylation by Jmjd2 demethylases is vital for <scp>ESC</scp> selfâ€ r enewal and early development. EMBO Journal, 2016, 35, 1550-1564.	3.5	84
3103	Tension-Dependent Free Energies of Nucleosome Unwrapping. ACS Central Science, 2016, 2, 660-666.	5.3	67
3104	PEDLA: predicting enhancers with a deep learning-based algorithmic framework. Scientific Reports, 2016, 6, 28517.	1.6	88
3105	Protein kinase Msk1 physically and functionally interacts with the KMT2A/MLL1 methyltransferase complex and contributes to the regulation of multiple target genes. Epigenetics and Chromatin, 2016, 9, 52.	1.8	26
3106	Modulation of mRNA and IncRNA expression dynamics by the Set2–Rpd3S pathway. Nature Communications, 2016, 7, 13534.	5.8	93
3107	Deconvolution of Ensemble Chromatin Interaction Data Reveals the Latent Mixing Structures in Cell Subpopulations. Journal of Computational Biology, 2016, 23, 425-438.	0.8	17
3108	Dynamic epigenetic mode analysis using spatial temporal clustering. BMC Bioinformatics, 2016, 17, 537.	1.2	4
3109	Capture reveals preformed chromatin interactions between <scp>HIF</scp> â€binding sites and distant promoters. EMBO Reports, 2016, 17, 1410-1421.	2.0	63
3110	CloudControl. , 2016, , .		4

#	Article	IF	CITATIONS
3111	Histones and histone modifications in perinuclear chromatin anchoring: from yeast to man. EMBO Reports, 2016, 17, 139-155.	2.0	128
3112	CAME: identification of chromatin accessibility from nucleosome occupancy and methylome sequencing. Bioinformatics, 2017, 33, 1139-1146.	1.8	4
3113	Negative reciprocal regulation between Sirt1 and Per2 modulates the circadian clock and aging. Scientific Reports, 2016, 6, 28633.	1.6	80
3114	Genome-wide epigenomic profiling for biomarker discovery. Clinical Epigenetics, 2016, 8, 122.	1.8	67
3115	Evaluation of Possible Proximate Mechanisms Underlying the Kinship Theory of Intragenomic Conflict in Social Insects. Integrative and Comparative Biology, 2016, 56, 1206-1214.	0.9	7
3116	NF-E2, FLI1 and RUNX1 collaborate at areas of dynamic chromatin to activate transcription in mature mouse megakaryocytes. Scientific Reports, 2016, 6, 30255.	1.6	26
3117	The sub-nucleolar localization of PHF6 defines its role in rDNA transcription and early processing events. European Journal of Human Genetics, 2016, 24, 1453-1459.	1.4	21
3118	MatP regulates the coordinated action of topoisomerase IV and MukBEF in chromosome segregation. Nature Communications, 2016, 7, 10466.	5.8	114
3119	Epigenetic Changes During Food-Specific Immunotherapy. Current Allergy and Asthma Reports, 2016, 16, 87.	2.4	10
3120	Minireview: Therapeutic Implications of Epigenetic Signaling in Breast Cancer. Endocrinology, 2017, 158, en.2016-1716.	1.4	8
3121	Hypoxia increases genome-wide bivalent epigenetic marking by specific gain of H3K27me3. Epigenetics and Chromatin, 2016, 9, 46.	1.8	63
3122	SUV4-20 activity in the preimplantation mouse embryo controls timely replication. Genes and Development, 2016, 30, 2513-2526.	2.7	26
3123	Involvement of PARP1 in the regulation of alternative splicing. Cell Discovery, 2016, 2, 15046.	3.1	63
3125	Computational Prediction of the Global Functional Genomic Landscape: Applications, Methods, and Challenges. Human Heredity, 2016, 81, 88-105.	0.4	3
3126	A deformation energy-based model for predicting nucleosome dyads and occupancy. Scientific Reports, 2016, 6, 24133.	1.6	14
3127	In vitro effects of the small-molecule protein kinase C agonists on HIV latency reactivation. Scientific Reports, 2016, 6, 39032.	1.6	27
3128	Chromatin remodeling effects on enhancer activity. Cellular and Molecular Life Sciences, 2016, 73, 2897-2910.	2.4	25
3130	Clinical Epigenetics and Epigenomics. Translational Bioinformatics, 2016, , 269-293.	0.0	0

#	Article	IF	CITATIONS
3131	Regulation of expression of venom toxins: silencing of prothrombin activator trocarin D by AGâ€rich motifs. FASEB Journal, 2016, 30, 2411-2425.	0.2	9
3132	Transcriptomic and epigenomic characterization of the developing bat wing. Nature Genetics, 2016, 48, 528-536.	9.4	64
3133	The epigenetic regulation of embryonic myogenesis and adult muscle regeneration by histone methylation modification. Biochemistry and Biophysics Reports, 2016, 6, 209-219.	0.7	43
3134	Biological function and regulation of histone and non-histone lysine methylation in response to DNA damage. Acta Biochimica Et Biophysica Sinica, 2016, 48, 603-616.	0.9	40
3135	Reprogramming of the Epigenome by MLL1 Links Early-Life Environmental Exposures to Prostate Cancer Risk. Molecular Endocrinology, 2016, 30, 856-871.	3.7	68
3136	Epithelial-mesenchymal transition and FOXA genes during tobacco smoke carcinogen induced transformation of human bronchial epithelial cells. Toxicology in Vitro, 2016, 35, 55-65.	1.1	25
3137	Inhibitors of enzymes catalyzing modifications to histone lysine residues: structure, function and activity. Future Medicinal Chemistry, 2016, 8, 879-897.	1.1	13
3138	Acquired Tissue-Specific Promoter Bivalency Is a Basis for PRC2 Necessity in Adult Cells. Cell, 2016, 165, 1389-1400.	13.5	101
3139	Don't worry; be informed about the epigenetics of anxiety. Pharmacology Biochemistry and Behavior, 2016, 146-147, 60-72.	1.3	32
3140	Epigenetic Advancements in Cancer. , 2016, , .		1
3141	RNA Polymerase II Regulates Topoisomerase 1 Activity to Favor Efficient Transcription. Cell, 2016, 165, 357-371.	13.5	211
3142	Combinations of Histone Modifications for Pattern Genes. Acta Biotheoretica, 2016, 64, 121-132.	0.7	2
3143	Proteomic profiling of nuclear fractions from native renal inner medullary collecting duct cells. Physiological Genomics, 2016, 48, 154-166.	1.0	13
3144	Dynamic Long-Range Chromatin Interaction Controls Expression of IL-21 in CD4+ T Cells. Journal of Immunology, 2016, 196, 4378-4389.	0.4	26
3145	Histone epigenetic marks in heterochromatin and euchromatin of the Chagas' disease vector, Triatoma infestans. Acta Histochemica, 2016, 118, 401-412.	0.9	10
3146	The Determinants of Directionality in Transcriptional Initiation. Trends in Genetics, 2016, 32, 322-333.	2.9	31
3147	FOXA1 defines cancer cell specificity. Science Advances, 2016, 2, e1501473.	4.7	41
3148	H2A.Z acetylation and transcription: ready, steady, go!. Epigenomics, 2016, 8, 583-586.	1.0	11

		CITATION R	EPORT	
#	Article		IF	Citations
3149	Evolution of Epigenetic Regulation in Vertebrate Genomes. Trends in Genetics, 2016, 3	2, 269-283.	2.9	86
3150	<i>De novo</i> deciphering three-dimensional chromatin interaction and topological d wavelet transformation of epigenetic profiles. Nucleic Acids Research, 2016, 44, e106-		6.5	33
3151	Bivalent Regions of Cytosine Methylation and H3K27 Acetylation Suggest an Active Ro Methylation at Enhancers. Molecular Cell, 2016, 62, 422-431.	ole for DNA	4.5	106
3152	CREB engages C/EBPδto initiate leukemogenesis. Leukemia, 2016, 30, 1887-1896.		3.3	28
3153	Role of Chromatin Structural Changes in Regulating Human CYP3A Ontogeny. Drug M Disposition, 2016, 44, 1027-1037.	etabolism and	1.7	5
3154	Regenerative Medicine - from Protocol to Patient. , 2016, , .			2
3155	Chromatin immunoprecipitation from fixed clinical tissues reveals tumor-specific enhar Nature Medicine, 2016, 22, 685-691.	ncer profiles.	15.2	64
3156	†Traffic light rules': Chromatin states direct miRNA-mediated network motifs run epigenome and regulatome. Biochimica Et Biophysica Acta - General Subjects, 2016, 18		1.1	9
3157	Molecular Architecture of the Circadian Clock in Mammals. Research and Perspectives Interactions, 2016, , 13-24.	in Endocrine	0.2	48
3158	Nongenomic regulation of gene expression. Current Opinion in Pediatrics, 2016, 28, 52	21-528.	1.0	2
3159	Setd1a and NURF mediate chromatin dynamics and gene regulation during erythroid li commitment and differentiation. Nucleic Acids Research, 2016, 44, gkw327.	neage	6.5	39
3160	Promoter H3K4 methylation dynamically reinforces activation-induced pathways in hur Genes and Immunity, 2016, 17, 283-297.	nan CD4 T cells.	2.2	30
3161	Genetically Encoded Voltage Indicators. , 2016, , 252-269.			2
3162	Targeting histone methyltransferases and demethylases in clinical trials for cancer ther Epigenetics, 2016, 8, 57.	apy. Clinical	1.8	333
3163	Impaired removal of H3K4 methylation affects cell fate determination and gene transcr Development (Cambridge), 2016, 143, 3751-3762.	ription.	1.2	15
3164	Epigenetic regulation of alternative promoters and enhancers in progenitor, immature, gonadotrope cell lines. Molecular and Cellular Endocrinology, 2016, 434, 250-265.	and mature	1.6	19
3165	Lineage relationship of CD8+ T cell subsets is revealed by progressive changes in the ep landscape. Cellular and Molecular Immunology, 2016, 13, 502-513.	pigenetic	4.8	99
3166	Regulation of gene expression in human cancers by TRIM24. Drug Discovery Today: Teo 19, 57-63.	chnologies, 2016,	4.0	36

		CITATION REPORT		
#	Article		IF	CITATIONS
3167	Synthesis and Assays of Inhibitors of Methyltransferases. Methods in Enzymology, 201	.6, 574, 245-308.	0.4	21
3168	Environmental contaminants and microRNA regulation: Transcription factors as regular toxicant-altered microRNA expression. Toxicology and Applied Pharmacology, 2016, 31	tors of 12, 61-66.	1.3	21
3169	Targeted next generation sequencing of a panel of autism-related genes identifies an E in a Kleefstra syndrome patient with autism and normal intellectual performance. Gene 131-141.		1.0	25
3170	Dysregulation of histone methyltransferases in breast cancer – Opportunities for ner therapies?. Molecular Oncology, 2016, 10, 1497-1515.	w targeted	2.1	56
3171	Maps of context-dependent putative regulatory regions and genomic signal interaction Acids Research, 2016, 44, gkw800.	ns. Nucleic	6.5	10
3173	Reversible Regulation of Promoter and Enhancer Histone Landscape by DNA Methylatic Embryonic Stem Cells. Cell Reports, 2016, 17, 289-302.	on in Mouse	2.9	92
3174	MIST1 and PTF1 Collaborate in Feed-Forward Regulatory Loops That Maintain the Panc Phenotype in Adult Mice. Molecular and Cellular Biology, 2016, 36, 2945-2955.	reatic Acinar	1.1	38
3175	The emerging role of lysine methyltransferase SETD8 in human diseases. Clinical Epiger 102.	netics, 2016, 8,	1.8	77
3176	Epigenetics and Cancer. Energy Balance and Cancer, 2016, , 1-28.		0.2	2
3177	Histone modification patterns in highly differentiation cells. Neurocomputing, 2016, 20	06, 42-49.	3.5	Ο
3178	Epigenetic regulation of active Chinese herbal components for cancer prevention and t follow-up review. Pharmacological Research, 2016, 114, 1-12.	treatment: A	3.1	43
3179	Exposure to the widely used herbicide atrazine results in deregulation of global tissues transcription in the third generation and is associated with a global decrease of histon trimethylation in mice. Nucleic Acids Research, 2016, 44, gkw840.		6.5	47
3180	A Survey of the Computational Methods for Enhancers and Enhancer-target Prediction	ıs. , 2016, , 3-27.		1
3181	Analysis RNA-seq and Noncoding RNA. Methods in Molecular Biology, 2016, 1480, 125	5-135.	0.4	21
3182	Toward development of epigenetic drugs for central nervous system disorders: Modula neuroplasticity <i>via</i> <scp>H3K4</scp> methylation. Psychiatry and Clinical Neuro 70, 536-550.		1.0	14
3183	ATP-binding cassette transmembrane transporters and their epigenetic control in canc Expert Opinion on Drug Metabolism and Toxicology, 2016, 12, 1419-1432.	er: an overview.	1.5	46
3184	Roles for <scp>SUMO</scp> in preâ€ <scp>mRNA</scp> processing. Wiley Interdiscipl 2016, 7, 105-112.	inary Reviews RNA,	3.2	13
3185	ZMYND8 Reads the Dual Histone Mark H3K4me1-H3K14ac to Antagonize the Expressi Metastasis-Linked Genes. Molecular Cell, 2016, 63, 470-484.	on of	4.5	112

#	Article	IF	CITATIONS
3186	One arbon metabolism and epigenetics: understanding the specificity. Annals of the New York Academy of Sciences, 2016, 1363, 91-98.	1.8	289
3187	Histone variants and melanoma: facts and hypotheses. Pigment Cell and Melanoma Research, 2016, 29, 426-433.	1.5	11
3188	Gene expression classification using epigenetic features and DNA sequence composition in the human embryonic stem cell line H1. Gene, 2016, 592, 227-234.	1.0	10
3189	Expression and regulation of human endogenous retrovirus W elements. Apmis, 2016, 124, 52-66.	0.9	47
3190	Nitric oxide, the new architect of epigenetic landscapes. Nitric Oxide - Biology and Chemistry, 2016, 59, 54-62.	1.2	48
3191	Vitamin D-dependent chromatin association of CTCF in human monocytes. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2016, 1859, 1380-1388.	0.9	37
3192	TBP loading by AF4 through SL1 is the major rate-limiting step in MLL fusion-dependent transcription. Cell Cycle, 2016, 15, 2712-2722.	1.3	21
3193	Next-Generation Sequencing Technologies and Plant Improvement. , 2016, , 271-294.		0
3194	Systems medicine in colorectal cancer: from a mathematical model toward a new type of clinical trial. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2016, 8, 314-336.	6.6	11
3195	Polycomb repressive complex 2 (PRC2) silences genes responsible for neurodegeneration. Nature Neuroscience, 2016, 19, 1321-1330.	7.1	178
3196	Genome-Wide Techniques for the Study of Clinical Epigenetic Biomarkers. , 2016, , 119-135.		0
3197	Chromatin Landscape and Epigenetic Signatures in Neurological Disorders. , 2016, , 519-537.		1
3198	Optimizing ChIP-seq peak detectors using visual labels and supervised machine learning. Bioinformatics, 2017, 33, 491-499.	1.8	28
3199	Epigenetic legacy of parental experiences: Dynamic and interactive pathways to inheritance. Development and Psychopathology, 2016, 28, 1219-1228.	1.4	77
3200	reChIP-seq reveals widespread bivalency of H3K4me3 and H3K27me3 in CD4+ memory T cells. Nature Communications, 2016, 7, 12514.	5.8	69
3201	Structural Insights into Substrate Recognition and Catalysis in Outer Membrane Protein B (OmpB) by Protein-lysine Methyltransferases from Rickettsia. Journal of Biological Chemistry, 2016, 291, 19962-19974.	1.6	18
3202	Rapid Conversion of Mutant IDH1 from Driver to Passenger in a Model of Human Gliomagenesis. Molecular Cancer Research, 2016, 14, 976-983.	1.5	84
3203	Comprehensive analysis of epigenetic pattern of long noncoding RNA loci in colorectal cancer. Gene, 2016, 595, 9-17.	1.0	4

#	Article	IF	CITATIONS
3204	Epigenetic Modifications in Neurological Diseases: Natural Products as Epigenetic Modulators a Treatment Strategy. Advances in Neurobiology, 2016, 12, 1-25.	1.3	10
3205	Allosteric control of mammalian DNA methyltransferases – a new regulatory paradigm. Nucleic Acids Research, 2016, 44, 8556-8575.	6.5	156
3206	Assay of LGI1 gene epigenetic alterations by posttranslational modifications of H3 histone in malignant gliomas. Cell and Tissue Biology, 2016, 10, 259-263.	0.2	0
3207	Epigenetics and approaches to targeted epigenetic therapy in acute myeloid leukemia. Blood, 2016, 127, 42-52.	0.6	234
3208	Polycomb-dependent epigenetic landscape in adult T-cell leukemia. Blood, 2016, 127, 1790-1802.	0.6	135
3209	Modeling <i>cis</i> -regulation with a compendium of genome-wide histone H3K27ac profiles. Genome Research, 2016, 26, 1417-1429.	2.4	75
3210	The Differentiation and Function of Th2 and Th9 Cells. , 2016, , 294-306.		0
3211	Regulatory Single-Nucleotide Variant Predictor Increases Predictive Performance of Functional Regulatory Variants. Human Mutation, 2016, 37, 1137-1143.	1.1	13
3212	Mutant <i>IDH</i> : a targetable driver of leukemic phenotypes linking metabolism, epigenetics and transcriptional regulation. Epigenomics, 2016, 8, 945-957.	1.0	21
3213	The Molecular Landscape of the Developing Human Central Nervous System. , 2016, , 203-220.		1
3214	Chromatin remodeling inactivates activity genes and regulates neural coding. Science, 2016, 353, 300-305.	6.0	96
3215	ChIP-Sequencing to Map the Epigenome of Senescent Cells Using Benzonase Endonuclease. Methods in Enzymology, 2016, 574, 355-364.	0.4	6
3216	The role of signal transducer and activator of transcription 3 in Rift Valley fever virus infection. Virology, 2016, 496, 175-185.	1.1	12
3217	Combinatorial epigenetic regulation of non-coding RNAs has profound effects on oncogenic pathways in breast cancer subtypes. Briefings in Bioinformatics, 2018, 19, bbw099.	3.2	15
3218	Mutant IDH1 Expression Drives <i>TERT</i> Promoter Reactivation as Part of the Cellular Transformation Process. Cancer Research, 2016, 76, 6680-6689.	0.4	55
3219	Navigating Transcriptional Coregulator Ensembles to Establish Genetic Networks. Current Topics in Developmental Biology, 2016, 118, 205-244.	1.0	19
3220	ATAC-see reveals the accessible genome by transposase-mediated imaging and sequencing. Nature Methods, 2016, 13, 1013-1020.	9.0	199
3221	SnapShot: Epigenomic Assays. Cell, 2016, 167, 1430-1430.e1.	13.5	2

#	Article	IF	CITATIONS
3222	Nucleosome Density ChIP-Seq Identifies Distinct Chromatin Modification Signatures Associated with MNase Accessibility. Cell Reports, 2016, 17, 2112-2124.	2.9	46
3223	Dynamically reorganized chromatin is the key for the reprogramming of somatic cells to pluripotent cells. Scientific Reports, 2016, 5, 17691.	1.6	20
3224	Yin–yang actions of histone methylation regulatory complexes in the brain. Epigenomics, 2016, 8, 1689-1708.	1.0	28
3225	Enhancers and their dynamics during hematopoietic differentiation and emerging strategies for therapeutic action. FEBS Letters, 2016, 590, 4084-4104.	1.3	7
3226	Current and Emerging Technologies for the Analysis of the Genome-Wide and Locus-Specific DNA Methylation Patterns. Advances in Experimental Medicine and Biology, 2016, 945, 343-430.	0.8	22
3227	Enzymology of Mammalian DNA Methyltransferases. Advances in Experimental Medicine and Biology, 2016, 945, 87-122.	0.8	49
3228	The Role of Epigenetic Mechanisms in the Regulation of Gene Expression in the Nervous System. Journal of Neuroscience, 2016, 36, 11427-11434.	1.7	109
3229	A comparative study of ChIP-seq sequencing library preparation methods. BMC Genomics, 2016, 17, 816.	1.2	25
3230	S-2-hydroxyglutarate regulates CD8+ T-lymphocyte fate. Nature, 2016, 540, 236-241.	13.7	306
3231	HIPSTR and thousands of IncRNAs are heterogeneously expressed in human embryos, primordial germ cells and stable cell lines. Scientific Reports, 2016, 6, 32753.	1.6	35
3232	Broad H3K4me3 as A Novel Epigenetic Signature for Normal Development and Disease. Genomics, Proteomics and Bioinformatics, 2016, 14, 262-264.	3.0	8
3233	Regulation of PCGEM1 by p54/nrb in prostate cancer. Scientific Reports, 2016, 6, 34529.	1.6	40
3234	Single Molecule Localization and Discrimination of DNA–Protein Complexes by Controlled Translocation Through Nanocapillaries. Nano Letters, 2016, 16, 7882-7890.	4.5	34
3235	Early programming of the oocyte epigenome temporally controls late prophase I transcription and chromatin remodelling. Nature Communications, 2016, 7, 12331.	5.8	61
3236	Histone modification signature at myeloperoxidase and proteinase 3 in patients with anti-neutrophil cytoplasmic autoantibody-associated vasculitis. Clinical Epigenetics, 2016, 8, 85.	1.8	24
3237	Counteracting H3K4 methylation modulators Set1 and Jhd2 co-regulate chromatin dynamics and gene transcription. Nature Communications, 2016, 7, 11949.	5.8	50
3238	An Emerging Regulatory Landscape for Skeletal Development. Trends in Genetics, 2016, 32, 774-787.	2.9	16
3239	Bayesian Graphical Models for Differential Pathways. Bayesian Analysis, 2016, 11, .	1.6	21

#	Article	IF	CITATIONS
3240	Integrating Epigenomics into the Understanding of Biomedical Insight. Bioinformatics and Biology Insights, 2016, 10, BBI.S38427.	1.0	22
3241	Investigation of Viral and Host Chromatin by ChIPâ€PCR or ChIPâ€Seq Analysis. Current Protocols in Microbiology, 2016, 40, 1E.10.1-1E.10.21.	6.5	9
3242	Histone Modifications in a Mouse Model of Early Adversities and Panic Disorder: Role for Asic1 and Neurodevelopmental Genes. Scientific Reports, 2016, 6, 25131.	1.6	33
3243	Neonatal monocytes exhibit a unique histone modification landscape. Clinical Epigenetics, 2016, 8, 99.	1.8	39
3244	Transcriptional, epigenetic and retroviral signatures identify regulatory regions involved in hematopoietic lineage commitment. Scientific Reports, 2016, 6, 24724.	1.6	18
3245	Enzymatic and chemical mapping of nucleosome distribution in purified micro- and macronuclei of the ciliated model organism, Tetrahymena thermophila. Science China Life Sciences, 2016, 59, 909-919.	2.3	27
3246	Molecular Mechanisms of Anesthetic Neurotoxicity: A Review of the Current Literature. Journal of Neurosurgical Anesthesiology, 2016, 28, 361-372.	0.6	30
3247	DGW: an exploratory data analysis tool for clustering and visualisation of epigenomic marks. BMC Bioinformatics, 2016, 17, 447.	1.2	3
3248	Genome-wide positioning of bivalent mononucleosomes. BMC Medical Genomics, 2016, 9, 60.	0.7	19
3249	DIVAN: accurate identification of non-coding disease-specific risk variants using multi-omics profiles. Genome Biology, 2016, 17, 252.	3.8	67
3250	Quantitative analysis of ChIP-seq data uncovers dynamic and sustained H3K4me3 and H3K27me3 modulation in cancer cells under hypoxia. Epigenetics and Chromatin, 2016, 9, 48.	1.8	23
3251	A maximum-likelihood approach for building cell-type trees by lifting. BMC Genomics, 2016, 17, 14.	1.2	6
3252	Mapping Protein–DNA Interactions Using ChIP-exo and Illumina-Based Sequencing. Methods in Molecular Biology, 2016, 1443, 119-137.	0.4	4
3253	Features that define the best ChIP-seq peak calling algorithms. Briefings in Bioinformatics, 2017, 18, bbw035.	3.2	96
3254	Recruitment of Rod Photoreceptors from Short-Wavelength-Sensitive Cones during the Evolution of Nocturnal Vision in Mammals. Developmental Cell, 2016, 37, 520-532.	3.1	103
3255	Chromatin Immunoprecipitation: Application to the Study of Asthma. Methods in Molecular Biology, 2016, 1434, 121-137.	0.4	2
3256	The molecular hallmarks of epigenetic control. Nature Reviews Genetics, 2016, 17, 487-500.	7.7	1,945
3257	Dynamic regulation of histone H3K9 is linked to the switch between replication and transcription at the Dbf4 origin-promoter locus. Cell Cycle, 2016, 15, 2321-2335.	1.3	5

# 3258	ARTICLE Decidualization and Epigenetic Regulation. , 2016, , 125-137.	IF	CITATIONS
3259	Epigenetics in ENS development and Hirschsprung disease. Developmental Biology, 2016, 417, 209-216.	0.9	36
3260	Hemoglobin genetics: recent contributions of GWAS and gene editing. Human Molecular Genetics, 2016, 25, R99-R105.	1.4	38
3261	Microglia development follows a stepwise program to regulate brain homeostasis. Science, 2016, 353, aad8670.	6.0	911
3262	Mechanism of chromatin segregation to the nuclear periphery in <i>C. elegans</i> embryos. Worm, 2016, 5, e1190900.	1.0	7
3263	An epigenetic mechanism mediates developmental nicotine effects on neuronal structure and behavior. Nature Neuroscience, 2016, 19, 905-914.	7.1	78
3264	Definition of mutations in polyautoimmunity. Journal of Autoimmunity, 2016, 72, 65-72.	3.0	19
3265	Differential patterns of histone methylase EHMT2 and its catalyzed histone modifications H3K9me1 and H3K9me2 during maturation of central auditory system. Cell and Tissue Research, 2016, 365, 247-264.	1.5	13
3266	Pbx1 is required for adult SVZ neurogenesis. Development (Cambridge), 2016, 143, 2281-91.	1.2	43
3267	Nerve Injury Diminishes Opioid Analgesia through Lysine Methyltransferase-mediated Transcriptional Repression of μ-Opioid Receptors in Primary Sensory Neurons. Journal of Biological Chemistry, 2016, 291, 8475-8485.	1.6	56
3268	Transcriptomic analysis of mouse EL4 T cells upon T cell activation and in response to protein synthesis inhibition via cycloheximide treatment. Genomics Data, 2016, 7, 148-151.	1.3	2
3269	The Nuclear Receptor Superfamily. Methods in Molecular Biology, 2016, , .	0.4	0
3270	Uterine Endometrial Function. , 2016, , .		2
3271	Cladribine, gemcitabine, busulfan, and SAHA combination as a potential pretransplant conditioning regimen for lymphomas: A preclinical study. Experimental Hematology, 2016, 44, 458-465.	0.2	7
3272	Discovery of Novel Dot1L Inhibitors through a Structure-Based Fragmentation Approach. ACS Medicinal Chemistry Letters, 2016, 7, 735-740.	1.3	53
3273	The dual specificity phosphatase 2 gene is hypermethylated in human cancer and regulated by epigenetic mechanisms. BMC Cancer, 2016, 16, 49.	1.1	19
3274	RISC-mediated control of selected chromatin regulators stabilizes ground state pluripotency of mouse embryonic stem cells. Genome Biology, 2016, 17, 94.	3.8	12
3275	Application of recombinant TAF3 PHD domain instead of anti-H3K4me3 antibody. Epigenetics and Chromatin, 2016, 9, 11.	1.8	18

#	Article	IF	CITATIONS
3276	H3K4 tri-methylation breadth at transcription start sites impacts the transcriptome of systemic lupus erythematosus. Clinical Epigenetics, 2016, 8, 14.	1.8	47
3277	Magnetofection based on superparamagnetic iron oxide nanoparticle-mediated low lncRNA HOTAIR expression decreases the proliferation and invasion of glioma stem cells. International Journal of Oncology, 2016, 49, 509-518.	1.4	56
3278	Molecular Genetics of Asthma. Methods in Molecular Biology, 2016, , .	0.4	0
3279	HDAC3 Is Required for the Downregulation of RORÎ ³ t during Thymocyte Positive Selection. Journal of Immunology, 2016, 197, 541-554.	0.4	29
3280	Epigenetics of Colorectal Cancer. , 2016, , 97-121.		1
3281	Genetic susceptibility to rheumatoid arthritis and its implications for novel drug discovery. Expert Opinion on Drug Discovery, 2016, 11, 805-813.	2.5	9
3282	Zerone: a ChIP-seq discretizer for multiple replicates with built-in quality control. Bioinformatics, 2016, 32, 2896-2902.	1.8	11
3283	Structure and function of histone methylation-binding proteins in plants. Biochemical Journal, 2016, 473, 1663-1680.	1.7	23
3284	Epigenetic regulation of <i>KLK7</i> gene expression in pancreatic and cervical cancer cells. Biological Chemistry, 2016, 397, 1135-1146.	1.2	13
3285	Changes in gene expression of histone modification enzymes in rat granulosa cells undergoing luteinization during ovulation. Journal of Ovarian Research, 2016, 9, 15.	1.3	16
3286	Next generation sequencing technology and genomewide data analysis: Perspectives for retinal research. Progress in Retinal and Eye Research, 2016, 55, 1-31.	7.3	58
3287	SET DOMAIN GROUP 708, a histone H3 lysine 36â€specific methyltransferase, controls flowering time in rice (Oryza sativa). New Phytologist, 2016, 210, 577-588.	3.5	49
3288	Influence of Arsenic on Global Levels of Histone Posttranslational Modifications: a Review of the Literature and Challenges in the Field. Current Environmental Health Reports, 2016, 3, 225-237.	3.2	51
3289	Differentially Isotopeâ€Labeled Nucleosomes To Study Asymmetric Histone Modification Crosstalk by Timeâ€Resolved NMR Spectroscopy. Angewandte Chemie, 2016, 128, 8402-8405.	1.6	2
3290	Differentially Isotope‣abeled Nucleosomes To Study Asymmetric Histone Modification Crosstalk by Timeâ€Resolved NMR Spectroscopy. Angewandte Chemie - International Edition, 2016, 55, 8262-8265.	7.2	25
3291	HMGNs: The enhancer charmers. BioEssays, 2016, 38, 226-231.	1.2	11
3292	DOT1L-mediated H3K79me2 modification critically regulates gene expression during cardiomyocyte differentiation. Cell Death and Differentiation, 2016, 23, 555-564.	5.0	57
3293	Herpesviral ICPO Protein Promotes Two Waves of Heterochromatin Removal on an Early Viral Promoter during Lytic Infection. MBio, 2016, 7, e02007-15.	1.8	61

#	Article	IF	CITATIONS
3294	The H3K4me3/2 histone demethylase RBR-2 controls axon guidance by repressing the actin-remodeling gene wsp-1. Development (Cambridge), 2016, 143, 851-63.	1.2	24
3295	Pleiotropic Functions of H3K27Me3 Demethylases in Immune Cell Differentiation. Trends in Immunology, 2016, 37, 102-113.	2.9	42
3296	Pharmacological Priming of Adipose-Derived Stem Cells Promotes Myocardial Repair. Journal of Investigative Medicine, 2016, 64, 50-62.	0.7	9
3297	Opposing Chromatin Signals Direct and Regulate the Activity of Lysine Demethylase 4C (KDM4C). Journal of Biological Chemistry, 2016, 291, 6060-6070.	1.6	28
3298	Genomic determinants of somatic copy number alterations across human cancers. Human Molecular Genetics, 2016, 25, 1019-1030.	1.4	10
3299	Role of Histone-Modifying Enzymes and Their Complexes in Regulation of Chromatin Biology. Biochemistry, 2016, 55, 1584-1599.	1.2	80
3300	Promoter architectures and developmental gene regulation. Seminars in Cell and Developmental Biology, 2016, 57, 11-23.	2.3	53
3301	Inhibition of the histone demethylase Kdm5b promotes neurogenesis and derepresses <i>Reln</i> (reelin) in neural stem cells from the adult subventricular zone of mice. Molecular Biology of the Cell, 2016, 27, 627-639.	0.9	20
3302	Blood-based biomarkers for diagnosis, prognosis and treatment of colorectal cancer. Clinica Chimica Acta, 2016, 455, 26-32.	0.5	59
3303	Genome-wide Profiling Reveals Remarkable Parallels Between Insertion Site Selection Properties of the MLV Retrovirus and the piggyBac Transposon in Primary Human CD4+ T Cells. Molecular Therapy, 2016, 24, 592-606.	3.7	122
3304	ΔNp63 regulates IL-33 and IL-31 signaling in atopic dermatitis. Cell Death and Differentiation, 2016, 23, 1073-1085.	5.0	38
3305	Molecular control of activation and priming in macrophages. Nature Immunology, 2016, 17, 26-33.	7.0	392
3306	Epigenetics mechanisms in renal development. Pediatric Nephrology, 2016, 31, 1055-1060.	0.9	19
3307	DNA methylation changes in plasticity genes accompany the formation and maintenance of memory. Nature Neuroscience, 2016, 19, 102-110.	7.1	307
3308	Non-coding RNAs in Mammary Gland Development and Disease. Advances in Experimental Medicine and Biology, 2016, 886, 121-153.	0.8	25
3309	Imprinting control regions (ICRs) are marked by mono-allelic bivalent chromatin when transcriptionally inactive. Nucleic Acids Research, 2016, 44, 621-635.	6.5	41
3310	SON and Its Alternatively Spliced Isoforms Control MLL Complex-Mediated H3K4me3 and Transcription of Leukemia-Associated Genes. Molecular Cell, 2016, 61, 859-873.	4.5	41
3311	Next generation transcriptomics and genomics elucidate biological complexity of microglia in health and disease. Clia, 2016, 64, 197-213.	2.5	112

#	Article	IF	CITATIONS
3312	Oxidative Stress Under Ambient and Physiological Oxygen Tension in Tissue Culture. Current Pharmacology Reports, 2016, 2, 64-72.	1.5	100
3313	Up-regulation of Histone Methyltransferase, DOT1L, by Matrix Hyaluronan Promotes MicroRNA-10 Expression Leading to Tumor Cell Invasion and Chemoresistance in Cancer Stem Cells from Head and Neck Squamous Cell Carcinoma. Journal of Biological Chemistry, 2016, 291, 10571-10585.	1.6	64
3314	A positive role for polycomb in transcriptional regulation via H4K20me1. Cell Research, 2016, 26, 529-542.	5.7	18
3315	Dysregulation of protein methyltransferases in human cancer: An emerging target class for anticancer therapy. Cancer Science, 2016, 107, 377-384.	1.7	67
3316	Decoding the non oding genome: elucidating genetic risk outside the coding genome. Genes, Brain and Behavior, 2016, 15, 187-204.	1.1	32
3317	Mutations in chromatin machinery and pediatric high-grade glioma. Science Advances, 2016, 2, e1501354.	4.7	69
3319	Clonal Dynamics In Vivo of Virus Integration Sites of T Cells Expressing a Safety Switch. Molecular Therapy, 2016, 24, 736-745.	3.7	11
3320	Structural basis for activity regulation of MLL family methyltransferases. Nature, 2016, 530, 447-452.	13.7	189
3321	Fineâ€ŧuning of CD8 ⁺ Tâ€cell effector functions by targeting the 2B4â€CD48 interaction. Immunology and Cell Biology, 2016, 94, 583-592.	1.0	6
3322	Morphology of nuclear transcription. Histochemistry and Cell Biology, 2016, 145, 343-358.	0.8	18
3323	DNA Replication and Histone Modification. , 2016, , 469-488.		2
3325	Epigenetic engineering shows that a human centromere resists silencing mediated by H3K27me3/K9me3. Molecular Biology of the Cell, 2016, 27, 177-196.	0.9	30
3326	The Histone Variant MacroH2A1.2 Is Necessary for the Activation of Muscle Enhancers and Recruitment of the Transcription Factor Pbx1. Cell Reports, 2016, 14, 1156-1168.	2.9	49
3327	Epigenomic Studies in Epidemiology. , 2016, , 163-182.		1
3328	Epigenetics, the Environment, and Childrenâ \in $^{ m Ms}$ Health Across Lifespans. , 2016, , .		7
3329	The effects of LSD1 inhibition on self-renewal and differentiation of human induced pluripotent stem cells. Experimental Cell Research, 2016, 340, 227-237.	1.2	7
3330	AID hits the jackpot when missing the target. Current Opinion in Immunology, 2016, 39, 96-102.	2.4	10
3331	Mapping the chromatin state dynamics in myoblasts. Gene Reports, 2016, 3, 5-13.	0.4	1

ARTICLE IF CITATIONS Tetracyanoresorcin[4]arene selectively recognises trimethyllysine and inhibits its enzyme-catalysed 3332 18 1.5 demethylation. Supramolecular Chemistry, 2016, 28, 575-581. Integrating RNA-seq and ChIP-seq data to characterize long non-coding RNAs in Drosophila 1.2 19 melanogaster. BMC Genomics, 2016, 17, 220. An interactive environment for agile analysis and visualization of ChIP-sequencing data. Nature 3334 3.6 223 Structural and Molecular Biology, 2016, 23, 349-357. The retrovirus HTLV-1 inserts an ectopic CTCF-binding site into the human genome. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 3054-3059. Epigenomic Landscape of Human Fetal Brain, Heart, and Liver. Journal of Biological Chemistry, 2016, 3336 1.6 45 291, 4386-4398. Understanding Suicide., 2016,,. Enhancers as non-coding RNA transcription units: recent insights and future perspectives. Nature 3338 7.7 614 Reviews Genetics, 2016, 17, 207-223. Histone H4 Lysine 20 (H4K20) Methylation, Expanding the Signaling Potential of the Proteome One 3339 2.5 Methyl Moiety at a Time. Molécular and Cellular Proteomics, 2016, 15, 755-764. ChIP-BIT: Bayesian inference of target genes using a novel joint probabilistic model of ChIP-seq 3340 6.5 15 profiles. Nucleic Acids Research, 2016, 44, e65-e65. Comprehensive benchmarking reveals H2BK20 acetylation as a distinctive signature of 3341 2.4 29 cell-state-specific enhancers and promoters. Genome Research, 2016, 26, 612-623. Epigenetics - A Different Way of Looking at Genetics. Epigenetics and Human Health, 2016, , . 3342 0.2 0 HDAC inhibitors induce global changes in histone lysine and arginine methylation and alter 3343 1.2 expression of lysine demethylases. Journal of Proteomics, 2016, 133, 125-133. ChIP bias as a function of cross-linking time. Chromosome Research, 2016, 24, 175-181. 3344 1.0 72 Epigenetics in Personalized Management of Lung Cancer. Advances in Experimental Medicine and 3345 0.8 Biology, 2016, 890, 111-122. Standardizing chromatin research: a simple and universal method for ChIP-seq. Nucleic Acids 3346 6.5 97 Research, 2016, 44, e67-e67. Estradiol differentially induces progesterone receptor isoforms expression through alternative 3347 1.1 promoter regulation in a mouse embryonic hypothalamic cell line. Endocrine, 2016, 52, 618-631. Fatty acid induced metabolic memory involves alterations in renal histone H3K36me2 and H3K27me3. 3348 1.6 36 Molecular and Cellular Endocrinology, 2016, 422, 233-242. Adsorption of histones on natural polysaccharides: The potential as agent for multiple organ failure 3349 in sepsis. International Journal of Biological Macromolecules, 2016, 84, 54-57.

#	Article	IF	CITATIONS
3350	An integrated genomic analysis of Tudor domain–containing proteins identifies PHD finger protein 20â€like 1 (PHF20L1) as a candidate oncogene in breast cancer. Molecular Oncology, 2016, 10, 292-302.	2.1	24
3351	Epigenome-based personalized medicine in human cancer. Epigenomics, 2016, 8, 119-133.	1.0	76
3353	Discovery of a Novel Inhibitor of Histone Lysine-Specific Demethylase 1A (KDM1A/LSD1) as Orally Active Antitumor Agent. Journal of Medicinal Chemistry, 2016, 59, 1501-1517.	2.9	70
3354	Histone modifying enzymes: novel disease biomarkers and assay development. Expert Review of Molecular Diagnostics, 2016, 16, 297-306.	1.5	25
3355	JARID1D Is a Suppressor and Prognostic Marker of Prostate Cancer Invasion and Metastasis. Cancer Research, 2016, 76, 831-843.	0.4	99
3356	An assessment of molecular pathways of obesity susceptible to nutrient, toxicant and genetically induced epigenetic perturbation. Journal of Nutritional Biochemistry, 2016, 30, 1-13.	1.9	17
3357	EMERGE: a flexible modelling framework to predict genomic regulatory elements from genomic signatures. Nucleic Acids Research, 2016, 44, e42-e42.	6.5	34
3358	Dot1l deficiency leads to increased intercalated cells and upregulation of V-ATPase B1 in mice. Experimental Cell Research, 2016, 344, 167-175.	1.2	18
3359	Transcriptomics and Gene Regulation. Translational Bioinformatics, 2016, , .	0.0	2
3361	A Nonparametric Bayesian Model for Nested Clustering. Methods in Molecular Biology, 2016, 1362, 129-141.	0.4	0
3363	Genome architecture: from linear organisation of chromatin to the 3D assembly in the nucleus. Chromosoma, 2016, 125, 455-469.	1.0	30
3364	Th22 cells control colon tumorigenesis through STAT3 and Polycomb Repression complex 2 signaling. Oncolmmunology, 2016, 5, e1082704.	2.1	29
3365	Epigenetic control of the immune system: a lesson from Kabuki syndrome. Immunologic Research, 2016, 64, 345-359.	1.3	51
3366	Association analysis between the distributions of histone modifications and gene expression in the human embryonic stem cell. Gene, 2016, 575, 90-100.	1.0	10
3367	H3K9me3 facilitates hypoxia-induced p53-dependent apoptosis through repression of APAK. Oncogene, 2016, 35, 793-799.	2.6	55
3368	Regulation of cell differentiation and function by the euchromatin histone methyltranserfases G9a and GLP. Biochemistry and Cell Biology, 2016, 94, 26-32.	0.9	34
3369	Histone H3K4 trimethylation: dynamic interplay with pre-mRNA splicing. Biochemistry and Cell Biology, 2016, 94, 1-11.	0.9	37
3370	Elucidating the mechanisms of transcription regulation during heart development by next-generation sequencing. Journal of Human Genetics, 2016, 61, 5-12.	1.1	3

	CITATION REI	PORT	
#	Article	IF	CITATIONS
3371	Grabbing the genome by the NADs. Chromosoma, 2016, 125, 361-371.	1.0	40
3372	Histone Demethylase LSD1 Inhibitors Prevent Cell Growth by Regulating Gene Expression in Esophageal Squamous Cell Carcinoma Cells. Annals of Surgical Oncology, 2016, 23, 312-320.	0.7	25
3373	Abscisic-acid-dependent basic leucine zipper (bZIP) transcription factors in plant abiotic stress. Protoplasma, 2017, 254, 3-16.	1.0	234
3374	Practical Guidelines for High-Resolution Epigenomic Profiling of Nucleosomal Histones in Postmortem Human Brain Tissue. Biological Psychiatry, 2017, 81, 162-170.	0.7	48
3375	The maternal control in the embryonic development of zebrafish. General and Comparative Endocrinology, 2017, 245, 55-68.	0.8	30
3376	ABCC3 genetic variants are associated with postoperative morphine-induced respiratory depression and morphine pharmacokinetics in children. Pharmacogenomics Journal, 2017, 17, 162-169.	0.9	27
3377	Epigenetic regulation of bone cells. Connective Tissue Research, 2017, 58, 76-89.	1.1	27
3378	Increased expression of the histone H3 lysine 4 methyltransferase MLL4 and the histone H3 lysine 27 demethylase UTX prolonging the overall survival of patients with glioblastoma and a methylated MGMT promoter. Journal of Neurosurgery, 2017, 126, 1461-1471.	0.9	9
3379	Underrepresentation of active histone modification marks in evolutionarily young genes. Insect Science, 2017, 24, 174-186.	1.5	3
3380	INSPIIRED: Quantification and Visualization Tools for Analyzing Integration Site Distributions. Molecular Therapy - Methods and Clinical Development, 2017, 4, 17-26.	1.8	60
3381	Epigenetic modification in chromatin machinery and its deregulation in pediatric brain tumors: Insight into epigenetic therapies. Epigenetics, 2017, 12, 353-369.	1.3	36
3382	Different expression patterns of histone H3K27 demethylases in renal cell carcinoma and bladder cancer. Cancer Biomarkers, 2017, 18, 125-131.	0.8	9
3383	The Role of Chromatin Structure in Gene Regulation of the Human Malaria Parasite. Trends in Parasitology, 2017, 33, 364-377.	1.5	46
3384	Single-cell epigenomic variability reveals functional cancer heterogeneity. Genome Biology, 2017, 18, 15.	3.8	92
3385	Discovery of Potent and Selective Inhibitors for G9a-Like Protein (GLP) Lysine Methyltransferase. Journal of Medicinal Chemistry, 2017, 60, 1876-1891.	2.9	54
3386	Mediator cyclinâ€dependent kinases upregulate transcription of inflammatory genes in cooperation with <scp>NF</scp> â€PB and C/ <scp>EBP</scp> β on stimulation of Tollâ€like receptor 9. Genes To Cells, 2017, 22, 265-276.	0.5	17
3387	Rapid Recall Ability of Memory T cells is Encoded in their Epigenome. Scientific Reports, 2017, 7, 39785.	1.6	39
3388	Chromatin immunoprecipitation in microfluidic droplets: towards fast and cheap analyses. Lab on A Chip, 2017, 17, 530-537.	3.1	9

#	Article	IF	Citations
3389	Emerging role of SETDB1 as a therapeutic target. Expert Opinion on Therapeutic Targets, 2017, 21, 319-331.	1.5	54
3390	Toward a Taxonomy for Multi-Omics Science? Terminology Development for Whole Genome Study Approaches by Omics Technology and Hierarchy. OMICS A Journal of Integrative Biology, 2017, 21, 1-16.	1.0	44
3391	Sex-specific chromatin landscapes in an ultra-compact chordate genome. Epigenetics and Chromatin, 2017, 10, 3.	1.8	14
3392	Retrieving Chromatin Patterns from Deep Sequencing Data Using Correlation Functions. Biophysical Journal, 2017, 112, 473-490.	0.2	18
3393	Decoding transcriptional states in cancer. Current Opinion in Genetics and Development, 2017, 43, 82-92.	1.5	7
3394	The <i>Saccharomyces cerevisiae</i> Cdk8 Mediator Represses <i>AQY1</i> Transcription by Inhibiting Set1p-Dependent Histone Methylation. G3: Genes, Genomes, Genetics, 2017, 7, 1001-1010.	0.8	6
3395	The Histone Methyltransferase DOT1L Promotes Neuroblastoma by Regulating Gene Transcription. Cancer Research, 2017, 77, 2522-2533.	0.4	59
3396	Precision medicine driven by cancer systems biology. Cancer and Metastasis Reviews, 2017, 36, 91-108.	2.7	38
3397	Investigation of correlations between DNA methylation, suicidal behavior and aging. Bipolar Disorders, 2017, 19, 32-40.	1.1	27
3398	Epigenetic Regulation: A New Frontier for Biomedical Engineers. Annual Review of Biomedical Engineering, 2017, 19, 195-219.	5.7	135
3399	Structure, Function and Dynamics of Chromatin. Springer Theses, 2017, , 63-103.	0.0	0
3400	TOP2 synergizes with BAF chromatin remodeling for both resolution and formation of facultative heterochromatin. Nature Structural and Molecular Biology, 2017, 24, 344-352.	3.6	66
3401	Glucocorticoid receptor positively regulates transcription of FNDC5 in the liver. Scientific Reports, 2017, 7, 43296.	1.6	29
3402	Role of Chromatin Modifications in Drosophila Germline Stem Cell Differentiation. Results and Problems in Cell Differentiation, 2017, 59, 1-30.	0.2	13
3403	The SETD8/PR-Set7 Methyltransferase Functions as a Barrier to Prevent Senescence-Associated Metabolic Remodeling. Cell Reports, 2017, 18, 2148-2161.	2.9	58
3404	Identification of potential target genes of ROR-alpha in THP1 and HUVEC cell lines. Experimental Cell Research, 2017, 353, 6-15.	1.2	9
3405	Histone H3K4 and H3K36 Methylation Independently Recruit the NuA3 Histone Acetyltransferase in <i>Saccharomyces cerevisiae</i> . Genetics, 2017, 205, 1113-1123.	1.2	23
3406	Neuronal activity modifies the chromatin accessibility landscape in the adult brain. Nature Neuroscience, 2017, 20, 476-483.	7.1	218

#	Article	IF	CITATIONS
3407	A loop of cancer-stroma-cancer interaction promotes peritoneal metastasis of ovarian cancer via TNFα-TGFα-EGFR. Oncogene, 2017, 36, 3576-3587.	2.6	68
3408	Changes to histone modifications following prenatal alcohol exposure: An emerging picture. Alcohol, 2017, 60, 41-52.	0.8	41
3409	H3K4me3 induces allosteric conformational changes in the DNA-binding and catalytic regions of the V(D)J recombinase. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 1904-1909.	3.3	24
3411	The SUV39H1 Protein Lysine Methyltransferase Methylates Chromatin Proteins Involved in Heterochromatin Formation and VDJ Recombination. ACS Chemical Biology, 2017, 12, 958-968.	1.6	26
3412	Multicellular Tumor Spheroids Combined with Mass Spectrometric Histone Analysis To Evaluate Epigenetic Drugs. Analytical Chemistry, 2017, 89, 2773-2781.	3.2	27
3413	Aorta macrophage inflammatory and epigenetic changes in a murine model of obstructive sleep apnea: Potential role of CD36. Scientific Reports, 2017, 7, 43648.	1.6	47
3414	Inhibiting histone deacetylases suppresses glucose metabolism and hepatocellular carcinoma growth by restoring FBP1 expression. Scientific Reports, 2017, 7, 43864.	1.6	72
3416	The Role of Nuclear Receptor–Binding SET Domain Family Histone Lysine Methyltransferases in Cancer. Cold Spring Harbor Perspectives in Medicine, 2017, 7, a026708.	2.9	122
3417	Wolf-Hirschhorn syndrome candidate 1-like 1 epigenetically regulates nephrin gene expression. American Journal of Physiology - Renal Physiology, 2017, 312, F1184-F1199.	1.3	4
3418	New Generation DNA Sequencing (NGS): Mining for Genes and the Potential of Extremophiles. , 2017, , 255-268.		3
3419	Chromatin and Polycomb: Biology and bioinformatics. Molecular Biology, 2017, 51, 14-24.	0.4	0
3420	Gene Regulatory Elements, Major Drivers of Human Disease. Annual Review of Genomics and Human Genetics, 2017, 18, 45-63.	2.5	115
3421	H3K4 demethylase KDM5B regulates global dynamics of transcription elongation and alternative splicing in embryonic stem cells. Nucleic Acids Research, 2017, 45, 6427-6441.	6.5	42
3422	Epigenetic programming of the neuroendocrine stress response by adult life stress. Journal of Molecular Endocrinology, 2017, 59, R11-R31.	1.1	63
3423	Polycomb Group Gene E(z) Is Required for Spermatogonial Dedifferentiation in Drosophila Adult Testis. Journal of Molecular Biology, 2017, 429, 2030-2041.	2.0	11
3424	Maternal low-protein diet decreases brain-derived neurotrophic factor expression in the brains of the neonatal rat offspring. Journal of Nutritional Biochemistry, 2017, 45, 54-66.	1.9	21
3425	Identification of <scp>FERM</scp> domainâ€containing protein 5 as a novel target of βâ€catenin/ <scp>TCF</scp> 7L2 complex. Cancer Science, 2017, 108, 612-619.	1.7	8
3426	The promise of epigenetic therapy: reprogramming the cancer epigenome. Current Opinion in Genetics and Development, 2017, 42, 68-77.	1.5	136

#	Article	IF	CITATIONS
3427	Interaction of a common painkiller piroxicam and copper-piroxicam with chromatin causes structural alterations accompanied by modulation at the epigenomic/genomic level. Biochimica Et Biophysica Acta - General Subjects, 2017, 1861, 2048-2059.	1.1	8
3428	The histone demethylase PHF8 is a molecular safeguard of the IFNÎ ³ response. Nucleic Acids Research, 2017, 45, gkw1346.	6.5	12
3429	Epigenetic modulation associated with carcinogenesis and prognosis of human gastric cancer. Oncology Letters, 2017, 13, 3363-3368.	0.8	14
3430	RNF8 mediates histone H3 ubiquitylation and promotes glycolysis and tumorigenesis. Journal of Experimental Medicine, 2017, 214, 1843-1855.	4.2	27
3431	Divergent Requirements for EZH1 in Heart Development Versus Regeneration. Circulation Research, 2017, 121, 106-112.	2.0	60
3432	Histone methylation is critical in monocyte to macrophage differentiation. FEBS Journal, 2017, 284, 1306-1308.	2.2	4
3433	Planarians SET New Paths for Innate Immune Memory. EBioMedicine, 2017, 20, 7-8.	2.7	2
3434	Different reaction of the core histones H2A and H2B to red laser irradiation. , 2017, , .		1
3435	S100-alarmin-induced innate immune programming protects newborn infants from sepsis. Nature Immunology, 2017, 18, 622-632.	7.0	131
3436	Nucleosome Positioning and NDR Structure at RNA Polymerase III Promoters. Scientific Reports, 2017, 7, 41947.	1.6	29
3437	Mocap: large-scale inference of transcription factor binding sites from chromatin accessibility. Nucleic Acids Research, 2017, 45, 4315-4329.	6.5	30
3438	DNA Methylation in Plants and Its Implications in Development, Hybrid Vigour, and Evolution. RNA Technologies, 2017, , 263-280.	0.2	1
3439	Writing, erasing and reading histone lysine methylations. Experimental and Molecular Medicine, 2017, 49, e324-e324.	3.2	800
3440	Deciphering Histone Code Enigmas Sheds New Light on Cardiac Regeneration. Circulation Research, 2017, 120, 1370-1372.	2.0	0
3442	KDM3 epigenetically controls tumorigenic potentials of human colorectal cancer stem cells through Wnt/β-catenin signalling. Nature Communications, 2017, 8, 15146.	5.8	93
3443	PAX3–FOXO1 Establishes Myogenic Super Enhancers and Confers BET Bromodomain Vulnerability. Cancer Discovery, 2017, 7, 884-899.	7.7	221
3444	Modulation of gene expression dynamics by co-transcriptional histone methylations. Experimental and Molecular Medicine, 2017, 49, e326-e326.	3.2	57
3445	Transcriptional Regulator CNOT3 Defines an Aggressive Colorectal Cancer Subtype. Cancer Research, 2017, 77, 766-779.	0.4	21

ARTICLE IF CITATIONS Epigenetic modifications in multiple myeloma: recent advances on the role of DNA and histone 3446 1.5 54 methylation. Expert Opinion on Therapeutic Targets, 2017, 21, 91-101. Histone chaperone HIRA regulates neural progenitor cell proliferation and neurogenesis via Î²-catenin. 3447 2.3 38 Journal of Cell Biology, 2017, 216, 1975-1992 Genetic advances in systemic lupus erythematosus: an update. Current Opinion in Rheumatology, 2017, 3448 2.0 112 29, 423-433. Lamina-Associated Domains: Links with Chromosome Architecture, Heterochromatin, and Gene 3450 798 Repression. Cell, 2017, 169, 780-791. Enhancers and chromatin structures: regulatory hubs in gene expression and diseases. Bioscience 3451 1.1 58 Reports, 2017, 37, . Bioinformatics Tools for Genome-Wide Epigenetic Research. Advances in Experimental Medicine and Biology, 2017, 978, 489-512. 3454 0.8 Epigenetic regulation during salinity and drought stress in plants: Histone modifications and DNA 3455 1.4 65 methylation. Plant Gene, 2017, 11, 199-204. Epigenetics in endometrial carcinogenesis – part 2: histone modifications, chromatin remodeling and 3456 1.0 noncoding RNAs. Epigenomics, 2017, 9, 873-892. 3457 GLANET: genomic loci annotation and enrichment tool. Bioinformatics, 2017, 33, 2818-2828. 1.8 15 Defining the 5Î,, and 3Î,, landscape of the Drosophila transcriptome with Exo-seq and RNaseH-seq. Nucleic 3458 6.5 Acids Research, 2017, 45, e95-e95. RNA Activation. Advances in Experimental Medicine and Biology, 2017, , . 3459 0.8 1 ChromBiSim: Interactive chromatin biclustering using a simple approach. Genomics, 2017, 109, 353-361. 3460 1.3 Dynamic balance between master transcription factors determines the fates and functions of CD4 T 3461 4.2 165 cell and innate lymphoid cell subsets. Journal of Experimental Medicine, 2017, 214, 1861-1876. Histone demethylase KDM5A regulates the ZMYND8–NuRD chromatin remodeler to promote DNA 3462 2.3 132 repair. Journal of Cell Biology, 2017, 216, 1959-1974. Recognition of long-range enhancer-promoter interactions by adding genomic signatures of 3463 1.3 15 segmented regulatory regions. Genomics, 2017, 109, 341-352. Structural Variation Shapes the Landscape of Recombination in Mouse. Genetics, 2017, 206, 603-619. 3464 1.2 Estrogen Receptor-Î² Modulation of the ERα-p53 Loop Regulating Gene Expression, Proliferation, and 3465 4.9 39 Apoptosis in Breast Cancer. Hormones and Cancer, 2017, 8, 230-242. Epigenetic effects of inhibition of heat shock protein 90 (HSP90) in human pancreatic and colon 3466 3.2 19 cancer. Cancer Letters, 2017, 402, 110-116.

#	Article	IF	CITATIONS
3467	EpiCompare: an online tool to define and explore genomic regions with tissue or cell type-specific epigenomic features. Bioinformatics, 2017, 33, 3268-3275.	1.8	17
3468	Protein post-translational modifications: In silico prediction tools and molecular modeling. Computational and Structural Biotechnology Journal, 2017, 15, 307-319.	1.9	145
3469	ChIP-seq for the Identification of Functional Elements in the Human Genome. Methods in Molecular Biology, 2017, 1543, 3-18.	0.4	9
3470	Identification of Candidate Functional Elements in the Genome from ChIP-seq Data. Methods in Molecular Biology, 2017, 1543, 19-43.	0.4	2
3472	How does chromatin package DNA within nucleus and regulate gene expression?. International Journal of Biological Macromolecules, 2017, 101, 862-881.	3.6	10
3473	GenoGAM: genome-wide generalized additive models for ChIP-Seq analysis. Bioinformatics, 2017, 33, 2258-2265.	1.8	9
3474	Epigenomic Promoter Alterations Amplify Gene Isoform and Immunogenic Diversity in Gastric Adenocarcinoma. Cancer Discovery, 2017, 7, 630-651.	7.7	48
3475	Perturbed Signaling and Role of Posttranslational Modifications in Cancer Drug Resistance. , 2017, , 483-510.		7
3476	Crosstalk between epigenetics and metabolism—Yin and Yang of histone demethylases and methyltransferases in cancer. Briefings in Functional Genomics, 2017, 16, 320-325.	1.3	26
3477	Quantitative chromatin proteomics reveals a dynamic histone post-translational modification landscape that defines asexual and sexual Plasmodium falciparum parasites. Scientific Reports, 2017, 7, 607.	1.6	60
3478	A comprehensive analysis of cancer-driving mutations and genes in kidney cancer. Oncology Letters, 2017, 13, 2151-2160.	0.8	4
3479	Transcriptional landscape of the human cell cycle. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 3473-3478.	3.3	110
3480	Microfluidics for genome-wide studies involving next generation sequencing. Biomicrofluidics, 2017, 11, 021501.	1.2	29
3481	Software tools for visualizing Hi-C data. Genome Biology, 2017, 18, 26.	3.8	53
3482	Drug Resistance in Bacteria, Fungi, Malaria, and Cancer. , 2017, , .		13
3483	KDM4B histone demethylase and G9a regulate expression of vascular adhesion proteins in cerebral microvessels. Scientific Reports, 2017, 7, 45005.	1.6	23
3484	Traffic-derived particulate matter exposure and histone H3 modification: A repeated measures study. Environmental Research, 2017, 153, 112-119.	3.7	52
3485	Characterization of hundreds of regulatory landscapes in developing limbs reveals two regimes of chromatin folding. Genome Research, 2017, 27, 223-233.	2.4	123

#	Article	IF	CITATIONS
3486	Epigenetic dysfunctional diseases and therapy for infection and inflammation. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2017, 1863, 518-528.	1.8	36
3487	Probing Chromatin Modifications in Response to ERK Signaling. Methods in Molecular Biology, 2017, 1487, 289-301.	0.4	3
3488	The Binding Specificity of the PHD-Finger Domain of VIN3 Moderates Vernalization Response. Plant Physiology, 2017, 173, 1258-1268.	2.3	21
3489	Epigenetic activation of SIN1 promotes NSCLC cell proliferation and metastasis by affecting the epithelial–mesenchymal transition. Biochemical and Biophysical Research Communications, 2017, 483, 645-651.	1.0	7
3490	Is H3K4me3 instructive for transcription activation?. BioEssays, 2017, 39, 1-12.	1.2	373
3491	A Flowering Locus C Homolog Is a Vernalization-Regulated Repressor in <i>Brachypodium</i> and Is Cold Regulated in Wheat. Plant Physiology, 2017, 173, 1301-1315.	2.3	78
3492	Chromatin priming elements establish immunological memory in T cells without activating transcription. BioEssays, 2017, 39, 1600184.	1.2	25
3493	Epigenetics and Control of RNAs. Methods in Molecular Biology, 2017, 1488, 217-237.	0.4	3
3494	Smarca4 ATPase mutations disrupt direct eviction of PRC1 from chromatin. Nature Genetics, 2017, 49, 282-288.	9.4	165
3495	Transcriptional architecture of the mammalian circadian clock. Nature Reviews Genetics, 2017, 18, 164-179.	7.7	1,766
3496	Mechanisms of pluripotency maintenance in mouse embryonic stem cells. Cellular and Molecular Life Sciences, 2017, 74, 1805-1817.	2.4	22
3497	Epigenetic Networks Regulate the Transcriptional Program in Memory and Terminally Differentiated CD8+ T Cells. Journal of Immunology, 2017, 198, 937-949.	0.4	55
3498	Regulation of endothelial intracellular adenosine via adenosine kinase epigenetically modulates vascular inflammation. Nature Communications, 2017, 8, 943.	5.8	69
3499	Naked Mole Rat Cells Have a Stable Epigenome that Resists iPSCÂReprogramming. Stem Cell Reports, 2017, 9, 1721-1734.	2.3	71
3500	Prediction of genome-wide DNA methylation in repetitive elements. Nucleic Acids Research, 2017, 45, 8697-8711.	6.5	106
3501	Concise Review: Epigenetic Regulation of Hematopoiesis: Biological Insights and Therapeutic Applications. Stem Cells Translational Medicine, 2017, 6, 2106-2114.	1.6	26
3502	Temporal regulation of chromatin during myoblast differentiation. Seminars in Cell and Developmental Biology, 2017, 72, 77-86.	2.3	17
3503	H2A.Z Represses Gene Expression by Modulating Promoter Nucleosome Structure and Enhancer Histone Modifications in Arabidopsis. Molecular Plant, 2017, 10, 1274-1292.	3.9	102

#	Article	IF	CITATIONS
3504	Ligand-dependent corepressor (LCoR) represses the transcription factor C/EBPÎ ² during early adipocyte differentiation. Journal of Biological Chemistry, 2017, 292, 18973-18987.	1.6	10
3505	Molecular Regulation of Cellular Senescence by MicroRNAs: Implications in Cancer and Age-Related Diseases. International Review of Cell and Molecular Biology, 2017, 334, 27-98.	1.6	16
3506	JMJD5 cleaves monomethylated histone H3 Nâ€ŧail under DNA damaging stress. EMBO Reports, 2017, 18, 2131-2143.	2.0	45
3507	Histone H3K4 methylation-dependent and -independent functions of Set1A/COMPASS in embryonic stem cell self-renewal and differentiation. Genes and Development, 2017, 31, 1732-1737.	2.7	68
3508	H3K27 Methylation Dynamics during CD4 T Cell Activation: Regulation of JAK/STAT and IL12RB2 Expression by JMJD3. Journal of Immunology, 2017, 199, 3158-3175.	0.4	29
3509	Effect of carbamazepine on expression of UDP-glucuronosyltransferase 1A6 and 1A7 in rat brain. Drug Metabolism and Pharmacokinetics, 2017, 32, 286-292.	1.1	7
3510	NEUROG1 Regulates CDK2 to Promote Proliferation in Otic Progenitors. Stem Cell Reports, 2017, 9, 1516-1529.	2.3	27
3511	Pattern-based Search of Epigenomic Data Using GeNemo. Journal of Visualized Experiments, 2017, , .	0.2	0
3512	Enzymatic methods for genome-wide profiling of protein binding sites. Briefings in Functional Genomics, 2018, 17, 138-145.	1.3	11
3513	Global inhibition of transcription causes an increase in histone H2A.Z incorporation within gene bodies. Nucleic Acids Research, 2017, 45, 12715-12722.	6.5	28
3514	A hyperdynamic H3.3 nucleosome marks promoter regions in pluripotent embryonic stem cells. Nucleic Acids Research, 2017, 45, 12181-12194.	6.5	28
3515	Chromatin proteomics reveals novel combinatorial histone modification signatures that mark distinct subpopulations of macrophage enhancers. Nucleic Acids Research, 2017, 45, 12195-12213.	6.5	26
3516	High-Resolution Chromatin Immunoprecipitation: ChIP-Sequencing. Methods in Molecular Biology, 2017, 1624, 61-73.	0.4	7
3517	The Impact of Post-Translational Regulation of Histone on Cancer Metastasis and Cancer Chemoresistance. Current Pharmacology Reports, 2017, 3, 253-267.	1.5	1
3518	DNA methylation of intragenic CpG islands depends on their transcriptional activity during differentiation and disease. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E7526-E7535.	3.3	125
3519	Mathematical Modeling of Avidity Distribution and Estimating General Binding Properties of Transcription Factors from Genome-Wide Binding Profiles. Methods in Molecular Biology, 2017, 1613, 193-276.	0.4	4
3520	Global Inhibition with Specific Activation: How p53 and MYC Redistribute the Transcriptome in the DNA Double-Strand Break Response. Molecular Cell, 2017, 67, 1013-1025.e9.	4.5	55
3521	LSD1-Mediated Epigenetic Reprogramming Drives CENPE Expression and Prostate Cancer Progression. Cancer Research, 2017, 77, 5479-5490.	0.4	71

#	Article	IF	CITATIONS
3522	DNA and Histone Methylation in Lung Cancer. Cancer Drug Discovery and Development, 2017, , 403-436.	0.2	3
3523	Genome-wide comparative analysis of H3K4me3 profiles between diploid and allotetraploid cotton to refine genome annotation. Scientific Reports, 2017, 7, 9098.	1.6	10
3524	FOXF1 transcription factor promotes lung regeneration after partial pneumonectomy. Scientific Reports, 2017, 7, 10690.	1.6	46
3525	The Schistosoma mansoni genome encodes thousands of long non-coding RNAs predicted to be functional at different parasite life-cycle stages. Scientific Reports, 2017, 7, 10508.	1.6	48
3526	Novel detection of post-translational modifications in human monocyte-derived dendritic cells after chronic alcohol exposure: Role of inflammation regulator H4K12ac. Scientific Reports, 2017, 7, 11236.	1.6	11
3527	CTCF-Mediated Enhancer-Promoter Interaction Is a Critical Regulator of Cell-to-Cell Variation of Gene Expression. Molecular Cell, 2017, 67, 1049-1058.e6.	4.5	219
3528	Bivalent Epigenetic Control of Oncofetal Gene Expression in Cancer. Molecular and Cellular Biology, 2017, 37, .	1.1	42
3529	Epigenetic Regulation of Dendritic Cell Development and Function. Cancer Journal (Sudbury, Mass), 2017, 23, 302-307.	1.0	30
3530	An embryonic system to assess direct and indirect Wnt transcriptional targets. Scientific Reports, 2017, 7, 11092.	1.6	4
3531	KDM4A regulates HIF-1 levels through H3K9me3. Scientific Reports, 2017, 7, 11094.	1.6	41
3532	Genome-wide identification of histone H2A and histone variant H2A.Z-interacting proteins by bPPI-seq. Cell Research, 2017, 27, 1258-1274.	5.7	14
3533	VEGF amplifies transcription through ETS1 acetylation to enable angiogenesis. Nature Communications, 2017, 8, 383.	5.8	79
3534	DNA and Histone Modifications in Cancer Therapy. Cancer Drug Discovery and Development, 2017, , 585-604.	0.2	0
3535	The Molecular Basis of Histone Demethylation. Cancer Drug Discovery and Development, 2017, , 151-219.	0.2	8
3536	Misregulation of Histone Methylation Regulators in Cancer. Cancer Drug Discovery and Development, 2017, , 221-248.	0.2	2
3537	Histone Methylation by SET Domain Proteins in Fungi. Annual Review of Microbiology, 2017, 71, 413-439.	2.9	106
3538	Recruitment of histone modifications to assist mRNA dosage maintenance after degeneration of cytosine DNA methylation during animal evolution. Genome Research, 2017, 27, 1513-1524.	2.4	8
3539	Coactivators and general transcription factors have two distinct dynamic populations dependent onAtranscription. EMBO Journal, 2017, 36, 2710-2725.	3.5	19

		CITATION REPORT		
#	Article		IF	CITATIONS
3540	The Epigenomic Revolution in Breast Cancer. American Journal of Pathology, 2017, 187,	, 2163-2174.	1.9	27
3541	Do social insects support Haig's kin theory for the evolution of genomic imprinting?. Ep 12, 725-742.	igenetics, 2017,	1.3	25
3542	ChIP-Seq Analysis for Identifying Genome-Wide Histone Modifications Associated with Stress-Responsive Genes in Plants. Methods in Molecular Biology, 2017, 1631, 139-149		0.4	2
3543	Chromatin Immunoprecipitation (ChIP) in Mouse T-cell Lines. Journal of Visualized Exper	iments, 2017, , .	0.2	12
3544	Epigenetic mechanisms underlying the toxic effects associated with arsenic exposure ar development of diabetes. Food and Chemical Toxicology, 2017, 107, 406-417.	1d the	1.8	34
3545	Kmt5a Controls Hepatic Metabolic Pathways by Facilitating RNA Pol II Release from Pror Regions. Cell Reports, 2017, 20, 909-922.	noter-Proximal	2.9	24
3546	How to tame an endogenous retrovirus: HERVH and the evolution of human pluripotenc Opinion in Virology, 2017, 25, 49-58.	zy. Current	2.6	35
3547	A role of human RNase P subunits, Rpp29 and Rpp21, in homology directed-repair of do breaks. Scientific Reports, 2017, 7, 1002.	uble-strand	1.6	22
3548	NRF1 coordinates with DNA methylation to regulate spermatogenesis. FASEB Journal, 20 4959-4970.	017, 31,	0.2	41
3549	MLL4 prepares the enhancer landscape for Foxp3 induction via chromatin looping. Natu Immunology, 2017, 18, 1035-1045.	re	7.0	63
3550	Repression of Stress-Induced LINE-1 Expression Protects Cancer Cell Subpopulations fro Exposure. Cancer Cell, 2017, 32, 221-237.e13.	m Lethal Drug	7.7	177
3551	Effects of high progesterone level on the day of human chorionic gonadotrophin admini inÂvitro fertilization cycles on epigenetic modification of endometrium in the peri-impla Fertility and Sterility, 2017, 108, 269-276.e1.	stration in ntation period.	0.5	55
3552	Epigenetic regulation of EC-SOD expression in aging lung fibroblasts: Role of histone ac Radical Biology and Medicine, 2017, 112, 212-223.	etylation. Free	1.3	14
3553	Histone Modification Is Correlated With Reverse Left Ventricular Remodeling in Nonisch Cardiomyopathy. Annals of Thoracic Surgery, 2017, 104, 1531-1539.	emic Dilated	0.7	29
3554	Running training experience attenuates disuse atrophy in fast-twitch skeletal muscles or of Applied Physiology, 2017, 123, 902-913.	f rats. Journal	1.2	15
3555	HISTONE DEACETYLASE6 Acts in Concert with Histone Methyltransferases SUVH4, SUV Regulate Transposon Silencing. Plant Cell, 2017, 29, 1970-1983.	H5, and SUVH6 to	3.1	72
3556	Phosphorylation of Histone H2A at Serine 95: A Plant-Specific Mark Involved in Flowerin Regulation and H2A.Z Deposition. Plant Cell, 2017, 29, 2197-2213.	g Time	3.1	76
3557	Neuronal-expressed microRNA-targeted pseudogenes compete with coding genes in the Translational Psychiatry, 2017, 7, e1199-e1199.	e human brain.	2.4	18

#	Article	IF	CITATIONS
3558	OCT4 and SOX2 Work as Transcriptional Activators in Reprogramming Human Fibroblasts. Cell Reports, 2017, 20, 1585-1596.	2.9	34
3559	Polycomb and Trithorax Group Genes in <i>Drosophila</i> . Genetics, 2017, 206, 1699-1725.	1.2	173
3560	Electrophoretic stretching and imaging of single native chromatin fibers in nanoslits. Biomicrofluidics, 2017, 11, 044108.	1.2	5
3561	Both DNA Polymerases δ and Îμ Contact Active and Stalled Replication Forks Differently. Molecular and Cellular Biology, 2017, 37, .	1.1	6
3563	MeCP2 and CTCF: enhancing the cross-talk of silencers. Biochemistry and Cell Biology, 2017, 95, 593-608.	0.9	7
3564	Chromatin Immunoprecipitation and Quantitative Real-Time PCR to Assess Binding of a Protein of Interest to Identified Predicted Binding Sites Within a Promoter. Methods in Molecular Biology, 2017, 1651, 23-32.	0.4	1
3565	Cell cycle transcription control: DREAM/MuvB and RB-E2F complexes. Critical Reviews in Biochemistry and Molecular Biology, 2017, 52, 638-662.	2.3	176
3566	Stochastics of Cellular Differentiation Explained by Epigenetics: The Case of Tâ€Cell Differentiation and Functional Plasticity. Scandinavian Journal of Immunology, 2017, 86, 184-195.	1.3	8
3567	An introduction to computational tools for differential binding analysis with ChIPâ€seq data. Quantitative Biology, 2017, 5, 226-235.	0.3	22
3568	Specific Acetylation Patterns of H2A.Z Form Transient Interactions with the BPTF Bromodomain. Biochemistry, 2017, 56, 4607-4615.	1.2	16
3569	Characterization of noncoding regulatory DNA in the human genome. Nature Biotechnology, 2017, 35, 732-746.	9.4	79
3570	Network analysis identifies chromosome intermingling regions as regulatory hotspots for transcription. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 13714-13719.	3.3	45
3571	H3K14ac is linked to methylation of H3K9 by the triple Tudor domain of SETDB1. Nature Communications, 2017, 8, 2057.	5.8	72
3572	The receptor tyrosine kinase EphA2 promotes glutamine metabolism in tumors by activating the transcriptional coactivators YAP and TAZ. Science Signaling, 2017, 10, .	1.6	80
3573	Chromatin-state discovery and genome annotation with ChromHMM. Nature Protocols, 2017, 12, 2478-2492.	5.5	613
3574	In Situ Fixation Redefines Quiescence and Early Activation of Skeletal Muscle Stem Cells. Cell Reports, 2017, 21, 1982-1993.	2.9	217
3575	Functional annotation of structural ncRNAs within enhancer RNAs in the human genome: implications for human disease. Scientific Reports, 2017, 7, 15518.	1.6	26
3576	Characteristics and Unmet Clinical Needs Related to Hepatocellular Carcinoma. Digestive Disease Interventions, 2017, 01, 074-082.	0.3	0

#	Article	IF	CITATIONS
3577	Two approaches reveal a new paradigm of †̃switchable or genetics-influenced allele-specific DNA methylation' with potential in human disease. Cell Discovery, 2017, 3, 17038.	3.1	25
3578	iTRAQ-Based Proteomic Analysis of Neonatal Kidney from Offspring of Protein Restricted Rats Reveals Abnormalities in Intraflagellar Transport Proteins. Cellular Physiology and Biochemistry, 2017, 44, 185-199.	1.1	32
3579	High-intensity UV laser ChIP-seq for the study of protein-DNA interactions in living cells. Nature Communications, 2017, 8, 1303.	5.8	25
3580	Determinants of Histone H3K4 Methylation Patterns. Molecular Cell, 2017, 68, 773-785.e6.	4.5	158
3581	Genome-wide profiling of nardilysin target genes reveals its role in epigenetic regulation and cell cycle progression. Scientific Reports, 2017, 7, 14801.	1.6	8
3582	Variant Histone H2afv reprograms DNA methylation during early zebrafish development. Epigenetics, 2017, 12, 811-824.	1.3	19
3583	HiHiMap: single-cell quantitation of histones and histone posttranslational modifications across the cell cycle by high-throughput imaging. Molecular Biology of the Cell, 2017, 28, 2290-2302.	0.9	20
3584	Common variant rs356182 near SNCA defines a Parkinson's disease endophenotype. Annals of Clinical and Translational Neurology, 2017, 4, 15-25.	1.7	40
3585	Context-specific effects of genetic variants associated with autoimmune disease. Human Molecular Genetics, 2017, 26, R185-R192.	1.4	38
3586	Small molecules for reprogramming and transdifferentiation. Cellular and Molecular Life Sciences, 2017, 74, 3553-3575.	2.4	84
3587	<scp>GT</scp> â€rich promoters can drive <scp>RNA</scp> pol <scp>II</scp> transcription and deposition of H2A.Z in African trypanosomes. EMBO Journal, 2017, 36, 2581-2594.	3.5	68
3588	The Role of Epigenetic Regulation in Transcriptional Memory in the Immune System. Advances in Protein Chemistry and Structural Biology, 2017, 106, 43-69.	1.0	14
3589	Mass Spectrometry-Based Methodology for Identification of Native Histone Variant Modifications From Mammalian Tissues and Solid Tumors. Methods in Enzymology, 2017, 586, 275-290.	0.4	1
3590	Histone 3 modifications and blood pressure in the Beijing Truck Driver Air Pollution Study. Biomarkers, 2017, 22, 584-593.	0.9	16
3591	Genome-wide Mapping of the Nucleosome Landscape by Micrococcal Nuclease and Chemical Mapping. Trends in Genetics, 2017, 33, 495-507.	2.9	34
3592	Epigenetic Changes in Chronic Inflammatory Diseases. Advances in Protein Chemistry and Structural Biology, 2017, 106, 139-189.	1.0	48
3593	Confident gene activity prediction based on single histone modification H2BK5ac in human cell lines. BMC Bioinformatics, 2017, 18, 67.	1.2	11
3594	iHMS: a database integrating human histone modification data across developmental stages and tissues. BMC Bioinformatics, 2017, 18, 103.	1.2	4

		CITATION RE	PORT	
#	Article		IF	CITATIONS
3595	Widespread of horizontal gene transfer in the human genome. BMC Genomics, 2017, 2	18, 274.	1.2	21
3596	SMYD5 regulates H4K20me3-marked heterochromatin to safeguard ES cell self-renewa spurious differentiation. Epigenetics and Chromatin, 2017, 10, 8.	l and prevent	1.8	45
3597	Histone peptide microarray screen of chromo and Tudor domains defines new histone methylation interactions. Epigenetics and Chromatin, 2017, 10, 12.	ysine	1.8	47
3598	The quest for epigenetic regulation underlying unisexual flower development in Cucum Epigenetics and Chromatin, 2017, 10, 22.	is melo.	1.8	27
3599	Type 2 diabetes and obesity induce similar transcriptional reprogramming in human my Medicine, 2017, 9, 47.	vocytes. Genome	3.6	37
3600	IDH1 or -2 mutations do not predict outcome and do not cause loss of 5-hydroxymethy altered histone modifications in central chondrosarcomas. Clinical Sarcoma Research, 2		2.3	50
3601	Histone demethylases UTX and JMJD3 are required for NKT cell development in mice. Co Bioscience, 2017, 7, 25.	ell and	2.1	28
3602	Dynamic and Antagonistic Allele-Specific Epigenetic Modifications Controlling the Expr Imprinted Genes in Maize Endosperm. Molecular Plant, 2017, 10, 442-455.	ession of	3.9	38
3603	Targeting chromatin defects in selected solid tumors based on oncogene addiction, syn lethality and epigenetic antagonism. Annals of Oncology, 2017, 28, 254-269.	nthetic	0.6	66
3604	Computational Methods and Correlation of Exon-skipping Events with Splicing, Transcr Epigenetic Factors. Methods in Molecular Biology, 2017, 1513, 163-170.	iption, and	0.4	12
3605	Functional Roles of Acetylated Histone Marks at Mouse Meiotic Recombination Hot Sp and Cellular Biology, 2017, 37, .	ots. Molecular	1.1	35
3606	Insights into inner ear-specific gene regulation: Epigenetics and non-coding RNAs in inr development and regeneration. Seminars in Cell and Developmental Biology, 2017, 65,	ier ear 69-79.	2.3	33
3607	Fluorescence In Situ Hybridization (FISH). Springer Protocols, 2017, , .		0.1	47
3608	Epigenetic Mechanisms in Cancer Development. , 2017, , 263-275.			3
3609	Cancer Genomics. , 2017, , 43-63.			0
3610	Histone Lysine Demethylase Inhibitors. Cold Spring Harbor Perspectives in Medicine, 20	017, 7, a026484.	2.9	57
3611	SET/MLL family proteins in hematopoiesis and leukemia. International Journal of Hemat 7-16.	ology, 2017, 105,	0.7	42
3612	Transcription Factor Trps1 Promotes Tubular Cell Proliferation after Ischemia-Reperfusion through cAMP–Specific 3′,5′-Cyclic Phosphodiesterase 4D and AKT. Journal of 1 Nephrology: JASN, 2017, 28, 532-544.		3.0	15

#	Article	IF	CITATIONS
3613	Epigenetic Regulation of Caveolin-1 Gene Expression in Lung Fibroblasts. American Journal of Respiratory Cell and Molecular Biology, 2017, 56, 50-61.	1.4	29
3614	Dependence-induced increase of alcohol self-administration and compulsive drinking mediated by the histone methyltransferase PRDM2. Molecular Psychiatry, 2017, 22, 1746-1758.	4.1	47
3615	Reprogramming of <scp>mPFC</scp> transcriptome and function in alcohol dependence. Genes, Brain and Behavior, 2017, 16, 86-100.	1.1	38
3616	Decrypting ENCODEd epigenetic marks of human tRN-A-RS genes in normal, stem and cancer cell lines. Journal of Biomolecular Structure and Dynamics, 2017, 35, 2759-2771.	2.0	0
3617	Regulatory cis-elements are located in accessible promoter regions of the CAT2 promoter and affect activating histone modifications in Arabidopsis thaliana. Plant Molecular Biology, 2017, 93, 49-60.	2.0	4
3618	Epigenetic Regulation of the Thermogenic Adipose Program. Trends in Endocrinology and Metabolism, 2017, 28, 19-31.	3.1	28
3619	InÂvitro reconstitution and biochemical analyses of the Schizosaccharomyces pombe nucleosome. Biochemical and Biophysical Research Communications, 2017, 482, 896-901.	1.0	10
3620	The epigenetic landscape of renal cancer. Nature Reviews Nephrology, 2017, 13, 47-60.	4.1	99
3621	The Effects of Replication Stress on S Phase Histone Management and Epigenetic Memory. Journal of Molecular Biology, 2017, 429, 2011-2029.	2.0	28
3622	Cistrome Data Browser: a data portal for ChIP-Seq and chromatin accessibility data in human and mouse. Nucleic Acids Research, 2017, 45, D658-D662.	6.5	451
3623	Transcriptional activation by MLL fusion proteins in leukemogenesis. Experimental Hematology, 2017, 46, 21-30.	0.2	32
3624	Activation and clustering of a <i>Plasmodium falciparum var</i> gene are affected by subtelomeric sequences. FEBS Journal, 2017, 284, 237-257.	2.2	9
3625	Genomeâ€wide DNA methylation analysis identifies <i>MEGF10</i> as a novel epigenetically repressed candidate tumor suppressor gene in neuroblastoma. Molecular Carcinogenesis, 2017, 56, 1290-1301.	1.3	23
3626	Identifying Nuclear Matrixâ€Attached DNA Across the Genome. Journal of Cellular Physiology, 2017, 232, 1295-1305.	2.0	19
3627	Differential deposition of H2A.Z in combination with histone modifications within related genes in Oryza sativa callus and seedling. Plant Journal, 2017, 89, 264-277.	2.8	38
3628	Evolution of the Human Genome I. Evolutionary Studies, 2017, , .	0.2	1
3629	Transcription Factor Genes. Evolutionary Studies, 2017, , 241-263.	0.2	1
3630	Defining baseline epigenetic landscapes in the rat liver. Epigenomics, 2017, 9, 1503-1527.	1.0	5

#	Article	IF	CITATIONS
3631	Revisiting medial preoptic area plasticity induced in male mice by sexual experience. Scientific Reports, 2017, 7, 17846.	1.6	21
3632	Regulation of H3K4me3 at Transcriptional Enhancers Characterizes Acquisition of Virus-Specific CD8+ T Cell-Lineage-Specific Function. Cell Reports, 2017, 21, 3624-3636.	2.9	53
3633	Erythropoietin Signaling Regulates Key Epigenetic and Transcription Networks in Fetal Neural Progenitor Cells. Scientific Reports, 2017, 7, 14381.	1.6	11
3634	Independence between pre-mRNA splicing and DNA methylation in an isogenic minigene resource. Nucleic Acids Research, 2017, 45, 12780-12797.	6.5	4
3635	Transcription factor-dependent â€~anti-repressive' mammalian enhancers exclude H3K27me3 from extended genomic domains. Genes and Development, 2017, 31, 2391-2404.	2.7	34
3636	DNA sequence+shape kernel enables alignment-free modeling of transcription factor binding. Bioinformatics, 2017, 33, 3003-3010.	1.8	25
3637	Higher-Order Chromatin Organization in Diseases: From Chromosomal Position Effect to Phenotype Variegation. , 2017, , 73-92.		4
3638	Putative enhancer sites in the bovine genome are enriched with variants affecting complex traits. Genetics Selection Evolution, 2017, 49, 56.	1.2	41
3639	Purification of nanogram-range immunoprecipitated DNA in ChIP-seq application. BMC Genomics, 2017, 18, 985.	1.2	34
3640	The Truncated Isoform of the Receptor Tyrosine Kinase ALK Generated by Alternative Transcription Initiation (ALK ^{ATI}) Induces Chromatin Structural Changes in the Nucleus in a Kinase Activity-Dependent Manner. Biological and Pharmaceutical Bulletin, 2017, 40, 1968-1975.	0.6	4
3641	Composition and dosage of a multipartite enhancer cluster control developmental expression of Ihh (Indian hedgehog). Nature Genetics, 2017, 49, 1539-1545.	9.4	107
3642	Ritornello: high fidelity control-free chromatin immunoprecipitation peak calling. Nucleic Acids Research, 2017, 45, e173-e173.	6.5	8
3643	Prediction of enhancer RNA activity levels from ChIP-seq-derived histone modification combinatorial codes. , 2017, , .		1
3644	Higher-order partial least squares for predicting gene expression levels from chromatin states. , 2017,		0
3645	Discover the semantic structure of human reference epigenome by differential latent dirichlet allocation. , 2017, , .		1
3647	Epigenetic Modifications to H3K9 in Renal Tubulointerstitial Cells after Unilateral Ureteric Obstruction and TGF-β1 Stimulation. Frontiers in Pharmacology, 2017, 8, 307.	1.6	38
3648	Potential New Therapies for Pediatric Diffuse Intrinsic Pontine Glioma. Frontiers in Pharmacology, 2017, 8, 495.	1.6	48
3649	Novel Function of a Transcription Factor WT1 in Regulating Decidualization in Human Endometrial Stromal Cells and Its Molecular Mechanism. Endocrinology, 2017, 158, 3696-3707.	1.4	23

		CITATION RE	PORT	
#	Article		IF	CITATIONS
3650	Epigenetic Modifications and Head and Neck Cancer: Implications for Tumor Progressi Resistance to Therapy. International Journal of Molecular Sciences, 2017, 18, 1506.	on and	1.8	129
3651	DNA methylation regulates discrimination of enhancers from promoters through a H31 seesaw mechanism. BMC Genomics, 2017, 18, 964.	(4me1-H3K4me3	1.2	80
3652	Role of Epigenetics in Uveal Melanoma. International Journal of Biological Sciences, 20	17, 13, 426-433.	2.6	33
3653	Epigenetics and alcohol use disorders. , 2017, , 361-397.			0
3654	Activating Mutations of the EZH2 Histone Methyltransferase in Cancer. , 2017, , 259-2	.88.		1
3655	The protective effect of PRMT6 overexpression on cigarette smoke extract-induced mu model. International Journal of COPD, 2017, Volume 12, 3245-3254.	rine emphysema	0.9	16
3656	Regulation of PRC2 Activity. , 2017, , 225-258.			0
3657	Epigenome Aberrations: Emerging Driving Factors of the Clear Cell Renal Cell Carcinon International Journal of Molecular Sciences, 2017, 18, 1774.	ha.	1.8	46
3658	GH/IGF-1 Signaling and Current Knowledge of Epigenetics; a Review and Consideratior Therapeutic Options. International Journal of Molecular Sciences, 2017, 18, 1624.	s on Possible	1.8	29
3659	Prenatal Exposure to a Maternal High-Fat Diet Affects Histone Modification of Cardion in Newborn Rats. Nutrients, 2017, 9, 407.	etabolic Genes	1.7	28
3660	Epigenetic Landscape during Coronavirus Infection. Pathogens, 2017, 6, 8.		1.2	96
3661	Regulation of zygotic gene activation by chromatin structure and epigenetic factors. Jo Reproduction and Development, 2017, 63, 359-363.	burnal of	0.5	13
3662	Forward and Reverse Genetics to Model Human Diseases in the Mouse. , 2017, , 727-7	52.		1
3663	Genome-Wide Epigenetic Studies in Chicken: A Review. Epigenomes, 2017, 1, 20.		0.8	11
3664	Matrix Metalloproteinase Gene Activation Resulting from Disordred Epigenetic Mechar Rheumatoid Arthritis. International Journal of Molecular Sciences, 2017, 18, 905.	nisms in	1.8	82
3665	T Cell Receptor and Cytokine Signaling Can Function at Different Stages to Establish a Transcriptional Memory and Enable T Helper Cell Differentiation. Frontiers in Immunolo 204.	nd Maintain 9gy, 2017, 8,	2.2	25
3666	The Lysine Methyltransferase G9a in Immune Cell Differentiation and Function. Frontie Immunology, 2017, 8, 429.	rs in	2.2	64
3667	"Multi-Omics―Analyses of the Development and Function of Natural Killer Cells. F Immunology, 2017, 8, 1095.	rontiers in	2.2	20

# 3668	ARTICLE Mechanisms of Histone Modifications. , 2017, , 25-46.	IF	CITATIONS 3
3669	The Histone Modification Code in the Pathogenesis of Autoimmune Diseases. Mediators of Inflammation, 2017, 2017, 1-12.	1.4	70
3670	Epigenetic Manipulation Facilitates the Generation of Skeletal Muscle Cells from Pluripotent Stem Cells. Stem Cells International, 2017, 2017, 1-8.	1.2	5
3671	Analyses of Genome-Wide Histone Modifications in the Mammalian Genome. , 2017, , 135-152.		1
3672	GTRD: a database of transcription factor binding sites identified by ChIP-seq experiments. Nucleic Acids Research, 2017, 45, D61-D67.	6.5	206
3673	DNA methylation at the mu-1 opioid receptor gene (OPRM1) promoter predicts preoperative, acute, and chronic postsurgical pain after spine fusion. Pharmacogenomics and Personalized Medicine, 2017, Volume 10, 157-168.	0.4	40
3674	Automatic identification of informative regions with epigenomic changes associated to hematopoiesis. Nucleic Acids Research, 2017, 45, 9244-9259.	6.5	19
3675	Krox20 hindbrain regulation incorporates multiple modes of cooperation between cis-acting elements. PLoS Genetics, 2017, 13, e1006903.	1.5	18
3676	Identification of the early and late responder genes during the generation of induced pluripotent stem cells from mouse fibroblasts. PLoS ONE, 2017, 12, e0171300.	1.1	6
3677	Muscle-relevant genes marked by stable H3K4me2/3 profiles and enriched MyoD binding during myogenic differentiation. PLoS ONE, 2017, 12, e0179464.	1.1	10
3678	Epigenetic Targeted Therapy for Diffuse Intrinsic Pontine Glioma. Neurologia Medico-Chirurgica, 2017, 57, 331-342.	1.0	36
3679	Functional convergence of histone methyltransferases EHMT1 and KMT2C involved in intellectual disability and autism spectrum disorder. PLoS Genetics, 2017, 13, e1006864.	1.5	116
3680	A conceptual and computational framework for modelling and understanding the non-equilibrium gene regulatory networks of mouse embryonic stem cells. PLoS Computational Biology, 2017, 13, e1005713.	1.5	7
3681	Genome-Wide Binding of Posterior HOXA/D Transcription Factors Reveals Subgrouping and Association with CTCF. PLoS Genetics, 2017, 13, e1006567.	1.5	38
3682	Host factors that promote retrotransposon integration are similar in distantly related eukaryotes. PLoS Genetics, 2017, 13, e1006775.	1.5	7
3683	Modular function of long noncoding RNA, COLDAIR, in the vernalization response. PLoS Genetics, 2017, 13, e1006939.	1.5	115
3684	Binding of high mobility group A proteins to the mammalian genome occurs as a function of AT-content. PLoS Genetics, 2017, 13, e1007102.	1.5	16
3685	ciRS-7 exonic sequence is embedded in a long non-coding RNA locus. PLoS Genetics, 2017, 13, e1007114.	1.5	66

# 3686	ARTICLE Application of dual reading domains as novel reagents in chromatin biology reveals a new H3K9me3 and H3K36me2/3 bivalent chromatin state. Epigenetics and Chromatin, 2017, 10, 45.	IF 1.8	CITATIONS 27
3687	Genome-wide profiling of transcribed enhancers during macrophage activation. Epigenetics and Chromatin, 2017, 10, 50.	1.8	41
3688	Software for rapid time dependent ChIP-sequencing analysis (TDCA). BMC Bioinformatics, 2017, 18, 521.	1.2	1
3689	Mechanism of Progesterone Action in the Brain. , 2017, , 181-214.		5
3690	The Epigenetic Link between Prenatal Adverse Environments and Neurodevelopmental Disorders. Genes, 2017, 8, 104.	1.0	134
3691	Recent Advancement in Methodology for Understanding Epigenetic Modifications. Journal of Clinical Epigenetics, 2017, 03, .	0.3	5
3692	LSD1 binds to HPV16 E7 and promotes the epithelial-mesenchymal transition in cervical cancer by demethylating histones at the Vimentin promoter. Oncotarget, 2017, 8, 11329-11342.	0.8	23
3693	Polycomb Function and Nuclear Organization. , 2017, , 131-163.		2
3694	Omicseq: a web-based search engine for exploring omics datasets. Nucleic Acids Research, 2017, 45, W445-W452.	6.5	11
3695	Nucleosome Positioning of Intronless Genes in the Human Genome. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 1111-1121.	1.9	3
3696	Transformation of Accessible Chromatin and 3D Nucleome Underlies Lineage Commitment of Early T Cells. Immunity, 2018, 48, 227-242.e8.	6.6	188
3697	Chromatin dynamics at the core of kidney fibrosis. Matrix Biology, 2018, 68-69, 194-229.	1.5	6
3698	A Non-catalytic Function of SETD1A Regulates Cyclin K and the DNA Damage Response. Cell, 2018, 172, 1007-1021.e17.	13.5	97
3699	BCL11B Drives Human Mammary Stem Cell Self-Renewal InÂVitro by Inhibiting Basal Differentiation. Stem Cell Reports, 2018, 10, 1131-1145.	2.3	9
3700	Application of the red fluorescent protein mCherry in mycelial labeling and organelle tracing in the dermatophyte Trichophyton mentagrophytes. FEMS Microbiology Letters, 2018, 365, .	0.7	5
3701	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
3702	ChIP-ping the branches of the tree: functional genomics and the evolution of eukaryotic gene regulation. Briefings in Functional Genomics, 2018, 17, 116-137.	1.3	5
3703	The Histone Variant MacroH2A Blocks Cellular Reprogramming by Inhibiting Mesenchymal-to-Epithelial Transition. Molecular and Cellular Biology, 2018, 38, .	1.1	13

#	Article	IF	CITATIONS
3704	PARP14 Controls the Nuclear Accumulation of a Subset of Type I IFN–Inducible Proteins. Journal of Immunology, 2018, 200, 2439-2454.	0.4	70
3705	Redox control in cancer development and progression. Molecular Aspects of Medicine, 2018, 63, 88-98.	2.7	103
3706	Low-input and multiplexed microfluidic assay reveals epigenomic variation across cerebellum and prefrontal cortex. Science Advances, 2018, 4, eaar8187.	4.7	35
3707	Functional Assays to Screen and Dissect Genomic Hits. Circulation Genomic and Precision Medicine, 2018, 11, e002178.	1.6	18
3708	Enhancer reprogramming in tumor progression: a new route towards cancer cell plasticity. Cellular and Molecular Life Sciences, 2018, 75, 2537-2555.	2.4	26
3709	Computational Methods for Assessing Chromatin Hierarchy. Computational and Structural Biotechnology Journal, 2018, 16, 43-53.	1.9	22
3710	Single-Cell Chromatin Modification Profiling Reveals Increased Epigenetic Variations with Aging. Cell, 2018, 173, 1385-1397.e14.	13.5	250
3711	Melatonin disturbs <scp>SUMO</scp> ylationâ€mediated crosstalk between câ€Myc and nestin via <scp>MT</scp> 1 activation and promotes the sensitivity of paclitaxel in brain cancer stem cells. Journal of Pineal Research, 2018, 65, e12496.	3.4	36
3712	Polymer physics predicts the effects of structural variants on chromatin architecture. Nature Genetics, 2018, 50, 662-667.	9.4	179
3713	Theoretical and Applied Epigenetics in Plants. , 2018, , 265-286.		0
3713 3714		4.5	0
	Theoretical and Applied Epigenetics in Plants. , 2018, , 265-286. Allosteric Activation Dictates PRC2 Activity Independent of Its Recruitment to Chromatin. Molecular	4.5	
3714	Theoretical and Applied Epigenetics in Plants. , 2018, , 265-286. Allosteric Activation Dictates PRC2 Activity Independent of Its Recruitment to Chromatin. Molecular Cell, 2018, 70, 422-434.e6. H3K36me3-mediated mismatch repair preferentially protects actively transcribed genes from mutation.		100
3714 3715	Theoretical and Applied Epigenetics in Plants. , 2018, , 265-286. Allosteric Activation Dictates PRC2 Activity Independent of Its Recruitment to Chromatin. Molecular Cell, 2018, 70, 422-434.e6. H3K36me3-mediated mismatch repair preferentially protects actively transcribed genes from mutation. Journal of Biological Chemistry, 2018, 293, 7811-7823.		100 77
3714 3715 3716	Theoretical and Applied Epigenetics in Plants. , 2018, , 265-286. Allosteric Activation Dictates PRC2 Activity Independent of Its Recruitment to Chromatin. Molecular Cell, 2018, 70, 422-434.e6. H3K36me3-mediated mismatch repair preferentially protects actively transcribed genes from mutation. Journal of Biological Chemistry, 2018, 293, 7811-7823. Applied RNA Bioscience. , 2018, , . Targeted in situ genome-wide profiling with high efficiency for low cell numbers. Nature Protocols,	1.6	100 77 1
3714 3715 3716 3717	Theoretical and Applied Epigenetics in Plants. , 2018, , 265-286. Allosteric Activation Dictates PRC2 Activity Independent of Its Recruitment to Chromatin. Molecular Cell, 2018, 70, 422-434.e6. H3K36me3-mediated mismatch repair preferentially protects actively transcribed genes from mutation. Journal of Biological Chemistry, 2018, 293, 7811-7823. Applied RNA Bioscience. , 2018, , . Targeted in situ genome-wide profiling with high efficiency for low cell numbers. Nature Protocols, 2018, 13, 1006-1019. FOXF1 Inhibits Pulmonary Fibrosis by Preventing CDH2-CDH11 Cadherin Switch in Myofibroblasts. Cell	1.6 5.5	100 77 1 572
3714 3715 3716 3717 3718	Theoretical and Applied Epigenetics in Plants. , 2018, , 265-286. Allosteric Activation Dictates PRC2 Activity Independent of Its Recruitment to Chromatin. Molecular Cell, 2018, 70, 422-434.e6. H3K36me3-mediated mismatch repair preferentially protects actively transcribed genes from mutation. Journal of Biological Chemistry, 2018, 293, 7811-7823. Applied RNA Bioscience. , 2018, , . Targeted in situ genome-wide profiling with high efficiency for low cell numbers. Nature Protocols, 2018, 13, 1006-1019. FOXF1 Inhibits Pulmonary Fibrosis by Preventing CDH2-CDH11 Cadherin Switch in Myofibroblasts. Cell Reports, 2018, 23, 442-458. PHF20 collaborates with PARP1 to promote stemness and aggressiveness of neuroblastoma cells	1.6 5.5 2.9	100 77 1 572 64

		CITATION RE	PORT	
#	Article		IF	CITATIONS
3722	Visualizing transcription factor dynamics in living cells. Journal of Cell Biology, 2018, 2	17, 1181-1191.	2.3	159
3723	Features and regulation of non-enzymatic post-translational modifications. Nature Che 2018, 14, 244-252.	emical Biology,	3.9	118
3724	Ring1A and Ring1B inhibit expression of Glis2 to maintain murine MOZ-TIF2 AML stem 131, 1833-1845.	cells. Blood, 2018,	0.6	15
3725	Human ex vivo prostate tissue model system identifies ING3 as an oncoprotein. British Cancer, 2018, 118, 713-726.	Journal of	2.9	28
3726	From Genotype to Phenotype. Circulation Genomic and Precision Medicine, 2018, 11,		1.6	16
3727	Double duty: ZMYND8 in the DNA damage response and cancer. Cell Cycle, 2018, 17,	414-420.	1.3	26
3728	The chromatin basis of neurodevelopmental disorders: Rethinking dysfunction along tl and temporal axes. Progress in Neuro-Psychopharmacology and Biological Psychiatry, 2		2.5	73
3729	The IncRNA GATA6-AS epigenetically regulates endothelial gene expression via interact Nature Communications, 2018, 9, 237.	ion with LOXL2.	5.8	154
3730	Octopus-toolkit: a workflow to automate mining of public epigenomic and transcripto next-generation sequencing data. Nucleic Acids Research, 2018, 46, e53-e53.	mic	6.5	61
3731	LSD1 interacts with cMYB to demethylate repressive histone marks and maintains inne identity. Development (Cambridge), 2018, 145, .	er ear progenitor	1.2	16
3732	Beyond the genetic code in leaf senescence. Journal of Experimental Botany, 2018, 69	, 801-810.	2.4	45
3733	Epigenetics, microbiota, and intraocular inflammation: New paradigms of immune regueree. Progress in Retinal and Eye Research, 2018, 64, 84-95.	lation in the	7.3	46
3734	Nuclear receptors in cancer — uncovering new and evolving roles through genomic a Reviews Genetics, 2018, 19, 160-174.	nalysis. Nature	7.7	74
3735	MLL2 conveys transcription-independent H3K4 trimethylation in oocytes. Nature Struc Molecular Biology, 2018, 25, 73-82.	tural and	3.6	127
3736	Trithoraxâ€group proteins ARABIDOPSIS TRITHORAX4 (ATX4) and <scp>ATX</scp> 5 f acid and dehydration stress responses. New Phytologist, 2018, 217, 1582-1597.	unction in abscisic	3.5	59
3737	Characterization of H3.3 and HIRA expression and function in bovine early embryos. M Reproduction and Development, 2018, 85, 106-116.	olecular	1.0	8
3738	Polycomb Repressive Complex 2: Emerging Roles in the Central Nervous System. Neuro 24, 208-220.	oscientist, 2018,	2.6	22
3739	Phf8 histone demethylase deficiency causes cognitive impairments through the mTOR Communications, 2018, 9, 114.	pathway. Nature	5.8	47

ARTICLE IF CITATIONS LeNup: learning nucleosome positioning from DNA sequences with improved convolutional neural 3740 34 1.8 networks. Bioinformatics, 2018, 34, 1705-1712. Transcriptional interference by small transcripts in proximal promoter regions. Nucleic Acids 3741 6.5 Research, 2018, 46, 1069-1088. Epigenetics of breast cancer: Biology and clinical implication in the era of precision medicine. 3742 4.3 115 Seminars in Cancer Biology, 2018, 51, 22-35. Dynamics of promoter bivalency and RNAP II pausing in mouse stem and differentiated cells. BMC 3743 Developmental Biology, 2018, 18, 2. Position-specific intron retention is mediated by the histone methyltransferase SDG725. BMC Biology, 3744 1.7 41 2018, 16, 44. Transcriptional activator DOT1L putatively regulates human embryonic stem cell differentiation into 2.4 the cardiac lineage. Stem Cell Research and Therapy, 2018, 9, 97. Multiple functions of m6A RNA methylation in cancer. Journal of Hematology and Oncology, 2018, 11, 3746 6.9 255 48. Towards a map of cis-regulatory sequences in the human genome. Nucleic Acids Research, 2018, 46, 3747 6.5 5395-5409. Epigenetic regulation of transcriptional plasticity associated with developmental song learning. 3748 1.2 21 Proceedings of the Royal Society B: Biological Sciences, 2018, 285, 20180160. SUN2 Modulates HIV-1 Infection and Latency through Association with Lamin A/C To Maintain the 3749 1.8 Repressive Chromatin. MBio, 2018, 9, . <i>Toxoplasma gondii</i> Histone 4 Affects Some Functions of Murine Anaâ€1 Macrophages In Vitro. 3750 4 0.8 Journal of Eukaryotic Microbiology, 2018, 65, 860-869. Reappraising Preclinical Models of Separation Anxiety Disorder, Panic Disorder, and CO2 Sensitivity: Implications for Methodology and Translation into New Treatments. Current Topics in Behavioral Neurosciences, 2018, 40, 195-217. 0.8 Genome-Wide Mapping of Protein–DNA Interactions on Nascent Chromatin. Methods in Molecular 3753 0.4 11 Biology, 2018, 1766, 231-238. Potentially Functional Variants of ATG16L2 Predict Radiation Pneumonitis and Outcomes in Patients with Non–Small Cell Lung Cancer after Definitive Radiotherapy. Journal of Thoracic Oncology, 2018, 3754 29 13,660-675. Mutant IDH1 Cooperates with ATRX Loss to Drive the Alternative Lengthening of Telomere Phenotype in 3755 0.4 63 Glioma. Cancer Research, 2018, 78, 2966-2977. A decade of ChIP-seq. Briefings in Functional Genomics, 2018, 17, 77-79. Enhancer Activation by Pharmacologic Displacement of LSD1 from GFI1 Induces Differentiation in 3757 2.9 146 Acute Myeloid Leukemia. Cell Reports, 2018, 22, 3641-3659. Genome-Wide Association Studies and Heritability Estimation in the Functional Genomics Era. 3758 Population Genomics, 2018, , 361-425.

#	Article	IF	CITATIONS
3759	Three-dimensional organization and dynamics of the genome. Cell Biology and Toxicology, 2018, 34, 381-404.	2.4	41
3760	Satellite DNA evolution: old ideas, new approaches. Current Opinion in Genetics and Development, 2018, 49, 70-78.	1.5	142
3761	Mapping transcription factor occupancy using minimal numbers of cells in vitro and in vivo. Genome Research, 2018, 28, 592-605.	2.4	46
3762	A survey of recently emerged genome-wide computational enhancer predictor tools. Computational Biology and Chemistry, 2018, 74, 132-141.	1.1	29
3763	SEASTAR: systematic evaluation of alternative transcription start sites in RNA. Nucleic Acids Research, 2018, 46, e45-e45.	6.5	17
3764	Chromatin Immunoprecipitation and High-Throughput Sequencing (ChIP-Seq): Tips and Tricks Regarding the Laboratory Protocol and Initial Downstream Data Analysis. Methods in Molecular Biology, 2018, 1767, 271-288.	0.4	2
3765	Zinc Fingers, TALEs, and CRISPR Systems: A Comparison of Tools for Epigenome Editing. Methods in Molecular Biology, 2018, 1767, 19-63.	0.4	73
3766	Disease Mechanisms of <i>C9ORF72</i> Repeat Expansions. Cold Spring Harbor Perspectives in Medicine, 2018, 8, a024224.	2.9	75
3767	Evolution of Brain Active Gene Promoters in Human Lineage Towards the Increased Plasticity of Gene Regulation. Molecular Neurobiology, 2018, 55, 1871-1904.	1.9	12
3768	Inhibitors of Protein Methyltransferases and Demethylases. Chemical Reviews, 2018, 118, 989-1068.	23.0	222
3769	Histone methylation in the freeze-tolerant wood frog (Rana sylvatica). Journal of Comparative Physiology B: Biochemical, Systemic, and Environmental Physiology, 2018, 188, 113-125.	0.7	22
3770	Long Noncoding RNAs and Cardiac Disease. Antioxidants and Redox Signaling, 2018, 29, 880-901.	2.5	64
3771	Orchestration of H3K27 methylation: mechanisms and therapeutic implication. Cellular and Molecular Life Sciences, 2018, 75, 209-223.	2.4	61
3772	The impact of epigenomic nextâ€generation sequencing approaches on our understanding of neuropsychiatric disorders. Clinical Genetics, 2018, 93, 467-480.	1.0	11
3773	Basil polysaccharide attenuates hepatocellular carcinoma metastasis in rat by suppressing H3K9me2 histone methylation under hepatic artery ligation-induced hypoxia. International Journal of Biological Macromolecules, 2018, 107, 2171-2179.	3.6	19
3774	Transcription: Insights From the HIV-1 Promoter. International Review of Cell and Molecular Biology, 2018, 335, 191-243.	1.6	48
3775	The Evolution of Gene-Specific Transcriptional Noise Is Driven by Selection at the Pathway Level. Genetics, 2018, 208, 173-189.	1.2	41
3776	Genome-wide association study and meta-analysis in multiple populations identifies new loci for peanut allergy and establishes C11orf30/EMSY as a genetic risk factor for food allergy. Journal of Allergy and Clinical Immunology, 2018, 141, 991-1001.	1.5	57

			0
#	ARTICLE	IF	CITATIONS
3777	How low can you go? Pushing the limits of low-input ChIP-seq. Briefings in Functional Genomics, 2018, 17, 89-95.	1.3	15
3778	Epigenetics in multiple myeloma: From mechanisms to therapy. Seminars in Cancer Biology, 2018, 51, 101-115.	4.3	59
3779	Genome-wide analysis of SU(VAR)3-9 distribution in chromosomes of Drosophila melanogaster. Chromosoma, 2018, 127, 85-102.	1.0	7
3780	Early-Life Adversity and Suicide Risk: The Role of Epigenetics. , 2018, , 39-49.		1
3781	Phenomenology of Suicide. , 2018, , .		9
3782	Transcriptome Alterations in Posttraumatic Stress Disorder. Biological Psychiatry, 2018, 83, 840-848.	0.7	36
3783	MiR-17-5p enhances pancreatic cancer proliferation by altering cell cycle profiles via disruption of RBL2/E2F4-repressing complexes. Cancer Letters, 2018, 412, 59-68.	3.2	75
3784	Targeting Epigenetics in Cancer. Annual Review of Pharmacology and Toxicology, 2018, 58, 187-207.	4.2	185
3785	T Helper Cell Differentiation, Heterogeneity, and Plasticity. Cold Spring Harbor Perspectives in Biology, 2018, 10, a030338.	2.3	222
3786	Dominant-negative SMARCA4 mutants alter the accessibility landscape of tissue-unrestricted enhancers. Nature Structural and Molecular Biology, 2018, 25, 61-72.	3.6	140
3787	Label-free detection of histone based on cationic conjugated polymer-mediated fluorescence resonance energy transfer. Talanta, 2018, 180, 150-155.	2.9	9
3788	Prenatal influences on temperament development: The role of environmental epigenetics. Development and Psychopathology, 2018, 30, 1269-1303.	1.4	110
3789	Target specificity of mammalian DNA methylation and demethylation machinery. Organic and Biomolecular Chemistry, 2018, 16, 1419-1435.	1.5	43
3790	A Role for Monomethylation of Histone H3-K27 in Gene Activity in <i>Drosophila</i> . Genetics, 2018, 208, 1023-1036.	1.2	11
3791	Effects of adolescent social stress and antidepressant treatment on cognitive inflexibility and Bdnf epigenetic modifications in the mPFC of adult mice. Psychoneuroendocrinology, 2018, 88, 92-101.	1.3	48
3792	Nervous system development and disease: A focus on trithorax related proteins and chromatin remodelers. Molecular and Cellular Neurosciences, 2018, 87, 46-54.	1.0	16
3793	<i>Treponema denticola</i> increases MMP-2 expression and activation in the periodontium via reversible DNA and histone modifications. Cellular Microbiology, 2018, 20, e12815.	1.1	20
3794	Arsenite downregulates H3K4 trimethylation and H3K9 dimethylation during transformation of human bronchial epithelial cells. Journal of Applied Toxicology, 2018, 38, 480-488.	1.4	8

		CITATION REF	PORT	
#	Article		IF	CITATIONS
3795	Changes in chromatin state reveal ARNT2 at a node of a tumorigenic transcription factor sig driving glioblastoma cell aggressiveness. Acta Neuropathologica, 2018, 135, 267-283.	nature	3.9	19
3796	Elucidation of the Two H3K36me3 Histone Methyltransferases Set2 and Ash1 in <i>Fusariun fujikuroi</i> Unravels Their Different Chromosomal Targets and a Major Impact of Ash1 on C Stability. Genetics, 2018, 208, 153-171.		1.2	61
3797	Evidence for the implication of the histone code in building the genome structure. BioSyster 164, 49-59.	ns, 2018,	0.9	52
3798	Dynamic transcriptional control of macrophage miRNA signature via inflammation responsiv enhancers revealed using a combination of next generation sequencing-based approaches. E Et Biophysica Acta - Gene Regulatory Mechanisms, 2018, 1861, 14-28.	e Biochimica	0.9	8
3799	Deciphering adipose tissue heterogeneity. Annals of the New York Academy of Sciences, 202	18, 1411, 5-20.	1.8	77
3800	Novel epigenetic therapies in hematological malignancies: Current status and beyond. Semir Cancer Biology, 2018, 51, 198-210.	hars in	4.3	22
3801	Epigenomics. , 2018, , 258-265.			5
3802	Histone methyltransferase SUV39H2 serves oncogenic roles in osteosarcoma. Oncology Rep 41, 325-332.	oorts, 2018,	1.2	7
3803	The Landscape of Histone Modification in Cancer Metastasis. , 2018, , .			1
3804	Dempster-Shafer Theory for the Prediction of Auxin-Response Elements (AuxREs) in Plant Ge BioMed Research International, 2018, 2018, 1-13.	nomes.	0.9	4
3805	The Interplay between Transcription Factors and Epigenetic Modifications in Th2 Cells. , 201	8, , .		1
3806	Epigenetic Biomarkers for Risk Assessment of Particulate Matter Associated Lung Cancer. Co Drug Targets, 2018, 19, 1127-1147.	urrent	1.0	28
3807	Nucleosome Positioning and Its Role in Gene Regulation in Yeast. , 2018, , .			1
3809	From Single Level Analysis to Multi-Omics Integrative Approaches: A Powerful Strategy towa Precision Oncology. High-Throughput, 2018, 7, 33.	rds the	4.4	48
3810	The Heterochromatin Landscape in Migrating Cells and the Importance of H3K27me3 for Ast Transcriptome Alterations. Cells, 2018, 7, 205.	sociated	1.8	26
3811	Highly Selective 5-Formyluracil Labeling and Genome-wide Mapping Using (2-Benzimidazolyl)Acetonitrile Probe. IScience, 2018, 9, 423-432.		1.9	18
3812	Coordinate regulation of long non-coding RNAs and protein-coding genes in germ-free mice. Genomics, 2018, 19, 834.	ВМС	1.2	47
3813	A Rat Methyl-Seq Platform to Identify Epigenetic Changes Associated with Stress Exposure. J Visualized Experiments, 2018, , .	ournal of	0.2	3

#	Article	IF	CITATIONS
3814	Tackling malignant melanoma epigenetically: histone lysine methylation. Clinical Epigenetics, 2018, 10, 145.	1.8	26
3815	Histone H3 lysine 4 methylation signature associated with human undernutrition. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E11264-E11273.	3.3	23
3816	RNome and Chromatin Dynamics. , 2018, , 79-112.		0
3817	Distinct Roles of Two Histone Methyltransferases in Transmitting H3K36me3-Based Epigenetic Memory Across Generations in <i>Caenorhabditis elegans</i> . Genetics, 2018, 210, 969-982.	1.2	38
3818	The Regulation and Function of Histone Methylation. Journal of Plant Biology, 2018, 61, 347-357.	0.9	10
3819	Genomeâ€Wide Maps of Transcription Regulatory Elements and Transcription Enhancers in Development and Disease. , 2018, 9, 439-455.		12
3820	Chromatin Accessibility and Interactions in the Transcriptional Regulation of T Cells. Frontiers in Immunology, 2018, 9, 2738.	2.2	36
3821	EZH2 variants differentially regulate polycomb repressive complex 2 in histone methylation and cell differentiation. Epigenetics and Chromatin, 2018, 11, 71.	1.8	28
3822	Genetic accommodation and the role of ancestral plasticity in the evolution of insect eusociality. Journal of Experimental Biology, 2018, 221, .	0.8	20
3823	MAGEA1 inhibits the expression of BORIS via increased promoter methylation. Journal of Cell Science, 2018, 132, .	1.2	3
3824	Agnostic detection of genomic alterations by holistic DNA structural interrogation. PLoS ONE, 2018, 13, e0208054.	1.1	1
3825	The Histone H3 Lysine 4 Presenter WDR5 as an Oncogenic Protein and Novel Epigenetic Target in Cancer. Frontiers in Oncology, 2018, 8, 502.	1.3	67
3826	Molecular Lesions of Insulator CTCF and Its Paralogue CTCFL (BORIS) in Cancer: An Analysis from Published Genomic Studies. High-Throughput, 2018, 7, 30.	4.4	8
3827	MYC Interacts with the G9a Histone Methyltransferase to Drive Transcriptional Repression and Tumorigenesis. Cancer Cell, 2018, 34, 579-595.e8.	7.7	94
3828	Enhancement of transgene expression by nuclear transcription factor Y and CCCTCâ€binding factor. Biotechnology Progress, 2018, 34, 1581-1588.	1.3	7
3829	Molecular Mechanisms of Transdifferentiation of Adipose-Derived Stem Cells into Neural Cells: Current Status and Perspectives. Stem Cells International, 2018, 2018, 1-14.	1.2	15
3830	SETting up Methylation in Mammalian Cells: Role of Histone Methyltransferases in Disease and Development. , 2018, , 197-258.		0
3831	Waves of chromatin modifications in mouse dendritic cells in response to LPS stimulation. Genome Biology, 2018, 19, 138.	3.8	19

#	Article	IF	CITATIONS
3832	Low-cost HPV testing and the prevalence of cervical infection in asymptomatic populations in Guatemala. BMC Cancer, 2018, 18, 562.	1.1	9
3833	Overexpression of IL-9 induced by STAT3 phosphorylation is mediated by miR-155 and miR-21 in chronic lymphocytic leukemia. Oncology Reports, 2018, 39, 3064-3072.	1.2	13
3834	Thermal Response of Epigenetic Genes Informs Turtle Sex Determination with and without Sex Chromosomes. Sexual Development, 2018, 12, 308-319.	1.1	30
3835	The gene repressor complex NuRD interacts with the histone variant H3.3 at promoters of active genes. Genome Research, 2018, 28, 1646-1655.	2.4	17
3836	LncRNA HOTAIR regulates lipopolysaccharide-induced cytokine expression and inflammatory response in macrophages. Scientific Reports, 2018, 8, 15670.	1.6	74
3837	Engineering Lineage Potency and Plasticity of Stem Cells using Epigenetic Molecules. Scientific Reports, 2018, 8, 16289.	1.6	5
3838	Spindlinâ€I recognizes methylations of K20 and R23 of histone H4 tail. FEBS Letters, 2018, 592, 4098-4110.	1.3	12
3839	SETD2-dependent H3K36me3 plays a critical role in epigenetic regulation of the HPV31 life cycle. PLoS Pathogens, 2018, 14, e1007367.	2.1	18
3840	The Emerging Role of Epigenetics. Translational Bioinformatics, 2018, , 65-101.	0.0	1
3841	The KDM4A/KDM4C/NF-ήB and WDR5 epigenetic cascade regulates the activation of B cells. Nucleic Acids Research, 2018, 46, 5547-5560.	6.5	34
3842	Genomic Analysis of DNA Double-Strand Break Repair in Escherichia coli. Methods in Enzymology, 2018, 612, 523-554.	0.4	3
3844	Histone H3K9 demethylase JMJD2B induces hepatic steatosis through upregulation of PPARÎ ³ 2. Scientific Reports, 2018, 8, 13734.	1.6	23
3845	Impact of human sepsis on CCCTC-binding factor associated monocyte transcriptional response of Major Histocompatibility Complex II components. PLoS ONE, 2018, 13, e0204168.	1.1	7
3846	Topokaryotyping demonstrates single cell variability and stress dependent variations in nuclear envelope associated domains. Nucleic Acids Research, 2018, 46, e135-e135.	6.5	3
3847	Alternative splicing links histone modifications to stem cell fate decision. Genome Biology, 2018, 19, 133.	3.8	53
3849	Epigenome-Based Precision Medicine in Lung Cancer. Methods in Molecular Biology, 2018, 1856, 57-85.	0.4	5
3850	Sequence-based 5-mers highly correlated to epigenetic modifications in genes interactions. Genes and Genomics, 2018, 40, 1363-1371.	0.5	1
3851	Epigenetic mechanisms regulating T-cell responses. Journal of Allergy and Clinical Immunology, 2018, 142, 728-743.	1.5	100

#	Article	IF	CITATIONS
3852	The biological significance of histone modifiers in multiple myeloma: clinical applications. Blood Cancer Journal, 2018, 8, 83.	2.8	30
3853	Genomic Location of PRMT6-Dependent H3R2 Methylation Is Linked to the Transcriptional Outcome of Associated Genes. Cell Reports, 2018, 24, 3339-3352.	2.9	38
3854	Classifying Included and Excluded Exons in Exon Skipping Event Using Histone Modifications. Frontiers in Genetics, 2018, 9, 433.	1.1	23
3857	Examining the Roles of H3K4 Methylation States with Systematically Characterized Antibodies. Molecular Cell, 2018, 72, 162-177.e7.	4.5	90
3858	Inter-nucleosomal communication between histone modifications for nucleosome phasing. PLoS Computational Biology, 2018, 14, e1006416.	1.5	3
3859	Suv4‑20h1 promotes G1 to S phase transition by downregulating p21WAF1/CIP1 expression in chronic myeloid leukemia K562 cells. Oncology Letters, 2018, 15, 6123-6130.	0.8	6
3860	PRDM9, a driver of the genetic map. PLoS Genetics, 2018, 14, e1007479.	1.5	85
3861	Epioncogene Networks: Identification of Epigenomic and Transcriptomic Cooperation by Multi-omics Integration of ChIP-Seq and RNA-Seq Data. RNA Technologies, 2018, , 129-151.	0.2	1
3862	DNA mismatch repair preferentially safeguards actively transcribed genes. DNA Repair, 2018, 71, 82-86.	1.3	24
3863	Ablation of Ezh2 in neural crest cells leads to aberrant enteric nervous system development in mice. PLoS ONE, 2018, 13, e0203391.	1.1	13
3864	Hypoxia-inducible KDM3A addiction in multiple myeloma. Blood Advances, 2018, 2, 323-334.	2.5	50
3865	STAT5 is essential for IL-7–mediated viability, growth, and proliferation of T-cell acute lymphoblastic leukemia cells. Blood Advances, 2018, 2, 2199-2213.	2.5	58
3866	Mining for Structural Variations in Next-Generation Sequencing Data. , 2018, , .		0
3867	Computational functional genomics-based approaches in analgesic drug discovery and repurposing. Pharmacogenomics, 2018, 19, 783-797.	0.6	23
3868	CARIP-Seq and ChIP-Seq: Methods to Identify Chromatin-Associated RNAs and Protein-DNA Interactions in Embryonic Stem Cells. Journal of Visualized Experiments, 2018, , .	0.2	2
3869	Targeted inhibition of histone H3K27 demethylation is effective in high-risk neuroblastoma. Science Translational Medicine, 2018, 10, .	5.8	70
3870	KDM5B decommissions the H3K4 methylation landscape of self-renewal genes during trophoblast stem cell differentiation. Biology Open, 2018, 7, .	0.6	20
3871	Analysis of ChIP-Seq and RNA-Seq Data with BioWardrobe. Methods in Molecular Biology, 2018, 1783, 343-360.	0.4	11

#	Article		CITATIONS
3872	Advances of DNase-seq for mapping active gene regulatory elements across the genome in animals. Gene, 2018, 667, 83-94.	1.0	20
3873	Gene Expression Analysis. Methods in Molecular Biology, 2018, , .	0.4	3
3874	Microfluidic Low-Input Fluidized-Bed Enabled ChIP-seq Device for Automated and Parallel Analysis of Histone Modifications. Analytical Chemistry, 2018, 90, 7666-7674.	3.2	18
3875	Two-Hybrid Systems. Methods in Molecular Biology, 2018, , .	0.4	1
3876	MLL4 Is Required to Maintain Broad H3K4me3 Peaks and Super-Enhancers at Tumor Suppressor Genes. Molecular Cell, 2018, 70, 825-841.e6.	4.5	123
3877	Integrating ChIP-seq with other functional genomics data. Briefings in Functional Genomics, 2018, 17, 104-115.	1.3	63
3878	Long noncoding RNAs exchange during zygotic genome activation in goatâ€. Biology of Reproduction, 2018, 99, 707-717.	1.2	48
3879	Epigenetic mechanisms as a new approach in cancer treatment: An updated review. Genes and Diseases, 2018, 5, 304-311.	1.5	146
3880	Selective DOT1L, LSD1, and HDAC Class I Inhibitors Reduce HOXA9 Expression in MLL-AF9 Rearranged Leukemia Cells, But Dysregulate the Expression of Many Histone-Modifying Enzymes. Journal of Proteome Research, 2018, 17, 2657-2667.	1.8	17
3881	Crosstalk between metabolism and epigenetic modifications in autoimmune diseases: a comprehensive overview. Cellular and Molecular Life Sciences, 2018, 75, 3353-3369.	2.4	40
3882	Methods and Strategies to Determine Epigenetic Variation in Human Disease. , 2018, , 13-37.		2
3883	Alterations of Histone Modifications in Cancer. , 2018, , 141-217.		10
3884	The histone methyltransferase SETD1A regulates thrombomodulin transcription in vascular endothelial cells. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2018, 1861, 752-761.	0.9	48
3885	Eukaryotic core promoters and the functional basis of transcription initiation. Nature Reviews Molecular Cell Biology, 2018, 19, 621-637.	16.1	480
3886	Type 2 Immunity. Methods in Molecular Biology, 2018, , .	0.4	1
3887	The Molecular Basis of the Gastrula Organizer in Amphibians and Cnidarians. Diversity and Commonality in Animals, 2018, , 667-708.	0.7	3
3888	Histones and heart failure in diabetes. Cellular and Molecular Life Sciences, 2018, 75, 3193-3213.	2.4	23
3889	Histone methylation changes are required for life cycle progression in the human parasite Schistosoma mansoni. PLoS Pathogens, 2018, 14, e1007066.	2.1	57

#	Article	IF	CITATIONS
3890	Nonprotein-coding RNAs in Fetal Alcohol Spectrum Disorders. Progress in Molecular Biology and Translational Science, 2018, 157, 299-342.	0.9	14
3891	Emerging Role of Epigenetics in Human Neurodevelopmental Disorders. , 2018, , 269-304.		1
3892	Mapping dynamic histone modification patterns during arsenic-induced malignant transformation of human bladder cells. Toxicology and Applied Pharmacology, 2018, 355, 164-173.	1.3	18
3893	Methyl-CpG-binding (SmMBD2/3) and chromobox (SmCBX) proteins are required for neoblast proliferation and oviposition in the parasitic blood fluke Schistosoma mansoni. PLoS Pathogens, 2018, 14, e1007107.	2.1	16
3894	Chromatin Preparation from Murine Eosinophils for Genome-Wide Analyses. Methods in Molecular Biology, 2018, 1799, 265-274.	0.4	0
3895	The Epigenetics of Primary Biliary Cholangitis. , 2018, , 251-272.		0
3896	Inference of Developmental Gene Regulatory Networks Beyond Classical Model Systems: New Approaches in the Post-genomic Era. Integrative and Comparative Biology, 2018, 58, 640-653.	0.9	13
3897	GenoGAM 2.0: scalable and efficient implementation of genome-wide generalized additive models for gigabase-scale genomes. BMC Bioinformatics, 2018, 19, 247.	1.2	1
3898	Epigenetics in ovarian cancer: premise, properties, and perspectives. Molecular Cancer, 2018, 17, 109.	7.9	87
3899	A novel extended form of alpha-synuclein 3′UTR in the human brain. Molecular Brain, 2018, 11, 29.	1.3	12
3901	Fetal nucleic acids in maternal plasma from biology to clinical translation. Frontiers in Bioscience - Landmark, 2018, 23, 397-431.	3.0	9
3902	Plant Cell Culture Protocols. Methods in Molecular Biology, 2018, , .	0.4	14
3903	Mechanistic Insights Into the Interaction Between Transcription Factors and Epigenetic Modifications and the Contribution to the Development of Obesity. Frontiers in Endocrinology, 2018, 9, 370.	1.5	52
3904	Super-Resolution Imaging of Higher-Order Chromatin Structures at Different Epigenomic States in Single Mammalian Cells. Cell Reports, 2018, 24, 873-882.	2.9	141
3905	Global epigenetic analysis of BDNF Val66Met mice hippocampus reveals changes in dendrite and spine remodeling genes. Hippocampus, 2018, 28, 783-795.	0.9	13
3906	H4K20me3 co-localizes with activating histone modifications at transcriptionally dynamic regions in embryonic stem cells. BMC Genomics, 2018, 19, 514.	1.2	23
3907	Bioinformatic Analysis of Nucleosome and Histone Variant Positioning. Methods in Molecular Biology, 2018, 1832, 185-203.	0.4	1
3908	Human Artificial Chromosome with Regulated Centromere: A Tool for Genome and Cancer Studies. ACS Synthetic Biology, 2018, 7, 1974-1989.	1.9	26

ARTICLE IF CITATIONS Epigenetic Maintenance of Acquired Gene Expression Programs during Memory CD8 T Cell 3910 2.2 29 Homeostasis. Frontiers in Immunology, 2018, 9, 6. Potential Epigenetic Regulation in the Germinal Center Reaction of Lymphoid Tissues in HIV/SIV 2.2 Infection. Frontiers in Immunology, 2018, 9, 159. Dendritic Cells Actively Limit Interleukin-10 Production Under Inflammatory Conditions via DC-SCRIPT 3912 2.2 16 and Dual-Specificity Phosphatase 4. Frontiers in Immunology, 2018, 9, 1420. Chromatin Binding of c-REL and p65 Is Not Limiting for Macrophage IL12B Transcription During Immediate Suppression by Ovarian Carcinoma Ascites. Frontiers in Immunology, 2018, 9, 1425. Altered Gene-Regulatory Function of KDM5C by a Novel Mutation Associated With Autism and 3914 1.4 52 Intellectual Disability. Frontiers in Molecular Neuroscience, 2018, 11, 104. Bioinformatics of Epigenomic Data Generated From Next-Generation Sequencing., 2018, , 65-106. Selective modulation of local linkages between active transcription and oxidative demethylation 3916 1.2 4 activity shapes cardiomyocyte-specific gene-body epigenetic status in mice. BMC Genomics, 2018, 19, 349. Chromatin Immunoprecipitation (ChiP) Protocol for the Analysis of Gene Regulation by Histone 3917 0.4 Modifications in Agave angustifolia Haw. Methods in Molecular Biology, 2018, 1815, 371-383. Gestational exposure to chlordecone promotes transgenerational changes in the murine 3918 22 1.6 reproductive system of males. Scientific Reports, 2018, 8, 10274. DNA Methylation and Histone Modification in Hypertension. International Journal of Molecular 3919 1.8 74 Sciences, 2018, 19, 1174. Epigenetic Modulation of CD8+ T Cell Function in Lentivirus Infections: A Review. Viruses, 2018, 10, 227. 3920 2 1.5 3921 Therapy of Infectious Diseases Using Epigenetic Approaches., 2018, , 689-715. H3K4me2 and WDR5 enriched chromatin interacting long non-coding RNAs maintain transcriptionally 3922 6.5 28 competent chromatin at divergent transcriptional units. Nucleic Acids Research, 2018, 46, 9384-9400. Transcription factor <scp>ABI</scp>3 autoâ€activates its own expression during dehydration stress response. FEBS Letters, 2018, 592, 2594-2611. 1.3 Rpd3L HDAC links H3K4me3 to transcriptional repression memory. Nucleic Acids Research, 2018, 46, 3924 6.5 41 8261-8274. Epigenetic regulation in development: is the mouse a good model for the human?. Human Reproduction 5.2 99 Update, 2018, 24, 556-576. Nup153 Unlocks the Nuclear Pore Complex for HIV-1 Nuclear Translocation in Nondividing Cells. 3926 1.578 Journal of Virology, 2018, 92, . Plasmodium falciparum RUVBL3 protein: a novel DNA modifying enzyme and an interacting partner of 1.6 essential HAT protein MYST. Scientific Reports, 2018, 8, 10917.

#	Article	IF	CITATIONS
3928	CRISPR-based reagents to study the influence of the epigenome on gene expression. Clinical and Experimental Immunology, 2018, 194, 9-16.	1.1	9
3929	Temporal Changes in Nucleus Morphology, Lamin A/C and Histone Methylation During Nanotopography-Induced Neuronal Differentiation of Stem Cells. Frontiers in Bioengineering and Biotechnology, 2018, 6, 69.	2.0	35
3930	A Decade of Exploring the Mammalian Sperm Epigenome: Paternal Epigenetic and Transgenerational Inheritance. Frontiers in Cell and Developmental Biology, 2018, 6, 50.	1.8	134
3931	Higher-order partial least squares for predicting gene expression levels from chromatin states. BMC Bioinformatics, 2018, 19, 113.	1.2	5
3932	Modulation of nucleosomal DNA accessibility via charge-altering post-translational modifications in histone core. Epigenetics and Chromatin, 2018, 11, 11.	1.8	73
3933	Born to run: control of transcription elongation by RNA polymerase II. Nature Reviews Molecular Cell Biology, 2018, 19, 464-478.	16.1	304
3934	Thinking BIG rheumatology: how to make functional genomics data work for you. Arthritis Research and Therapy, 2018, 20, 29.	1.6	4
3935	A metadynamic approach to understand the recognition mechanism of the histone H3 tail with the ATRXADD domain. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2018, 1861, 594-602.	0.9	4
3936	Histone variant H2A.Z antagonizes the positive effect of the transcriptional activator CPC1 to regulate catalase-3 expression under normal and oxidative stress conditions. Free Radical Biology and Medicine, 2018, 121, 136-148.	1.3	16
3937	JMJD3 inhibition protects against isoproterenol-induced cardiac hypertrophy by suppressing β-MHC expression. Molecular and Cellular Endocrinology, 2018, 477, 1-14.	1.6	29
3938	Muscle type-specific RNA polymerase II recruitment during PGC-1α gene transcription after acute exercise in adult rats. Journal of Applied Physiology, 2018, 125, 1238-1245.	1.2	13
3939	Insights from multidimensional analyses of the panâ€cancer DNA methylome heterogeneity and the uncanonical CpG–gene associations. International Journal of Cancer, 2018, 143, 2814-2827.	2.3	12
3940	Identification of H4K20me3- and H3K4me3-associated RNAs using CARIP-Seq expands the transcriptional and epigenetic networks of embryonic stem cells. Journal of Biological Chemistry, 2018, 293, 15120-15135.	1.6	7
3941	ChromTime: modeling spatio-temporal dynamics of chromatin marks. Genome Biology, 2018, 19, 109.	3.8	10
3942	Epigenetics: An emerging field in the pathogenesis of nonalcoholic fatty liver disease. Mutation Research - Reviews in Mutation Research, 2018, 778, 1-12.	2.4	11
3943	DNMT1 modulates interneuron morphology by regulating <i>Pak6</i> expression through crosstalk with histone modifications. Epigenetics, 2018, 13, 536-556.	1.3	47
3944	Human cardiac <i>cis</i> -regulatory elements, their cognate transcription factors, and regulatory DNA sequence variants. Genome Research, 2018, 28, 1577-1588.	2.4	25
3945	Trac-looping measures genome structure and chromatin accessibility. Nature Methods, 2018, 15, 741-747.	9.0	74

#	Article	IF	CITATIONS
3946	Emerging EZH2 Inhibitors and Their Application in Lymphoma. Current Hematologic Malignancy Reports, 2018, 13, 369-382.	1.2	84
3947	Histone H2A.Z Suppression of Interferon-Stimulated Transcription and Antiviral Immunity Is Modulated by GCN5 and BRD2. IScience, 2018, 6, 68-82.	1.9	34
3948	Visualizing biologically active small molecules in cells using click chemistry. Nature Reviews Chemistry, 2018, 2, 202-215.	13.8	133
3949	Lysine-specific demethylase 1 cooperates with BRAF–histone deacetylase complex 80 to enhance HIV-1 Tat-mediated transactivation. Virus Genes, 2018, 54, 662-671.	0.7	3
3950	Prediction and identification of transcriptional regulatory elements at the lung cancer‑specific DKK1 locus. Oncology Letters, 2018, 16, 137-144.	0.8	11
3951	Gene Therapy in Skeletal Muscle Repair and Regeneration. , 2018, , 49-69.		0
3952	Epigenetic Regulation of Endothelial-to-Mesenchymal Transition in Chronic Heart Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2018, 38, 1986-1996.	1.1	63
3953	Structure and Conformational Dynamics of a COMPASS Histone H3K4 Methyltransferase Complex. Cell, 2018, 174, 1117-1126.e12.	13.5	84
3954	Deficiency of PKD2L1 (TRPP3) Exacerbates Pathological Cardiac Hypertrophy by Augmenting NCX1-Mediated Mitochondrial Calcium Overload. Cell Reports, 2018, 24, 1639-1652.	2.9	27
3955	A regulatory circuitry comprising TP53, <i>miR-29</i> family, and SETDB1 in non-small cell lung cancer. Bioscience Reports, 2018, 38, .	1.1	20
3956	Epigenetic Approaches to the Treatment of Dental Pulp Inflammation and Repair: Opportunities and Obstacles. Frontiers in Genetics, 2018, 9, 311.	1.1	36
3957	Sodium arsenite exposure inhibits histone acetyltransferase p300 for attenuating H3K27ac at enhancers in mouse embryonic fibroblast cells. Toxicology and Applied Pharmacology, 2018, 357, 70-79.	1.3	17
3958	Chromatin Immunoprecipitation for Identification of Protein–DNA Interactions in Human Cells. Methods in Molecular Biology, 2018, 1794, 335-352.	0.4	2
3959	Histone variants H3.3 and H2A.Z are incorporated into the β-globin locus during transcription activation via different mechanisms. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2018, 1861, 637-646.	0.9	9
3960	Gas41 links histone acetylation to H2A.Z deposition and maintenance of embryonic stem cell identity. Cell Discovery, 2018, 4, 28.	3.1	47
3961	Epigenetic Mechanisms of Alcohol Neuroadaptation: Insights from Drosophila. Journal of Experimental Neuroscience, 2018, 12, 117906951877980.	2.3	9
3962	An Introduction to Epigenetic Mechanisms. Progress in Molecular Biology and Translational Science, 2018, 158, 29-48.	0.9	13
3963	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

		CITATION REPORT		
#	Article		IF	CITATIONS
3964	Epigenetics and Epigenomic Studies in Asthma. Translational Bioinformatics, 2018, , 6	Э-101.	0.0	0
3965	Unraveling the 3D genome of human malaria parasites. Seminars in Cell and Developm 2019, 90, 144-153.	ental Biology,	2.3	6
3966	Marine Environmental Epigenetics. Annual Review of Marine Science, 2019, 11, 335-36	58.	5.1	223
3967	Sodium tungstate: Is it a safe option for a chronic disease setting, such as diabetes?. Jo Cellular Physiology, 2019, 234, 51-60.	burnal of	2.0	11
3968	HPV16 E7â€induced upregulation of KDM2A promotes cervical cancer progression by miRâ€132–radixin pathway. Journal of Cellular Physiology, 2019, 234, 2659-2671.	regulating	2.0	26
3969	Mapping histone modifications in low cell number and single cells using antibody-guid tagmentation (ACT-seq). Nature Communications, 2019, 10, 3747.	ed chromatin	5.8	111
3970	PAX5 is part of a functional transcription factor network targeted in lymphoid leukemi Genetics, 2019, 15, e1008280.	a. PLoS	1.5	33
3971	Targeting Chromatin Remodeling for Cancer Therapy. Current Molecular Pharmacolog, 215-229.	y, 2019, 12,	0.7	37
3972	PropaNet: Time-Varying Condition-Specific Transcriptional Network Construction by N Propagation. Frontiers in Plant Science, 2019, 10, 698.	etwork	1.7	6
3973	The pause-initiation limit restricts transcription activation in human cells. Nature Comr 2019, 10, 3603.	nunications,	5.8	60
3974	The histone modification reader ZCWPW1 is required for meiosis prophase I in male bu mice. Science Advances, 2019, 5, eaax1101.	ıt not in female	4.7	43
3975	One-Carbon Metabolism Supports S-Adenosylmethionine and Histone Methylation to Inflammatory Macrophages. Molecular Cell, 2019, 75, 1147-1160.e5.	Drive	4.5	186
3976	Genome-wide analysis of polymerase Ill–transcribed <i>Alu</i> elements suggests ce enhancer function. Genome Research, 2019, 29, 1402-1414.	ell-type–specific	2.4	69
3977	TET-Catalyzed 5-Carboxylcytosine Promotes CTCF Binding to Suboptimal Sequences G IScience, 2019, 19, 326-339.	enome-wide.	1.9	19
3978	DNA methylation and chromatin modifications. , 2019, , 13-36.			4
3979	KDM2 proteins constrain transcription from CpG island gene promoters independently histone demethylase activity. Nucleic Acids Research, 2019, 47, 9005-9023.	of their	6.5	26
3980	Insights for the design of protein lysine methyltransferase C9a inhibitors. Future Media Chemistry, 2019, 11, 993-1014.	sinal	1.1	23
3981	Peak calling by Sparse Enrichment Analysis for CUT&RUN chromatin profiling. Epi Chromatin, 2019, 12, 42.	genetics and	1.8	267

		CITATION RE	PORT	
#	Article		IF	Citations
3982	PRMT5 in gene regulation and hematologic malignancies. Genes and Diseases, 2019, 6	, 247-257.	1.5	56
3983	Inhibition of Histone Methyltransferases EHMT1/2 Reverses Amyloid-β-Induced Loss of in Human Stem Cell-Derived Cortical Neurons. Journal of Alzheimer's Disease, 2019, 70	AMPAR Currents , 1175-1185.	1.2	14
3984	Sequenceâ€dependent nucleosome nanoscale structure characterized by atomic force FASEB Journal, 2019, 33, 10916-10923.	microscopy.	0.2	13
3985	Coupling Fluorescence-Activated Cell Sorting and Targeted Analysis of Histone Modific in Primary Human Leukocytes. Journal of the American Society for Mass Spectrometry, 2526-2534.		1.2	9
3986	A Scalable Platform for Producing Recombinant Nucleosomes with Codified Histone Methyltransferase Substrate Preferences. Protein Expression and Purification, 2019, 16	4, 105455.	0.6	1
3987	Chemical genomics reveals histone deacetylases are required for core regulatory transc Nature Communications, 2019, 10, 3004.	ription.	5.8	107
3988	Physcomitrella STEMIN transcription factor induces stem cell formation with epigenetic reprogramming. Nature Plants, 2019, 5, 681-690.	2	4.7	32
3989	Epigenetic Regulation at the Interplay Between Gut Microbiota and Host Metabolism. F Genetics, 2019, 10, 638.	rontiers in	1.1	116
3990	Low-Affinity Binding Sites and the Transcription Factor Specificity Paradox in Eukaryote Review of Cell and Developmental Biology, 2019, 35, 357-379.	s. Annual	4.0	144
3991	Who's your daddy? Behavioral and epigenetic consequences of paternal drug exposure Journal of Developmental Neuroscience, 2019, 78, 109-121.	. International	0.7	13
3992	Genomeâ€Wide Measurement and Computational Analysis of Transcription Factor Bind Chromatin Accessibility in Lymphocytes. Current Protocols in Immunology, 2019, 126,		3.6	0
3993	Arabidopsis SWR1-associated protein methyl-CpC-binding domain 9 is required for hist deposition. Nature Communications, 2019, 10, 3352.	one H2A.Z	5.8	60
3994	Growth inhibitor of human hepatic carcinoma HepG2 cells by evodiamine is associated downregulation of PRAME. Naunyn-Schmiedeberg's Archives of Pharmacology, 2019, 3		1.4	5
3995	ZNF518B gene up-regulation promotes dissemination of tumour cells and is governed l mechanisms in colorectal cancer. Scientific Reports, 2019, 9, 9339.	oy epigenetic	1.6	11
3996	MicroRNA Regulation of Epigenetic Modifiers in Breast Cancer. Cancers, 2019, 11, 897		1.7	52
3997	Inferring changes in histone modification during cell differentiation by ancestral state e based on phylogenetic trees of cell types: Human hematopoiesis as a model case. Gene		2.3	2
3998	Early life stress and the propensity to develop addictive behaviors. International Journal Developmental Neuroscience, 2019, 78, 156-169.	of	0.7	23
3999	Enhancer signatures stratify and predict outcomes of non-functional pancreatic neuroe tumors. Nature Medicine, 2019, 25, 1260-1265.	ndocrine	15.2	120

#	Article	IF	CITATIONS
4000	Roles and regulation of histone methylation in animal development. Nature Reviews Molecular Cell Biology, 2019, 20, 625-641.	16.1	324
4001	Stress-Induced Epigenetic Changes in Hippocampal Mkp-1 Promote Persistent Depressive Behaviors. Molecular Neurobiology, 2019, 56, 8537-8556.	1.9	20
4002	Profiling histone modifications in the normal mouse kidney and after unilateral ureteric obstruction. American Journal of Physiology - Renal Physiology, 2019, 317, F606-F615.	1.3	2
4003	H3K4me2 functions as a repressive epigenetic mark in plants. Epigenetics and Chromatin, 2019, 12, 40.	1.8	51
4004	The transcription factor OsSUF4 interacts with SDG725 in promoting H3K36me3 establishment. Nature Communications, 2019, 10, 2999.	5.8	29
4005	Chromatin Immunoprecipitation Assay for Analyzing Transcription Factor Activity at the Level of Peripheral Myelin Gene Promoters. Methods in Molecular Biology, 2019, 2011, 647-658.	0.4	1
4007	Going low to reach high: Smallâ€scale ChIPâ€seq maps new terrain. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2020, 12, e1465.	6.6	8
4008	KDM3B suppresses APL progression by restricting chromatin accessibility and facilitating the ATRA-mediated degradation of PML/RARα. Cancer Cell International, 2019, 19, 256.	1.8	13
4009	Genome-wide allele-specific methylation is enriched at gene regulatory regions in a multi-generation pedigree from the Norfolk Island isolate. Epigenetics and Chromatin, 2019, 12, 60.	1.8	12
4010	MOWChIP-seq for low-input and multiplexed profiling of genome-wide histone modifications. Nature Protocols, 2019, 14, 3366-3394.	5.5	29
4011	Omics Approaches to Understanding Muscle Biology. , 2019, , .		3
4012	Phloroglucinol Treatment Induces Transgenerational Epigenetic Inherited Resistance Against Vibrio Infections and Thermal Stress in a Brine Shrimp (Artemia franciscana) Model. Frontiers in Immunology, 2019, 10, 2745.	2.2	42
4013	Native internally calibrated chromatin immunoprecipitation for quantitative studies of histone post-translational modifications. Nature Protocols, 2019, 14, 3275-3302.	5.5	14
4014	Histone modifications and their regulatory roles in plant development and environmental memory. Journal of Genetics and Genomics, 2019, 46, 467-476.	1.7	76
4015	JMJD3 in the regulation of human diseases. Protein and Cell, 2019, 10, 864-882.	4.8	68
4016	Transgenerational epigenetic inheritance: from phenomena to molecular mechanisms. Current Opinion in Neurobiology, 2019, 59, 189-206.	2.0	57
4017	CTCF and cellular heterogeneity. Cell and Bioscience, 2019, 9, 83.	2.1	14
4019	G9a promotes cell proliferation and suppresses autophagy in gastric cancer by directly activating mTOR. FASEB Journal, 2019, 33, 14036-14050.	0.2	37

#	Article	IF	Citations
4020	The Chromatin Environment Around Interneuron Genes in Oligodendrocyte Precursor Cells and Their Potential for Interneuron Reprograming. Frontiers in Neuroscience, 2019, 13, 829.	1.4	11
4021	Identification and Characterization of a Transcribed Distal Enhancer Involved in Cardiac Kcnh2 Regulation. Cell Reports, 2019, 28, 2704-2714.e5.	2.9	15
4023	Regulation of Genomic Output and (Pluri)potency in Regeneration. Annual Review of Genetics, 2019, 53, 327-346.	3.2	15
4024	Interplay of miR-137 and EZH2 contributes to the genome-wide redistribution of H3K27me3 underlying the Pb-induced memory impairment. Cell Death and Disease, 2019, 10, 671.	2.7	32
4025	Epigenetic Regulation of p21cip1/waf1 in Human Cancer. Cancers, 2019, 11, 1343.	1.7	22
4026	Changes in histone H3 lysine 4 trimethylation in Hashimoto's thyroiditis. Archives of Medical Science, 2019, 18, 153-163.	0.4	2
4027	DNA repair complex licenses acetylation of H2A.Z.1 by KAT2A during transcription. Nature Chemical Biology, 2019, 15, 992-1000.	3.9	20
4028	Targeting epigenetic machinery: Emerging novel allosteric inhibitors. , 2019, 204, 107406.		32
4029	Rapid Identification of Novel Allosteric PRC2 Inhibitors. ACS Chemical Biology, 2019, 14, 2134-2140.	1.6	5
4030	Nucleosome Dynamics: a new tool for the dynamic analysis of nucleosome positioning. Nucleic Acids Research, 2019, 47, 9511-9523.	6.5	12
4031	Weighted Gene Co-Expression Analyses Point to Long Non-Coding RNA Hub Genes at Different Schistosoma mansoni Life-Cycle Stages. Frontiers in Genetics, 2019, 10, 823.	1.1	22
4032	Mitochondrial calcium exchange links metabolism with the epigenome to control cellular differentiation. Nature Communications, 2019, 10, 4509.	5.8	93
4033	The Epigenetics of Aging in Invertebrates. International Journal of Molecular Sciences, 2019, 20, 4535.	1.8	15
4034	The internal interaction in RBBP5 regulates assembly and activity of MLL1 methyltransferase complex. Nucleic Acids Research, 2019, 47, 10426-10438.	6.5	16
4035	PRDM16 functions as a suppressor of lung adenocarcinoma metastasis. Journal of Experimental and Clinical Cancer Research, 2019, 38, 35.	3.5	30
4036	From Genotype to Phenotype: Through Chromatin. Genes, 2019, 10, 76.	1.0	31
4037	KDM5D-mediated H3K4 demethylation is required for sexually dimorphic gene expression in mouse embryonic fibroblasts. Journal of Biochemistry, 2019, 165, 335-342.	0.9	20
4038	C/EBPÎ ² regulates Vegf gene expression in granulosa cells undergoing luteinization during ovulation in female rats. Scientific Reports, 2019, 9, 714.	1.6	18

#	Article	IF	CITATIONS
4039	Leveraging chromatin accessibility for transcriptional regulatory network inference in T Helper 17 Cells. Genome Research, 2019, 29, 449-463.	2.4	87
4040	Epigenetics and memory: Emerging role of histone lysine methyltransferase G9a/GLP complex as bidirectional regulator of synaptic plasticity. Neurobiology of Learning and Memory, 2019, 159, 1-5.	1.0	16
4041	Chromatin accessibility and the regulatory epigenome. Nature Reviews Genetics, 2019, 20, 207-220.	7.7	1,112
4042	Inhibition of EHMT1/2 rescues synaptic and cognitive functions for Alzheimer's disease. Brain, 2019, 142, 787-807.	3.7	98
4043	Expression Changes of Structural Protein Genes May Be Related to Adaptive Skin Characteristics Specific to Humans. Genome Biology and Evolution, 2019, 11, 613-628.	1.1	8
4044	The complex architecture and epigenomic impact of plant T-DNA insertions. PLoS Genetics, 2019, 15, e1007819.	1.5	109
4045	Quantifying CRISPR off-target effects. Emerging Topics in Life Sciences, 2019, 3, 327-334.	1.1	9
4046	Global Quantitative Mapping of Enhancers in Rice by STARR-seq. Genomics, Proteomics and Bioinformatics, 2019, 17, 140-153.	3.0	43
4047	The histone variant H2A.Z in gene regulation. Epigenetics and Chromatin, 2019, 12, 37.	1.8	205
4048	The histone lysine demethylase <i>KDM7A</i> is required for normal development and first cell lineage specification in porcine embryos. Epigenetics, 2019, 14, 1088-1101.	1.3	13
4049	HMMRATAC: a Hidden Markov ModeleR for ATAC-seq. Nucleic Acids Research, 2019, 47, e91-e91.	6.5	67
4050	METTL3 promote tumor proliferation of bladder cancer by accelerating pri-miR221/222 maturation in m6A-dependent manner. Molecular Cancer, 2019, 18, 110.	7.9	475
4051	Antiproliferative effect of the histone demethylase inhibitor GSKâ€J4 in chondrosarcomas. IUBMB Life, 2019, 71, 1711-1719.	1.5	10
4052	Quantitative analysis of post-translational modifications of histone H3 variants during the cell cycle. Analytica Chimica Acta, 2019, 1080, 116-126.	2.6	2
4053	Preserving genome integrity and function: the DNA damage response and histone modifications. Critical Reviews in Biochemistry and Molecular Biology, 2019, 54, 208-241.	2.3	63
4054	Pharmacoepigenetics of Memantine in Dementia. , 2019, , 827-835.		0
4055	Epigenetics of Aging and Age-Related Disorders. , 2019, , 871-883.		1
4056	Regulation of subtelomeric fungal secondary metabolite genes by H3K4me3 regulators CclA and KdmB. Molecular Microbiology, 2019, 112, 837-853.	1.2	16

#	Article	IF	CITATIONS
4057	Chromatin Immunoprecipitation Assay Using Micrococcal Nucleases in Mammalian Cells. Journal of Visualized Experiments, 2019, , .	0.2	2
4058	Pinpointing the Genomic Localizations of Chromatinâ€Associated Proteins: The Yesterday, Today, and Tomorrow of ChIPâ€seq. Current Protocols in Cell Biology, 2019, 84, e89.	2.3	10
4059	Why are so many MLL lysine methyltransferases required for normal mammalian development?. Cellular and Molecular Life Sciences, 2019, 76, 2885-2898.	2.4	54
4060	Effects of histone deacetylase inhibitors on ATP‑binding cassette transporters in lung cancer A549 and colorectal cancer HCT116 cells. Oncology Letters, 2019, 18, 63-71.	0.8	9
4061	Sotos syndrome. , 2019, , 219-234.		0
4062	Chromatin and epigenetic signaling pathways. , 2019, , 1-23.		0
4063	Histone Modifications. , 2019, , 47-72.		6
4064	Epigenetics of Early Mammalian Development: A Pathway to Regenerative Medicine. , 2019, , 133-163.		1
4065	Rewiring the Epigenetic Networks in MLL-Rearranged Leukemias: Epigenetic Dysregulation and Pharmacological Interventions. Frontiers in Cell and Developmental Biology, 2019, 7, 81.	1.8	59
4066	Lysine demethylases KDM6A and UTY: The X and Y of histone demethylation. Molecular Genetics and Metabolism, 2019, 127, 31-44.	0.5	44
4067	Histone H3 Mutations: An Updated View of Their Role in Chromatin Deregulation and Cancer. Cancers, 2019, 11, 660.	1.7	105
4068	Human transposons are an abundant supply of transcription factor binding sites and promoter activities in breast cancer cell lines. Mobile DNA, 2019, 10, 16.	1.3	21
4069	ldentification of Cholecystokinin by Genome-Wide Profiling as Potential Mediator of Serotonin-Dependent Behavioral Effects of Maternal Separation in the Amygdala. Frontiers in Neuroscience, 2019, 13, 460.	1.4	11
4070	Improved Detection of Epigenomic Marks with Mixed-Effects Hidden Markov Models. Biometrics, 2019, 75, 1401-1413.	0.8	0
4071	Pathogenic and Therapeutic Role of H3K4 Family of Methylases and Demethylases in Cancers. Indian Journal of Clinical Biochemistry, 2019, 34, 123-132.	0.9	16
4072	Bookmarking by histone methylation ensures chromosomal integrity during mitosis. Archives of Pharmacal Research, 2019, 42, 466-480.	2.7	6
4073	Chromatin State-Based Analysis of Epigenetic H3K4me3 Marks of Arabidopsis in Response to Dark Stress. Frontiers in Genetics, 2019, 10, 306.	1.1	17
4074	A Variant of the Histone-Binding Protein sNASP Contributes to Mouse Lupus. Frontiers in Immunology, 2019, 10, 637.	2.2	6

#	Article	IF	CITATIONS
4075	Control of Intra-Thymic $\hat{l}\pm\hat{l}^2$ T Cell Selection and Maturation by H3K27 Methylation and Demethylation. Frontiers in Immunology, 2019, 10, 688.	2.2	4
4076	Age, but Not Amyloidosis, Induced Changes in Global Levels of Histone Modifications in Susceptible and Disease-Resistant Neurons in Alzheimer's Disease Model Mice. Frontiers in Aging Neuroscience, 2019, 11, 68.	1.7	12
4077	Epigenetically Down-Regulated Acetyltransferase PCAF Increases the Resistance of Colorectal Cancer to 5-Fluorouracil. Neoplasia, 2019, 21, 557-570.	2.3	28
4078	Retrotransposon elements among initial sites of hepatitis B virus integration into human genome in the HepG2-NTCP cell infection model. Cancer Genetics, 2019, 235-236, 39-56.	0.2	12
4079	ALFA: annotation landscape for aligned reads. BMC Genomics, 2019, 20, 250.	1.2	9
4080	ChlPmentation for Low-Input Profiling of In Vivo Protein–DNA Interactions. Methods in Molecular Biology, 2019, 1979, 269-282.	0.4	0
4081	Primed histone demethylation regulates shoot regenerative competency. Nature Communications, 2019, 10, 1786.	5.8	52
4082	Development of a high efficient promoter finding method based on transient transfection. Gene: X, 2019, 2, 100008.	2.3	3
4083	Broad domains of histone 3 lysine 4 trimethylation are associated with transcriptional activation in CA1 neurons of the hippocampus during memory formation. Neurobiology of Learning and Memory, 2019, 161, 149-157.	1.0	24
4084	Contribution of H3K4 demethylase KDM5B to nucleosome organization in embryonic stem cells revealed by micrococcal nuclease sequencing. Epigenetics and Chromatin, 2019, 12, 20.	1.8	8
4086	AlControl: replacing matched control experiments with machine learning improves ChIP-seq peak identification. Nucleic Acids Research, 2019, 47, e58-e58.	6.5	9
4087	Contrasting requirements during disease evolution identify EZH2 as a therapeutic target in AML. Journal of Experimental Medicine, 2019, 216, 966-981.	4.2	91
4088	Effective breast cancer combination therapy targeting BACH1 and mitochondrial metabolism. Nature, 2019, 568, 254-258.	13.7	233
4089	Combinatorial Pattern of Histone Modifications in Exon Skipping Event. Frontiers in Genetics, 2019, 10, 122.	1.1	5
4090	Znhit1 controls intestinal stem cell maintenance by regulating H2A.Z incorporation. Nature Communications, 2019, 10, 1071.	5.8	25
4091	Toward multiomics-based next-generation diagnostics for precision medicine. Personalized Medicine, 2019, 16, 157-170.	0.8	12
4092	Making headway towards understanding how epigenetic mechanisms contribute to early-life effects. Philosophical Transactions of the Royal Society B: Biological Sciences, 2019, 374, 20180126.	1.8	12
4093	Leveraging technological innovations to investigate evolutionary transitions to eusociality. Current Opinion in Insect Science, 2019, 34, 27-32.	2.2	2

#	Article	IF	CITATIONS
4094	Extensive Recovery of Embryonic Enhancer and Gene Memory Stored in Hypomethylated Enhancer DNA. Molecular Cell, 2019, 74, 542-554.e5.	4.5	65
4095	Measuring the reproducibility and quality of Hi-C data. Genome Biology, 2019, 20, 57.	3.8	125
4096	Single-cell chromatin immunocleavage sequencing (scChIC-seq) to profile histone modification. Nature Methods, 2019, 16, 323-325.	9.0	144
4097	Epigenetic Modifications in Acute Myeloid Leukemia: Prognosis, Treatment, and Heterogeneity. Frontiers in Genetics, 2019, 10, 133.	1.1	58
4098	KDM5D inhibit epithelialâ€mesenchymal transition of gastric cancer through demethylation in the promoter of Cul4A in male. Journal of Cellular Biochemistry, 2019, 120, 12247-12258.	1.2	23
4099	Chemoprobe-based assays of histone lysine demethylase 1A target occupation enable in vivo pharmacokinetics and pharmacodynamics studies of KDM1A inhibitors. Journal of Biological Chemistry, 2019, 294, 8311-8322.	1.6	12
4100	Stable H3K4me3 is associated with transcription initiation during early embryo development. Bioinformatics, 2019, 35, 3931-3936.	1.8	23
4101	Histone H3 trimethylation at lysine 36 guides m6A RNA modification co-transcriptionally. Nature, 2019, 567, 414-419.	13.7	452
4102	Epigenetic therapy in hematological cancers. Apmis, 2019, 127, 316-328.	0.9	16
4103	DeepTACT: predicting 3D chromatin contacts via bootstrapping deep learning. Nucleic Acids Research, 2019, 47, e60-e60.	6.5	101
4104	<scp>CFP</scp> â€l interacts with <scp>HDAC</scp> 1/2 complexes in <i>C.Âelegans</i> development. FEBS Journal, 2019, 286, 2490-2504.	2.2	6
4105	Zbtb7c is a critical gluconeogenic transcription factor that induces glucose-6-phosphatase and phosphoenylpyruvate carboxykinase 1 genes expression during mice fasting. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2019, 1862, 643-656.	0.9	17
4106	Genome-Wide Identification of Histone Modifications Involved in Placental Development in Pigs. Frontiers in Genetics, 2019, 10, 277.	1.1	21
4107	Targeting the Epigenome as a Therapeutic Strategy for Pancreatic Tumors: DNA and Histone Modifying Enzymes. , 2019, , 133-157.		0
4108	Transient Kinetic Analysis of SWR1C-Catalyzed H2A.Z Deposition Unravels the Impact of Nucleosome Dynamics and the Asymmetry of Histone Exchange. Cell Reports, 2019, 27, 374-386.e4.	2.9	26
4109	A Tail-Based Mechanism Drives Nucleosome Demethylation by the LSD2/NPAC Multimeric Complex. Cell Reports, 2019, 27, 387-399.e7.	2.9	31
4110	Deep learning: new computational modelling techniques for genomics. Nature Reviews Genetics, 2019, 20, 389-403.	7.7	717
4111	Enabling cell-type-specific behavioral epigenetics in Drosophila: a modified high-yield INTACT method reveals the impact of social environment on the epigenetic landscape in dopaminergic neurons. BMC Biology 2019, 17, 30	1.7	18

		CITATION RE	PORT	
#	Article		IF	CITATIONS
4112	Research in Computational Molecular Biology. Lecture Notes in Computer Science, 20	19,,.	1.0	0
4113	DeepHistone: a deep learning approach to predicting histone modifications. BMC Gen 193.	omics, 2019, 20,	1.2	50
4114	Human adipose tissue H3K4me3 histone mark in adipogenic, lipid metabolism and infl positively associated with BMI and HOMA-IR. PLoS ONE, 2019, 14, e0215083.	ammatory genes is	1.1	33
4115	Comparison of genotoxic versus nongenotoxic stabilization of p53 provides insight in stress-responsive transcriptional networks. Cell Cycle, 2019, 18, 809-823.	co parallel	1.3	11
4116	PIXUL-ChIP: integrated high-throughput sample preparation and analytical platform fo studies. Nucleic Acids Research, 2019, 47, e69-e69.	r epigenetic	6.5	16
4117	Profiling expression changes of genes associated with temperature and sex during hig temperature-induced masculinization in the Nile tilapia brain. Physiological Genomics,	h 2019, 51, 159-168.	1.0	13
4118	Aberrant regulation of epigenetic modifiers contributes to the pathogenesis in patient selenoprotein N <i>\hat{e}</i> /i> related myopathies. Human Mutation, 2019, 40, 962-974.	s with	1.1	13
4119	Multilocus Methylation Assays in Epigenetics. , 2019, , 2181-2202.			0
4120	Forward and Reverse Epigenomics in Embryonic Stem Cells. , 2019, , 2269-2288.			0
4121	Identification of ADGRE5 as discriminating MYC target between Burkitt lymphoma and B-cell lymphoma. BMC Cancer, 2019, 19, 322.	l diffuse large	1.1	8
4122	Mapping the Heterogeneity of Histone Modifications on Hepatitis B Virus DNA Using L Biopsies Obtained from Chronically Infected Patients. Journal of Virology, 2019, 93, .	iver Needle.	1.5	24
4123	The Epigenetic Targets of Berry Anthocyanins in Cancer Prevention. , 2019, , 129-148.			3
4124	DNA helicase RecQ1 regulates mutually exclusive expression of virulence genes in <i>Falciparum</i> via heterochromatin alteration. Proceedings of the National Academy o the United States of America, 2019, 116, 3177-3182.		3.3	16
4125	Mechanoâ€modulation of nuclear events regulating oligodendrocyte progenitor gene 2019, 67, 1229-1239.	expression. Glia,	2.5	18
4126	KDM4B: A Nail for Every Hammer?. Genes, 2019, 10, 134.		1.0	35
4127	Effects of Culture Condition on Epigenomic Profiles of Brain Tumor Cells. ACS Biomate and Engineering, 2019, 5, 1544-1552.	rials Science	2.6	14
4128	Serial genomic inversions induce tissue-specific architectural stripes, gene misexpressi congenital malformations. Nature Cell Biology, 2019, 21, 305-310.	on and	4.6	107
4129	Monitoring of chromatin organization in live cells by FRIC. Effects of the inner nuclear protein Samp1. Nucleic Acids Research, 2019, 47, e49-e49.	membrane	6.5	6

#	Article	IF	Citations
4130	The multiple mechanisms that regulate p53 activity and cell fate. Nature Reviews Molecular Cell Biology, 2019, 20, 199-210.	16.1	711
4131	Epigenetics and Epigenomics Analysis for Autoimmune Diseases. , 2019, , 365-395.		0
4132	Computational Analysis of Epigenetic Modifications in Melanoma. , 2019, , 327-342.		1
4133	Discovery of a Novel Chemotype of Histone Lysine Methyltransferase EHMT1/2 (GLP/G9a) Inhibitors: Rational Design, Synthesis, Biological Evaluation, and Co-crystal Structure. Journal of Medicinal Chemistry, 2019, 62, 2666-2689.	2.9	33
4134	Developmental Dioxin Exposure Alters the Methylome of Adult Male Zebrafish Gonads. Frontiers in Genetics, 2019, 9, 719.	1.1	19
4135	Lysine-Specific Histone Demethylases 1/2 (LSD1/2) and Their Inhibitors. Topics in Medicinal Chemistry, 2019, , 197-219.	0.4	1
4136	Critical role of Jumonji domain of JMJD1C in MLL-rearranged leukemia. Blood Advances, 2019, 3, 1499-1511.	2.5	21
4137	AUSPP: A universal short-read pre-processing package. Journal of Bioinformatics and Computational Biology, 2019, 17, 1950037.	0.3	3
4138	Technological advances in studying epigenetics biomarkers of prognostic potential for clinical research. , 2019, , 45-83.		1
4139	The Bdnf and Npas4 genes are targets of HDAC3-mediated transcriptional repression. BMC Neuroscience, 2019, 20, 65.	0.8	10
4140	A computational method to predict topologically associating domain boundaries combining histone Marks and sequence information. BMC Genomics, 2019, 20, 980.	1.2	13
4141	Histone hyperacetylation disrupts core gene regulatory architecture in rhabdomyosarcoma. Nature Genetics, 2019, 51, 1714-1722.	9.4	113
4142	Inhibitor of Growth 4 (ING4) is a positive regulator of rRNA synthesis. Scientific Reports, 2019, 9, 17235.	1.6	11
4143	A genome-wide DNA methylation signature for SETD1B-related syndrome. Clinical Epigenetics, 2019, 11, 156.	1.8	48
4144	The transcriptional co-activator NCOA6 promotes estrogen-induced GREB1 transcription by recruiting ERα and enhancing enhancer–promoter interactions. Journal of Biological Chemistry, 2019, 294, 19667-19682.	1.6	8
4145	Multivariable regulation of gene expression plasticity in metazoans. Open Biology, 2019, 9, 190150.	1.5	11
4146	CSA: a web service for the complete process of ChIP-Seq analysis. BMC Bioinformatics, 2019, 20, 515.	1.2	2
4147	DEEPSEN: a convolutional neural network based method for super-enhancer prediction. BMC Bioinformatics, 2019, 20, 598.	1.2	12

#	Article	IF	CITATIONS
4148	Reduced H3K27me3 leads to abnormal Hox gene expression in neural tube defects. Epigenetics and Chromatin, 2019, 12, 76.	1.8	28
4149	PDGFRA defines the mesenchymal stem cell Kaposi's sarcoma progenitors by enabling KSHV oncogenesis in an angiogenic environment. PLoS Pathogens, 2019, 15, e1008221.	2.1	23
4150	Dead Cas Systems: Types, Principles, and Applications. International Journal of Molecular Sciences, 2019, 20, 6041.	1.8	74
4151	uap: reproducible and robust HTS data analysis. BMC Bioinformatics, 2019, 20, 664.	1.2	14
4152	Functional genomic approaches to elucidate the role of enhancers during development. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2019, 12, e1467.	6.6	19
4153	Adipose-Derived Stem Cells and Ceiling Culture-Derived Preadipocytes Cultured from Subcutaneous Fat Tissue Differ in Their Epigenetic Characteristics and Osteogenic Potential. Plastic and Reconstructive Surgery, 2019, 144, 644-655.	0.7	7
4154	Transgenerational Inheritance of Environmentally Induced Epigenetic Alterations during Mammalian Development. Cells, 2019, 8, 1559.	1.8	66
4155	Co-incidence of RCC-susceptibility polymorphisms with HIF cis-acting sequences supports a pathway tuning model of cancer. Scientific Reports, 2019, 9, 18768.	1.6	9
4156	AWESOME: a database of SNPs that affect protein post-translational modifications. Nucleic Acids Research, 2019, 47, D874-D880.	6.5	53
4157	Characterizing protein–DNA binding event subtypes in ChIP-exo data. Bioinformatics, 2019, 35, 903-913.	1.8	29
4158	Sequencing in High Definition Drives a Changing Worldview of the Epigenome. Cold Spring Harbor Perspectives in Medicine, 2019, 9, a033076.	2.9	1
4158 4159		2.9 0.8	1 7
	Perspectives in Medicine, 2019, 9, a033076. Transcriptional Programs and Regeneration Enhancers Underlying Heart Regeneration. Journal of		
4159	Perspectives in Medicine, 2019, 9, a033076. Transcriptional Programs and Regeneration Enhancers Underlying Heart Regeneration. Journal of Cardiovascular Development and Disease, 2019, 6, 2. Identification of regulatory elements from nascent transcription using dREG. Genome Research, 2019,	0.8	7
4159 4160	 Perspectives in Medicine, 2019, 9, a033076. Transcriptional Programs and Regeneration Enhancers Underlying Heart Regeneration. Journal of Cardiovascular Development and Disease, 2019, 6, 2. Identification of regulatory elements from nascent transcription using dREG. Genome Research, 2019, 29, 293-303. Gain-of-function DNMT3A mutations cause microcephalic dwarfism and hypermethylation of 	0.8 2.4	7 85
4159 4160 4161	 Perspectives in Medicine, 2019, 9, a033076. Transcriptional Programs and Regeneration Enhancers Underlying Heart Regeneration. Journal of Cardiovascular Development and Disease, 2019, 6, 2. Identification of regulatory elements from nascent transcription using dREG. Genome Research, 2019, 29, 293-303. Gain-of-function DNMT3A mutations cause microcephalic dwarfism and hypermethylation of Polycomb-regulated regions. Nature Genetics, 2019, 51, 96-105. One-Carbon Metabolism: Linking Nutritional Biochemistry to Epigenetic Programming of Long-Term 	0.8 2.4 9.4	7 85 110
4159 4160 4161 4162	Perspectives in Medicine, 2019, 9, a033076. Transcriptional Programs and Regeneration Enhancers Underlying Heart Regeneration. Journal of Cardiovascular Development and Disease, 2019, 6, 2. Identification of regulatory elements from nascent transcription using dREG. Genome Research, 2019, 29, 293-303. Gain-of-function DNMT3A mutations cause microcephalic dwarfism and hypermethylation of Polycomb-regulated regions. Nature Genetics, 2019, 51, 96-105. One-Carbon Metabolism: Linking Nutritional Biochemistry to Epigenetic Programming of Long-Term Development. Annual Review of Animal Biosciences, 2019, 7, 263-287.	0.8 2.4 9.4	7 85 110 197

#	Article	IF	CITATIONS
4166	Cancer epigenetics and the potential of epigenetic drugs for treating solid tumors. Expert Review of Anticancer Therapy, 2019, 19, 139-149.	1.1	16
4167	Complexity of genome sequencing and reporting: Next generation sequencing (NGS) technologies and implementation of precision medicine in real life. Critical Reviews in Oncology/Hematology, 2019, 133, 171-182.	2.0	93
4168	Nucleosome Turnover Regulates Histone Methylation Patterns over the Genome. Molecular Cell, 2019, 73, 61-72.e3.	4.5	69
4169	Long noncoding RNA expression profiling in cancer: Challenges and opportunities. Genes Chromosomes and Cancer, 2019, 58, 191-199.	1.5	117
4170	Cistrome Data Browser: expanded datasets and new tools for gene regulatory analysis. Nucleic Acids Research, 2019, 47, D729-D735.	6.5	527
4171	Prediction of TF-binding site by inclusion of higher order position dependencies. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 17, 1-1.	1.9	6
4172	Histone H3 lysine K4 methylation and its role in learning and memory. Epigenetics and Chromatin, 2019, 12, 7.	1.8	113
4173	Role of Histone Modifications in Chronic Pain Development. , 2019, , 85-98.		1
4174	Pain-Induced Chromatin Modifications. , 2019, , 111-124.		0
4175	Putative contributions of the sex chromosome proteins SOX3 and SRY to neurodevelopmental disorders. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2019, 180, 390-414.	1.1	7
4176	Approaches for the study of epigenetic modifications in the inner ear and related tissues. Hearing Research, 2019, 376, 69-85.	0.9	6
4177	Crosstalk of Genetic Variants, Allele-Specific DNA Methylation, and Environmental Factors for Complex Disease Risk. Frontiers in Genetics, 2018, 9, 695.	1.1	63
4178	The impact of histone post-translational modifications in neurodegenerative diseases. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2019, 1865, 1982-1991.	1.8	33
4179	Loss of Stat6 affects chromatin condensation in intestinal epithelial cells causing diverse outcome in murine models of inflammation-associated and sporadic colon carcinogenesis. Oncogene, 2019, 38, 1787-1801.	2.6	13
4180	Endocrine Epigenetics, Epigenetic Profiling and Biomarker Identification. , 2019, , 31-35.		4
4181	The many lives of KATs — detectors, integrators and modulators of the cellular environment. Nature Reviews Genetics, 2019, 20, 7-23.	7.7	129
4182	Loss of the GPIâ€anchor in Bâ€lymphoblastic leukemia by epigenetic downregulation of <i>PIGH</i> expression. American Journal of Hematology, 2019, 94, 93-102.	2.0	8
4183	Disruption of FOXP3–EZH2 Interaction Represents a Pathobiological Mechanism in Intestinal Inflammation. Cellular and Molecular Gastroenterology and Hepatology, 2019, 7, 55-71.	2.3	23

#	Article	IF	CITATIONS
4184	RiboProP: a probabilistic ribosome positioning algorithm for ribosome profiling. Bioinformatics, 2019, 35, 1486-1493.	1.8	7
4185	Brain Tumor Stem Cells. Methods in Molecular Biology, 2019, , .	0.4	2
4186	Chromatin Immunoprecipitation (ChIP) Protocols for the Cancer and Developmental Biology Laboratory. Methods in Molecular Biology, 2019, 1869, 143-153.	0.4	2
4187	Lysine demethylase 5B (KDM5B): A potential anti-cancer drug target. European Journal of Medicinal Chemistry, 2019, 161, 131-140.	2.6	41
4188	DOT1L promotes progenitor proliferation and primes neuronal layer identity in the developing cerebral cortex. Nucleic Acids Research, 2019, 47, 168-183.	6.5	49
4189	Progesterone receptor integrates the effects of mutated MED12 and altered DNA methylation to stimulate RANKL expression and stem cell proliferation in uterine leiomyoma. Oncogene, 2019, 38, 2722-2735.	2.6	36
4190	Histopathological and Molecular Signatures of a Mouse Model of Acute-on-Chronic Alcoholic Liver Injury Demonstrate Concordance With Human Alcoholic Hepatitis. Toxicological Sciences, 2019, 170, 427-437.	1.4	15
4191	Proteomic approaches for cancer epigenetics research. Expert Review of Proteomics, 2019, 16, 33-47.	1.3	5
4192	Machine learning for integrating data in biology and medicine: Principles, practice, and opportunities. Information Fusion, 2019, 50, 71-91.	11.7	340
4193	ChIPprimersDB: a public repository of verified qPCR primers for chromatin immunoprecipitation (ChIP). Nucleic Acids Research, 2019, 47, D46-D49.	6.5	9
4194	It is a complex issue: emerging connections between epigenetic regulators in drug addiction. European Journal of Neuroscience, 2019, 50, 2477-2491.	1.2	16
4195	The relationship between histone posttranslational modification and DNA damage signaling and repair. International Journal of Radiation Biology, 2019, 95, 382-393.	1.0	12
4196	Genome-wide meta-analysis identifies <i>BARX1</i> and <i>EML4-MTA3</i> as new loci associated with infantile hypertrophic pyloric stenosis. Human Molecular Genetics, 2019, 28, 332-340.	1.4	18
4197	Histone methylation and the DNA damage response. Mutation Research - Reviews in Mutation Research, 2019, 780, 37-47.	2.4	132
4198	Histone variants in environmental-stress-induced DNA damage repair. Mutation Research - Reviews in Mutation Research, 2019, 780, 55-60.	2.4	14
4199	Regulation of Astrocyte Functions in Multiple Sclerosis. Cold Spring Harbor Perspectives in Medicine, 2019, 9, a029009.	2.9	69
4200	Role of CTCF in DNA damage response. Mutation Research - Reviews in Mutation Research, 2019, 780, 61-68.	2.4	18
4201	Amelioration of autism-like social deficits by targeting histone methyltransferases EHMT1/2 in Shank3-deficient mice. Molecular Psychiatry, 2020, 25, 2517-2533.	4.1	57

#	Article	IF	CITATIONS
4202	The SETD6 Methyltransferase Plays an Essential Role in Hippocampus-Dependent Memory Formation. Biological Psychiatry, 2020, 87, 577-587.	0.7	8
4203	Effect of the key histone modifications on the expression of genes related to breast cancer. Genomics, 2020, 112, 853-858.	1.3	14
4204	Assaying epigenome functions of PRMTs and their substrates. Methods, 2020, 175, 53-65.	1.9	16
4205	Characterization and Analysis of Mammalian AKR7A Gene Promoters: Implications for Transcriptional Regulation. Biochemical Genetics, 2020, 58, 171-188.	0.8	7
4207	Dichotomous role of TGF-β controls inducible regulatory T-cell fate in allergic airway disease through Smad3 and TGF-β–activated kinase 1. Journal of Allergy and Clinical Immunology, 2020, 145, 933-946.e4.	1.5	8
4208	Determinants of enhancer and promoter activities of regulatory elements. Nature Reviews Genetics, 2020, 21, 71-87.	7.7	464
4209	Regulatory annotation of genomic intervals based on tissue-specific expression QTLs. Bioinformatics, 2020, 36, 690-697.	1.8	9
4210	Irregular Chromatin: Packing Density, Fiber Width, and Occurrence of Heterogeneous Clusters. Biophysical Journal, 2020, 118, 207-218.	0.2	21
4211	Knocking out histone methyltransferase PRMT1 leads to stalled tadpole development and lethality in Xenopus tropicalis. Biochimica Et Biophysica Acta - General Subjects, 2020, 1864, 129482.	1.1	7
4212	Epigenetic regulation of macrophages: from homeostasis maintenance to host defense. Cellular and Molecular Immunology, 2020, 17, 36-49.	4.8	196
4213	Identification of anoctamin 1 (ANO1) as a key driver of esophageal epithelial proliferation in eosinophilic esophagitis. Journal of Allergy and Clinical Immunology, 2020, 145, 239-254.e2.	1.5	24
4214	LncRNA-mediated regulation of <i>SOX9</i> expression in basal subtype breast cancer cells. Rna, 2020, 26, 175-185.	1.6	16
4215	JMJD2A sensitizes gastric cancer to chemotherapy by cooperating with CCDC8. Gastric Cancer, 2020, 23, 426-436.	2.7	15
4216	Distinct Pathogenic Genes Causing Intellectual Disability and Autism Exhibit a Common Neuronal Network Hyperactivity Phenotype. Cell Reports, 2020, 30, 173-186.e6.	2.9	44
4217	The expression of histone methyltransferases and distribution of selected histone methylations in testes of yak and cattle-yak hybrid. Theriogenology, 2020, 144, 164-173.	0.9	17
4218	Comparative Proteomic Analysis of Histone Modifications upon Acridone Derivative 8a -Induced CCRF-CEM Cells by Data Independent Acquisition. Journal of Proteome Research, 2020, 19, 819-831.	1.8	2
4219	Drug Discovery Researches on Modulators of Lysine-Modifying Enzymes Based on Strategic Chemistry Approaches. Chemical and Pharmaceutical Bulletin, 2020, 68, 34-45.	0.6	11
4220	Chromatin regulation and dynamics in stem cells. Current Topics in Developmental Biology, 2020, 138, 1-71.	1.0	12

# 4221	ARTICLE Epigenetic inheritance and plant evolution. Population Ecology, 2020, 62, 17-27.	IF 0.7	CITATIONS
4222	From Signaling Molecules to Circuits and Behaviors: Cell-Type–Specific Adaptations to Psychostimulant Exposure in the Striatum. Biological Psychiatry, 2020, 87, 944-953.	0.7	31
4223	Molecular systems in inflammatory bowel disease. , 2020, , 367-388.		1
4224	Epigenetic regulations in alternative telomere lengthening: Understanding the mechanistic insight in arsenic-induced skin cancer patients. Science of the Total Environment, 2020, 704, 135388.	3.9	22
4225	Structure of H3K36-methylated nucleosome–PWWP complex reveals multivalent cross-gyre binding. Nature Structural and Molecular Biology, 2020, 27, 8-13.	3.6	57
4226	High-throughput omics in the precision medicine ecosystem. , 2020, , 19-31.		1
4227	Proteasome inhibition creates a chromatin landscape favorable to RNA Pol II processivity. Journal of Biological Chemistry, 2020, 295, 1271-1287.	1.6	9
4228	A method for assessing histone surface accessibility genome-wide. Methods, 2020, 184, 61-69.	1.9	3
4229	The Bivalent Genome: Characterization, Structure, and Regulation. Trends in Genetics, 2020, 36, 118-131.	2.9	112
4230	Canonical Wnt Signaling Modulates the Expression of Pre- and Postsynaptic Components in Different Temporal Patterns. Molecular Neurobiology, 2020, 57, 1389-1404.	1.9	14
4231	De Novo Damaging DNA Coding Mutations Are Associated With Obsessive-Compulsive Disorder and Overlap With Tourette's Disorder and Autism. Biological Psychiatry, 2020, 87, 1035-1044.	0.7	59
4232	Increase in hippocampal histone H3K9me3 is negatively correlated with memory in old male mice. Biogerontology, 2020, 21, 175-189.	2.0	17
4233	P5 eHealth: An Agenda for the Health Technologies of the Future. , 2020, , .		21
4234	Systematic integration of GATA transcription factors and epigenomes via IDEAS paints the regulatory landscape of hematopoietic cells. IUBMB Life, 2020, 72, 27-38.	1.5	8
4235	Advances and applications of environmental stress adaptation research. Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology, 2020, 240, 110623.	0.8	12
4236	BMSC-EVs regulate Th17 cell differentiation in UC via H3K27me3. Molecular Immunology, 2020, 118, 191-200.	1.0	22
4237	Fumonisin B1 Epigenetically Regulates PTEN Expression and Modulates DNA Damage Checkpoint Regulation in HepG2 Liver Cells. Toxins, 2020, 12, 625.	1.5	16
4238	Contribution of the bone marrow stromal cells in mediating drug resistance in hematopoietic tumors. Current Opinion in Pharmacology, 2020, 54, 36-43.	1.7	13

#	Article	IF	CITATIONS
4239	DNA Methylation of Intragenic CpG Islands are Required for Differentiation from iPSC to NPC. Stem Cell Reviews and Reports, 2020, 16, 1316-1327.	1.7	6
4240	Chromatinâ€modifying drugs and metabolites in cell fate control. Cell Proliferation, 2020, 53, e12898.	2.4	11
4241	NSD3-Induced Methylation of H3K36 Activates NOTCH Signaling to Drive Breast Tumor Initiation and Metastatic Progression. Cancer Research, 2021, 81, 77-90.	0.4	41
4242	Histone Variants and Histone Modifications in Neurogenesis. Trends in Cell Biology, 2020, 30, 869-880.	3.6	23
4243	Regulatory Mechanisms of Epigenetic miRNA Relationships in Human Cancer and Potential as Therapeutic Targets. Cancers, 2020, 12, 2922.	1.7	84
4244	<p>Targeting of KDM5A by miR-421 in Human Ovarian Cancer Suppresses the Progression of Ovarian Cancer Cells</p> . OncoTargets and Therapy, 2020, Volume 13, 9419-9428.	1.0	12
4245	EpiMogrify Models H3K4me3 Data to Identify Signaling Molecules that Improve Cell Fate Control and Maintenance. Cell Systems, 2020, 11, 509-522.e10.	2.9	10
4246	Inhibition of PfMYST Histone Acetyltransferase Activity Blocks Plasmodium falciparum Growth and Survival. Antimicrobial Agents and Chemotherapy, 2020, 65, .	1.4	6
4247	μDamID: A Microfluidic Approach for Joint Imaging and Sequencing of Protein-DNA Interactions in Single Cells. Cell Systems, 2020, 11, 354-366.e9.	2.9	15
4248	Targeting histone demethylase KDM5B for cancer treatment. European Journal of Medicinal Chemistry, 2020, 208, 112760.	2.6	21
4249	DNA Processing in the Context of Noncoding Transcription. Trends in Biochemical Sciences, 2020, 45, 1009-1021.	3.7	20
4250	ChIA-PIPE: A fully automated pipeline for comprehensive ChIA-PET data analysis and visualization. Science Advances, 2020, 6, eaay2078.	4.7	22
4251	Approaching Sex Differences in Cardiovascular Non-Coding RNA Research. International Journal of Molecular Sciences, 2020, 21, 4890.	1.8	12
4252	CoryneRegNet 7, the reference database and analysis platform for corynebacterial gene regulatory networks. Scientific Data, 2020, 7, 142.	2.4	22
4253	Normal Patterns of Histone H3K27 Methylation Require the Histone Variant H2A.Z in Neurospora crassa. Genetics, 2020, 216, 51-66.	1.2	14
4254	Hypoxic Regulation of Gene Transcription and Chromatin: Cause and Effect. International Journal of Molecular Sciences, 2020, 21, 8320.	1.8	29
4255	Histone modifications associated with gene expression and genome accessibility are dynamically enriched at Plasmodium falciparum regulatory sequences. Epigenetics and Chromatin, 2020, 13, 50.	1.8	28
4256	Histone sumoylation promotes Set3 histone-deacetylase complex-mediated transcriptional regulation. Nucleic Acids Research, 2020, 48, 12151-12168.	6.5	28

ARTICLE IF CITATIONS Histone tail analysis reveals H3K36me2 and H4K16ac as epigenetic signatures of diffuse intrinsic 4257 3.5 16 pontine glioma. Journal of Experimental and Clinical Cancer Research, 2020, 39, 261. DNA Double-Strand Breaks Are a Critical Regulator of Fear Memory Reconsolidation. International 4259 1.8 Journal of Molecular Sciences, 2020, 21, 8995. Exposome and Immunity Training: How Pathogen Exposure Order Influences Innate Immune Cell Lineage 4260 1.8 18 Commitment and Function. International Journal of Molecular Sciences, 2020, 21, 8462. P<scp>eax</scp>: Interactive Visual Pattern Search in Sequential Data Using Unsupervised Deep 4261 1.8 Representation Learning. Computer Graphics Forum, 2020, 39, 167-179. The crucial role of epigenetic regulation in breast cancer anti-estrogen resistance: Current findings 4262 4.3 31 and future perspectives. Seminars in Cancer Biology, 2022, 82, 35-59. Conserved Epigenetic Regulatory Logic Infers Genes Governing Cell Identity. Cell Systems, 2020, 11, 625-639.e13 Highly Efficient Separation of Methylated Peptides Utilizing Selective Complexation between Lysine 4264 3.2 5 and 18-Crown-6. Analytical Chemistry, 2020, 92, 15663-15670. From thymus to periphery: Molecular basis of effector $\hat{I}^{3}\hat{a}\in \mathcal{I}$ cell differentiation. Immunological Reviews, 4265 2.8 2020, 298, 47-60. Evidence that miR-152-3p is a positive regulator of SETDB1-mediated H3K9 histone methylation and 4266 1.2 4 serves as a toggle between histone and DNA methylation. Experimental Cell Research, 2020, 395, 112216. Diploid genome architecture revealed by multi-omic data of hybrid mice. Genome Research, 2020, 30, 4267 2.4 1097-1106. Combinatorial ChIP and bisulfite sequencing (BisChIP-seq)., 2020, , 387-395. 0 4268 An atlas of dynamic chromatin landscapes in mouse fetal development. Nature, 2020, 583, 744-751. 4269 13.7 Networkâ€based approaches for understanding gene regulation and function in plants. Plant Journal, 4270 2.8 35 2020, 104, 302-317. Human L1 Transposition Dynamics Unraveled with Functional Data Analysis. Molecular Biology and Evolution, 2020, 37, 3576-3600. 4271 3.5 Transcriptome-wide stability analysis uncovers LARP4-mediated NFκB1 mRNA stabilization during TÂcell 4272 10 6.5 activation. Nucleic Acids Research, 2020, 48, 8724-8739. DNA mismatch repair promotes APOBEC3-mediated diffuse hypermutation in human cancers. Nature 4273 9.4 Genetics, 2020, 52, 958-968. Interactions With Histone H3 & amp; Tools to Study Them. Frontiers in Cell and Developmental Biology, 4274 1.8 17 2020, 8, 701. XACT-Seq Comprehensively Defines the Promoter-Position and Promoter-Sequence Determinants for 4.5 Initial-Transcription Pausing. Molecular Cell, 2020, 79, 797-811.e8.

#	Article	IF	CITATIONS
4276	Cell-free Chromatin Immunoprecipitation (cfChIP) from blood plasma can determine gene-expression in tumors from non-small-cell lung cancer patients. Lung Cancer, 2020, 147, 244-251.	0.9	12
4277	Principles and innovative technologies for decrypting noncoding RNAs: from discovery and functional prediction to clinical application. Journal of Hematology and Oncology, 2020, 13, 109.	6.9	60
4278	Crystal Structure of MLL2 Complex Guides the Identification of a Methylation Site on P53 Catalyzed by KMT2 Family Methyltransferases. Structure, 2020, 28, 1141-1148.e4.	1.6	14
4279	Post-translational modifications of PRC2: signals directing its activity. Epigenetics and Chromatin, 2020, 13, 47.	1.8	39
4280	Establishment and function of chromatin modification at enhancers. Open Biology, 2020, 10, 200255.	1.5	13
4281	Evaluation of post-translational modifications in histone proteins: A review on histone modification defects in developmental and neurological disorders. Journal of Biosciences, 2020, 45, 1.	0.5	79
4282	setd2 knockout zebrafish is viable and fertile: differential and developmental stress-related requirements for Setd2 and histone H3K36 trimethylation in different vertebrate animals. Cell Discovery, 2020, 6, 72.	3.1	8
4283	Single-Cell Sequencing of Mouse Thymocytes Reveals Mutational Landscape Shaped by Replication Errors, Mismatch Repair, and H3K36me3. IScience, 2020, 23, 101452.	1.9	5
4284	Leptin regulates exon-specific transcription of the Bdnf gene via epigenetic modifications mediated by an AKT/p300 HAT cascade. Molecular Psychiatry, 2021, 26, 3701-3722.	4.1	31
4285	Genome-wide chromatin accessibility is restricted by ANP32E. Nature Communications, 2020, 11, 5063.	5.8	29
4286	Chromatin Dynamics in Intestinal Epithelial Homeostasis: A Paradigm of Cell Fate Determination versus Cell Plasticity. Stem Cell Reviews and Reports, 2020, 16, 1062-1080.	1.7	7
4287	Prediction of transcription factors binding events based on epigenetic modifications in different human cells. Epigenomics, 2020, 12, 1443-1456.	1.0	20
4288	Changes in circulating miRNA19a-3p precede insulin resistance programmed by intra-uterine growth retardation in mice. Molecular Metabolism, 2020, 42, 101083.	3.0	12
4289	Interplay of m ⁶ A and H3K27 trimethylation restrains inflammation during bacterial infection. Science Advances, 2020, 6, eaba0647.	4.7	85
4290	Efficient chromatin profiling of H3K4me3 modification in cotton using CUT&Tag. Plant Methods, 2020, 16, 120.	1.9	31
4291	Cancer SLC43A2 alters T cell methionine metabolism and histone methylation. Nature, 2020, 585, 277-282.	13.7	280
4292	Changes in regeneration-responsive enhancers shape regenerative capacities in vertebrates. Science, 2020, 369, .	6.0	147
4293	The nuclear cap-binding complex as choreographer of gene transcription and pre-mRNA processing. Genes and Development, 2020, 34, 1113-1127.	2.7	41

#	Article	IF	CITATIONS
4294	Understanding the Interplay Between Health Disparities and Epigenomics. Frontiers in Genetics, 2020, 11, 903.	1.1	37
4295	CHD8 dosage regulates transcription in pluripotency and early murine neural differentiation. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 22331-22340.	3.3	27
4296	Estrogen Induces Selective Transcription of Caveolin1 Variants in Human Breast Cancer through Estrogen Responsive Element-Dependent Mechanisms. International Journal of Molecular Sciences, 2020, 21, 5989.	1.8	6
4297	Transcriptional regulation by methyltransferases and their role in the heart: highlighting novel emerging functionality. American Journal of Physiology - Heart and Circulatory Physiology, 2020, 319, H847-H865.	1.5	11
4298	LINC00673 Represses CDKN2C and Promotes the Proliferation of Esophageal Squamous Cell Carcinoma Cells by EZH2-Mediated H3K27 Trimethylation. Frontiers in Oncology, 2020, 10, 1546.	1.3	14
4299	Genome-Wide Transcriptional Regulation of the Long Non-coding RNA Steroid Receptor RNA Activator in Human Erythroblasts. Frontiers in Genetics, 2020, 11, 850.	1.1	6
4300	The Interplay Between Exercise Metabolism, Epigenetics, and Skeletal Muscle Remodeling. Exercise and Sport Sciences Reviews, 2020, 48, 188-200.	1.6	47
4301	Medulloblastoma epigenetics and the path to clinical innovation. Journal of Neuro-Oncology, 2020, 150, 35-46.	1.4	7
4302	Targeting Chromatin Complexes in Myeloid Malignancies and Beyond: From Basic Mechanisms to Clinical Innovation. Cells, 2020, 9, 2721.	1.8	13
4303	Epigenetic Variation Analysis Leads to Biomarker Discovery in Gastric Adenocarcinoma. Frontiers in Genetics, 2020, 11, 551787.	1.1	1
4304	Histone Variant H3.3 Mutations in Defining the Chromatin Function in Mammals. Cells, 2020, 9, 2716.	1.8	10
4305	Introduction to epigenetics: basic concepts and advancements in the field. , 2020, , xxv-xliv.		1
4306	RECOGNICER: A coarseâ€graining approach for identifying broad domains from ChIPâ€seq data. Quantitative Biology, 2020, 8, 359-368.	0.3	1
4307	H4K20 Methylation Is Differently Regulated by Dilution and Demethylation in Proliferating and Cell-Cycle-Arrested Xenopus Embryos. Cell Systems, 2020, 11, 653-662.e8.	2.9	6
4308	Nucleosome Positioning around Transcription Start Site Correlates with Gene Expression Only for Active Chromatin State in Drosophila Interphase Chromosomes. International Journal of Molecular Sciences, 2020, 21, 9282.	1.8	2
4309	Pituitary Tumor Transforming Gene 1 Orchestrates Gene Regulatory Variation in Mouse Ventral Midbrain During Aging. Frontiers in Genetics, 2020, 11, 566734.	1.1	4
4310	Broad genic repression domains signify enhanced silencing of oncogenes. Nature Communications, 2020, 11, 5560.	5.8	10
4311	Profiling chromatin regulatory landscape: insights into the development of ChIP-seq and ATAC-seq. Molecular Biomedicine, 2020, 1, 9.	1.7	34

ARTICLE IF CITATIONS Mimicking the Nucleosomal Context in Peptide-Based Binders of a H3K36me Reader Increases Binding 4312 1.7 0 Affinity While Altering the Binding Mode. Molecules, 2020, 25, 4951. Transcriptional regulation by the KMT2 histone H3K4 methyltransferases. Biochimica Et Biophysica 9 Acta - Gene Regulatory Mechanisms, 2020, 1863, 194545. An improved functional analysis of linker-mediated complex (iFALC) strategy. Biochemical and 4314 1.0 4 Biophysical Research Communications, 2020, 526, 1164-1169. Regulation of alternative polyadenylation in the yeast Saccharomyces cerevisiae by histone H3K4 and 24 H3K36 methyltransferases. Nucleic Acids Research, 2020, 48, 5407-5425. PIWIL4 Maintains HIV-1 Latency by Enforcing Epigenetically Suppressive Modifications on the $5\hat{a}\in^2$ Long 4316 1.5 8 Terminal Repeat. Journal of Virology, 2020, 94, . Epigenome signatures landscaped by histone H3K9me3 are associated with the synaptic dysfunction in Alzheimer's disease. Aging Cell, 2020, 19, e13153. 3.0 Histone H2A variants alpha1-extension helix directs RNF168-mediated ubiquitination. Nature 4318 5.8 18 Communications, 2020, 11, 2462. Population Genomics of Pearl Millet. Population Genomics, 2020, , 1. 0.2 4319 Extreme differences between human germline and tumor mutation densities are driven by ancestral 4320 9 5.8 human-specific deviations. Nature Communications, 2020, 11, 2512. Inhibition of LSD1 promotes the differentiation of human induced pluripotent stem cells into 2.4 insulin-producing cells. Stem Cell Research and Therapy, 2020, 11, 185. Epigenetic Alterations in Oesophageal Cancer: Expression and Role of the Involved Enzymes. 4322 7 1.8 International Journal of Molecular Sciences, 2020, 21, 3522. Polycomb-like 2 regulates PRC2 components to affect proliferation in glioma cells. Journal of 1.4 Neuro-Oncology, 2020, 148, 259-271 Transcriptional Control of Circadian Rhythms and Metabolism: A Matter of Time and Space. Endocrine 4324 8.9 66 Reviews, 2020, 41, 707-732. Improvements on the quantitative analysis of Trypanosoma cruzi histone post translational modifications: Study of changes in epigenetic marks through the parasite's metacyclogenesis and life cycle. Journal of Proteomics, 2020, 225, 103847. 1.2 Mutually suppressive roles of KMT2A and KDM5C in behaviour, neuronal structure, and histone H3K4 4326 2.0 26 methylation. Communications Biology, 2020, 3, 278. From GWAS to Function: Using Functional Genomics to Identify the Mechanisms Underlying Complex 335 Diseases. Frontiers in Genetics, 2020, 11, 424. The role of SETD1A and SETD1B in development and disease. Biochimica Et Biophysica Acta - Gene 4328 0.9 12 Regulatory Mechanisms, 2020, 1863, 194578. 4329 Chromatin remodelers in oligodendroglia. Glia, 2020, 68, 1604-1618.

#	Article	IF	CITATIONS
4330	Characterization of histone modification patterns and prediction of novel promoters using functional principal component analysis. PLoS ONE, 2020, 15, e0233630.	1.1	1
4331	Epigenetics of Drug Addiction. Cold Spring Harbor Perspectives in Medicine, 2021, 11, a040253.	2.9	21
4332	Epigenetics of spondyloarthritis. Joint Bone Spine, 2020, 87, 565-571.	0.8	8
4333	Modeling circRNA expression pattern with integrated sequence and epigenetic features demonstrates the potential involvement of H3K79me2 in circRNA expression. Bioinformatics, 2020, 36, 4739-4748.	1.8	3
4334	Translational Opportunities for Microfluidic Technologies to Enable Precision Epigenomics. Analytical Chemistry, 2020, 92, 7989-7997.	3.2	8
4335	Superresolution imaging reveals spatiotemporal propagation of human replication foci mediated by CTCF-organized chromatin structures. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 15036-15046.	3.3	27
4336	Emerging of lysine demethylases (KDMs): From pathophysiological insights to novel therapeutic opportunities. Biomedicine and Pharmacotherapy, 2020, 129, 110392.	2.5	30
4337	Modulation of KDM1A with vafidemstat rescues memory deficit and behavioral alterations. PLoS ONE, 2020, 15, e0233468.	1.1	29
4338	The Nâ€ŧerminal and Câ€ŧerminal halves of histone H2A.Z independently function in nucleosome positioning and stability. Genes To Cells, 2020, 25, 538-546.	0.5	10
4339	Genomic resources for dissecting the role of non-protein coding variation in gene-environment interactions. Toxicology, 2020, 441, 152505.	2.0	2
4340	Lysine acetyltransferase Tip60 is required for hematopoietic stem cell maintenance. Blood, 2020, 136, 1735-1747.	0.6	33
4341	Genomics of Pain and Co-Morbid Symptoms. , 2020, , .		0
4342	Epigenetic biomarkers and preterm birth. Environmental Epigenetics, 2020, 6, dvaa005.	0.9	19
4343	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
4344	A long noncoding RNA regulates inflammation resolution by mouse macrophages through fatty acid oxidation activation. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 14365-14375.	3.3	39
4345	Low-Phosphate Chromatin Dynamics Predict a Cell Wall Remodeling Network in Rice Shoots. Plant Physiology, 2020, 182, 1494-1509.	2.3	14
4346	Epigenetic mechanisms in the regulation of lymphocyte differentiation. , 2020, , 77-116.		3
4347	Epigenetics mechanisms driving immune memory cell differentiation and function. , 2020, , 117-137.		1

#	Article	IF	CITATIONS
4348	A review of epigenetic regulation in wound healing: Implications for the future of wound care. Wound Repair and Regeneration, 2020, 28, 710-718.	1.5	16
4349	Machine learning and deep learning for the advancement of epigenomics. , 2020, , 217-237.		0
4350	Dissecting myogenin-mediated retinoid X receptor signaling in myogenic differentiation. Communications Biology, 2020, 3, 315.	2.0	5
4351	Dynamic shifts in chromatin states differentially mark the proliferative basal cells and terminally differentiated cells of the developing epidermis. Epigenetics, 2020, 15, 932-948.	1.3	8
4352	The Role of Polycomb Repressive Complex in Malignant Peripheral Nerve Sheath Tumor. Genes, 2020, 11, 287.	1.0	17
4353	Chromatin Landscaping At Mitotic Exit Orchestrates Genome Function. Frontiers in Genetics, 2020, 11, 103.	1.1	8
4354	Probing the Diversity of Polycomb and Trithorax Proteins in Cultured and Environmentally Sampled Microalgae. Frontiers in Marine Science, 2020, 7, .	1.2	26
4355	Epigenetic regulation of oligodendrocyte differentiation: From development to demyelinating disorders. Glia, 2020, 68, 1619-1630.	2.5	23
4356	Regulation of gene expression by growth hormone. Molecular and Cellular Endocrinology, 2020, 507, 110788.	1.6	21
4357	Transgenerational acclimation to changes in ocean acidification in marine invertebrates. Marine Pollution Bulletin, 2020, 153, 111006.	2.3	26
4358	Exploring histone loading on HIV DNA reveals a dynamic nucleosome positioning between unintegrated and integrated viral genome. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 6822-6830.	3.3	26
4359	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
4360	Long INterspersed elementâ€4 mobility as a sensor of environmental stresses. Environmental and Molecular Mutagenesis, 2020, 61, 465-493.	0.9	15
4361	Purification and enrichment of specific chromatin loci. Nature Methods, 2020, 17, 380-389.	9.0	25
4362	Advances in applying of multi-omics approaches in the research of systemic lupus erythematosus. International Reviews of Immunology, 2020, 39, 163-173.	1.5	9
4363	Distinct roles for H4 and H2A.Z acetylation in RNA transcription in African trypanosomes. Nature Communications, 2020, 11, 1498.	5.8	35
4364	Genomic landscape of transcriptionally active histone arginine methylation marks, H3R2me2s and H4R3me2a, relative to nucleosome depleted regions. Gene, 2020, 742, 144593.	1.0	24
4365	H3K4me3 Is a Potential Mediator for Antiproliferative Effects of Calcitriol (1α,25(OH)2D3) in Ovarian Cancer Biology. International Journal of Molecular Sciences, 2020, 21, 2151.	1.8	8

#	Article	IF	CITATIONS
4366	Comparative analysis of ChIP-exo peak-callers: impact of data quality, read duplication and binding subtypes. BMC Bioinformatics, 2020, 21, 65.	1.2	2
4367	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
4368	Mass Spectrometry to Study Chromatin Compaction. Biology, 2020, 9, 140.	1.3	2
4369	Identification of Novel Molecular Markers of Human Th17 Cells. Cells, 2020, 9, 1611.	1.8	27
4370	Synoviocyte-targeted therapy synergizes with TNF inhibition in arthritis reversal. Science Advances, 2020, 6, eaba4353.	4.7	43
4371	miR-155 Accelerates the Growth of Human Liver Cancer Cells by Activating CDK2 via Targeting H3F3A. Molecular Therapy - Oncolytics, 2020, 17, 471-483.	2.0	16
4372	Regulation of inflammation in diabetes: From genetics to epigenomics evidence. Molecular Metabolism, 2020, 41, 101041.	3.0	23
4373	Sharing Marks: H3K4 Methylation and H2B Ubiquitination as Features of Meiotic Recombination and Transcription. International Journal of Molecular Sciences, 2020, 21, 4510.	1.8	12
4374	TRACE: transcription factor footprinting using chromatin accessibility data and DNA sequence. Genome Research, 2020, 30, 1040-1046.	2.4	12
4375	Epigenetic Regulation of Differentially Expressed Drug-Metabolizing Enzymes in Cancer. Drug Metabolism and Disposition, 2020, 48, 759-768.	1.7	14
4376	Epigenetic regulation of intestinal stem cell differentiation. American Journal of Physiology - Renal Physiology, 2020, 319, G189-G196.	1.6	11
4377	Skeletal muscle as an experimental model of choice to study tissue aging and rejuvenation. Skeletal Muscle, 2020, 10, 4.	1.9	32
4378	When function follows form: Nuclear compartment structure and the epigenetic landscape of the aging neuron. Experimental Gerontology, 2020, 133, 110876.	1.2	11
4379	Histone demethylase KDM4D cooperates with NFIB and MLL1 complex to regulate adipogenic differentiation of C3H10T1/2 mesenchymal stem cells. Scientific Reports, 2020, 10, 3050.	1.6	15
4380	Alteration of CTCF-associated chromatin neighborhood inhibits TAL1-driven oncogenic transcription program and leukemogenesis. Nucleic Acids Research, 2020, 48, 3119-3133.	6.5	19
4381	Reverse transcriptase inhibitors promote the remodelling of nuclear architecture and induce autophagy in prostate cancer cells. Cancer Letters, 2020, 478, 133-145.	3.2	14
4382	Simultaneous detection of site-specific histone methylations and acetylation assisted by single template oriented molecularly imprinted polymers. Analyst, The, 2020, 145, 1376-1383.	1.7	16
4383	Histone methyltransferase G9a diminishes expression of cannabinoid CB1 receptors in primary sensory neurons in neuropathic pain. Journal of Biological Chemistry, 2020, 295, 3553-3562.	1.6	18

#	Article	IF	CITATIONS
4384	Current Approaches Targeting the Wound Healing Phases to Attenuate Fibrosis and Scarring. International Journal of Molecular Sciences, 2020, 21, 1105.	1.8	117
4385	Measurement of differential chromatin interactions with absolute quantification of architecture (AQuA-HiChIP). Nature Protocols, 2020, 15, 1209-1236.	5.5	19
4386	Regulation of epigenetic state by non-histone chromatin proteins and transcription factors: Implications in disease. Journal of Biosciences, 2020, 45, 1.	0.5	4
4387	Genomic programming of IRF4-expressing human Langerhans cells. Nature Communications, 2020, 11, 313.	5.8	22
4388	ModHMM: A Modular Supra-Bayesian Genome Segmentation Method. Journal of Computational Biology, 2020, 27, 442-457.	0.8	6
4389	Towards a comprehensive catalogue of validated and target-linked human enhancers. Nature Reviews Genetics, 2020, 21, 292-310.	7.7	229
4390	Broad domains of histone H3 lysine 4 trimethylation in transcriptional regulation and disease. FEBS Journal, 2020, 287, 2891-2902.	2.2	51
4391	Role of a DEF/Y motif in histone H2A-H2B recognition and nucleosome editing. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 3543-3550.	3.3	19
4392	Ubiquitin-specific protease 7 is a drug-able target that promotes hepatocellular carcinoma and chemoresistance. Cancer Cell International, 2020, 20, 28.	1.8	20
4394	Decoding the Role of Satellite DNA in Genome Architecture and Plasticity—An Evolutionary and Clinical Affair. Genes, 2020, 11, 72.	1.0	47
4395	From reads to insight: a hitchhiker's guide to ATAC-seq data analysis. Genome Biology, 2020, 21, 22.	3.8	268
4396	Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. Nature Genetics, 2020, 52, 306-319.	9.4	275
4397	Oct4-Mediated Inhibition of Lsd1 Activity Promotes the Active and Primed State of Pluripotency Enhancers. Cell Reports, 2020, 30, 1478-1490.e6.	2.9	17
4398	H3K4me1 Distribution Predicts Transcription State and Poising at Promoters. Frontiers in Cell and Developmental Biology, 2020, 8, 289.	1.8	61
4399	Sex-specific epigenetic gene activation profiles are differentially modulated in human placentas affected by intrauterine growth restriction. Journal of Reproductive Immunology, 2020, 139, 103124.	0.8	2
4400	KMT2D Deficiency Impairs Super-Enhancers to Confer a Glycolytic Vulnerability in Lung Cancer. Cancer Cell, 2020, 37, 599-617.e7.	7.7	137
4401	Centromeric RNA and Its Function at and Beyond Centromeric Chromatin. Journal of Molecular Biology, 2020, 432, 4257-4269.	2.0	25
4402	Exposure to low doses of inorganic arsenic induces transgenerational changes on behavioral and epigenetic markers in zebrafish (Danio rerio). Toxicology and Applied Pharmacology, 2020, 396, 115002.	1.3	41

#	Article	IF	CITATIONS
4403	A G(enomic)P(ositioning)S(ystem) for Plant RNAPII Transcription. Trends in Plant Science, 2020, 25, 744-764.	4.3	30
4404	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
4405	The potential underlying mechanism of the leukemia caused by <i>MLL</i> â€fusion and potential treatments. Molecular Carcinogenesis, 2020, 59, 839-851.	1.3	6
4406	Predicting target genes of non-coding regulatory variants with IRT. Bioinformatics, 2020, 36, 4440-4448.	1.8	6
4407	Epigenetic regulation in human cancer: the potential role of epi-drug in cancer therapy. Molecular Cancer, 2020, 19, 79.	7.9	255
4408	Insights on the regulation of the MLL/SET1 family histone methyltransferases. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2020, 1863, 194561.	0.9	22
4409	CRISPR/Cas9 Epigenome Editing Potential for Rare Imprinting Diseases: A Review. Cells, 2020, 9, 993.	1.8	33
4411	Drosophila P75 safeguards oogenesis by preventing H3K9me2 spreading. Journal of Genetics and Genomics, 2020, 47, 187-199.	1.7	8
4412	Comparative proteomic analysis of protein methylation provides insight into the resistance of hepatocellular carcinoma to 5-fluorouracil. Journal of Proteomics, 2020, 219, 103738.	1.2	1
4413	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
4414	X-Linked RNA-Binding Motif Protein Modulates HIV-1 Infection of CD4 ⁺ T Cells by Maintaining the Trimethylation of Histone H3 Lysine 9 at the Downstream Region of the 5′ Long Terminal Repeat of HIV Proviral DNA. MBio, 2020, 11, .	1.8	8
4415	Data Integration for Immunology. Annual Review of Biomedical Data Science, 2020, 3, 113-136.	2.8	5
4416	BAMscale: quantification of next-generation sequencing peaks and generation of scaled coverage tracks. Epigenetics and Chromatin, 2020, 13, 21.	1.8	40
4417	Gain-of-Function Genetic Alterations of G9a Drive Oncogenesis. Cancer Discovery, 2020, 10, 980-997.	7.7	44
4418	EPIGENE: genome-wide transcription unit annotation using a multivariate probabilistic model of histone modifications. Epigenetics and Chromatin, 2020, 13, 20.	1.8	2
4419	Adaptive responses of histone modifications to resistance exercise in human skeletal muscle. PLoS ONE, 2020, 15, e0231321.	1.1	23
4420	Transcriptomic and ChIP-seq Integrative Analysis Reveals Important Roles of Epigenetically Regulated IncRNAs in Placental Development in Meishan Pigs. Genes, 2020, 11, 397.	1.0	6
4421	Upregulation of H3K27 Demethylase KDM6 During Respiratory Syncytial Virus Infection Enhances Proinflammatory Responses and Immunopathology. Journal of Immunology, 2020, 204, 159-168.	0.4	27

#		IF	CITATIONS
4423	TET3 controls the expression of the H3K27me3 demethylase Kdm6b during neural commitment. Cellular and Molecular Life Sciences, 2021, 78, 757-768.	2.4	11
4424	Computational annotation of miRNA transcription start sites. Briefings in Bioinformatics, 2021, 22, 380-392.	3.2	23
4425	Epigenetic and Transcriptional Control of the Epidermal Growth Factor Receptor Regulates the Tumor Immune Microenvironment in Pancreatic Cancer. Cancer Discovery, 2021, 11, 736-753.	7.7	73
4426	Upregulation of histone H3K9 methylation in fetal endothelial cells from preeclamptic pregnancies. Journal of Cellular Physiology, 2021, 236, 1866-1874.	2.0	4
4427	Histone variants in skeletal myogenesis. Epigenetics, 2021, 16, 243-262.	1.3	5
4428	CpG Islands Shape the Epigenome Landscape. Journal of Molecular Biology, 2021, 433, 166659.	2.0	16
4429	Metabolic Flexibility Assists Reprograming of Central and Peripheral Innate Immunity During Neurodevelopment. Molecular Neurobiology, 2021, 58, 703-718.	1.9	4
4430	Contributions of Histone Variants in Nucleosome Structure and Function. Journal of Molecular Biology, 2021, 433, 166678.	2.0	49
4431	Computational methods and next-generation sequencing approaches to analyze epigenetics data: Profiling of methods and applications. Methods, 2021, 187, 92-103.	1.9	24
4432	Epigenetic Signatures and Plasticity of Intestinal and Other Stem Cells. Annual Review of Physiology, 2021, 83, 405-427.	5.6	6
4433	Male hybrid sterility in the cattle-yak and other bovines: a review. Biology of Reproduction, 2021, 104, 495-507.	1.2	22
4434	SETD8 potentiates constitutive ERK1/2 activation via epigenetically silencing DUSP10 expression in pancreatic cancer. Cancer Letters, 2021, 499, 265-278.	3.2	16
4435	GTRD: an integrated view of transcription regulation. Nucleic Acids Research, 2021, 49, D104-D111.	6.5	137
4436	The epigenetic basis of cellular heterogeneity. Nature Reviews Genetics, 2021, 22, 235-250.	7.7	163
4437	Methylation of histone 4's lysine 20: a critical analysis of the state of the field. Physiological Genomics, 2021, 53, 22-32.	1.0	14
4438	Breaths, Twists, and Turns of Atomistic Nucleosomes. Journal of Molecular Biology, 2021, 433, 166744.	2.0	19
4439	Effects of chronic stress on depressive-like behaviors and JMJD3 expression in the prefrontal cortex and hippocampus of C57BL/6 and ob/ob mice. Journal of Psychiatric Research, 2021, 133, 142-155.	1.5	9
4440	MetaTX: deciphering the distribution of mRNA-related features in the presence of isoform ambiguity, with applications in epitranscriptome analysis. Bioinformatics, 2021, 37, 1285-1291.	1.8	10

#	Article	IF	CITATIONS
4441	To mock or not: a comprehensive comparison of mock IP and DNA input for ChIP-seq. Nucleic Acids Research, 2021, 49, e17-e17.	6.5	8
4442	Super enhancers—Functional cores under the 3D genome. Cell Proliferation, 2021, 54, e12970.	2.4	17
4443	Targeting EHMT2/ G9a for cancer therapy: Progress and perspective. European Journal of Pharmacology, 2021, 893, 173827.	1.7	23
4444	Targeting PRC2 for the treatment of cancer: an updated patent review (2016 - 2020). Expert Opinion on Therapeutic Patents, 2021, 31, 119-135.	2.4	28
4445	Significant compaction of H4 histone tail upon charge neutralization by acetylation and its mimics, possible effects on chromatin structure. Journal of Molecular Biology, 2021, 433, 166683.	2.0	4
4447	Epigenetic Reprogramming During Mouse Embryogenesis. Methods in Molecular Biology, 2021, , .	0.4	1
4448	Exploring Epigenetic Marks by Analysis of Noncovalent Interactions. ChemBioChem, 2021, 22, 408-415.	1.3	2
4449	Computer-aided screening for suppressor of variegation 4-20 homolog 1 inhibitors and their preliminary activity validation in human osteosarcoma. Journal of Biomolecular Structure and Dynamics, 2021, 39, 526-537.	2.0	4
4450	Secondary Metabolite Production in Plant Cell Culture: A New Epigenetic Frontier. , 2021, , 1-37.		2
4451	Pathogenic histone modifications in schizophrenia are targets for therapy. , 2021, , 309-319.		1
4452	Histone lysine demethylase inhibitor (HDMi) as chemo-sensitizing agent. , 2021, , 41-55.		0
4453	Regulation of Seed Dormancy and Germination Mechanisms in a Changing Environment. International Journal of Molecular Sciences, 2021, 22, 1357.	1.8	44
4454	Histone modifications, DNA methylation, and the epigenetic code of alcohol use disorder. International Review of Neurobiology, 2021, 156, 1-62.	0.9	21
4455	Biclustering via Semiparametric Bayesian Inference. Bayesian Analysis, 2022, 17, .	1.6	1
4456	Native Chromatin Proteomics (N-ChroP) to Characterize Histone Post-translational Modification (PTM) Combinatorics at Distinct Genomic Regions. Methods in Molecular Biology, 2021, 2351, 251-274.	0.4	1
4457	Parental nucleosome segregation and the inheritance of cellular identity. Nature Reviews Genetics, 2021, 22, 379-392.	7.7	63
4458	Genome-Wide Histone Modifications and CTCF Enrichment Predict Gene Expression in Sheep Macrophages. Frontiers in Genetics, 2020, 11, 612031.	1.1	9
4459	Precision Surface Microtopography Regulates Cell Fate via Changes to Actomyosin Contractility and Nuclear Architecture. Advanced Science, 2021, 8, 2003186.	5.6	41

	Cı	TATION REP	PORT	
#	Article		IF	CITATIONS
4460	BACH1 recruits NANOG and histone H3 lysine 4 methyltransferase MLL/SET1 complexes to regulate enhancer–promoter activity and maintains pluripotency. Nucleic Acids Research, 2021, 49, 1972-19	986.	6.5	24
4461	Probiotics Stimulate Bone Formation in Obese Mice via Histone Methylations. Theranostics, 2021, 11 8605-8623.	,	4.6	22
4462	Targeting histone lysine methyltransferases for drug sensitization. , 2021, , 57-67.			0
4463	Exercise, epigenetics, and aging. , 2021, , 127-182.			1
4464	Épigénétique de la spondyloarthrite. Revue Du Rhumatisme (Edition Francaise), 2021, 88, 32-	39.	0.0	0
4465	H3K4 trimethylation dynamics impact diverse developmental and environmental responses in plants. Planta, 2021, 253, 4.		1.6	13
4466	Principles of epigenetics and DNA methylation. , 2021, , 3-26.			0
4469	Epigenetics concepts: An overview. , 2021, , 19-40.			0
4470	Genome-wide analysis of chromatin structure changes upon MyoD binding in proliferative myoblasts during the cell cycle. Journal of Biochemistry, 2021, 169, 653-661.		0.9	0
4471	Loss of FOXC1 contributes to the corneal epithelial fate switch and pathogenesis. Signal Transduction and Targeted Therapy, 2021, 6, 5.		7.1	12
4472	ChIP-seq of plasma cell-free nucleosomes identifies gene expression programs of the cells of origin. Nature Biotechnology, 2021, 39, 586-598.		9.4	81
4473	Insight into the multi-faceted role of the SUV family of H3K9 methyltransferases in carcinogenesis and cancer progression. Biochimica Et Biophysica Acta: Reviews on Cancer, 2021, 1875, 188498.	1	3.3	23
4474	Methylation multiplicity and its clinical values in cancer. Expert Reviews in Molecular Medicine, 2021, 23, e2.		1.6	45
4475	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
4476	Prioritization of regulatory variants with tissue-specific function in the non-coding regions of human genome. Nucleic Acids Research, 2022, 50, e6-e6.		6.5	13
4477	Genome-Wide Profiling of Protein–DNA Interactions with Chromatin Endogenous Cleavage and High-Throughput Sequencing (ChEC-Seq). Methods in Molecular Biology, 2021, 2351, 289-303.		0.4	2
4478	Epigenetic mechanisms of hepatocellular carcinoma progression: Potential therapeutic opportunities. , 2021, , 279-296.			0
4479	Histone modifications during the life cycle of the brown alga Ectocarpus. Genome Biology, 2021, 22, 12.		3.8	29

		CITATION REPORT		
#	Article		IF	Citations
4480	Brain stem gliomas and current landscape. Journal of Neuro-Oncology, 2021, 151, 21-2	28.	1.4	2
4481	CRISPR/dCas system as the modulator of gene expression. Progress in Molecular Biolo Translational Science, 2021, 178, 99-122.	gy and	0.9	10
4483	Histone lysine methyltransferase Prâ€set7/SETD8 promotes neural stem cell reactivati 2021, 22, e50994.	on. EMBO Reports,	2.0	12
4484	The histone demethylase KDM5 is required for synaptic structure and function at the I neuromuscular junction. Cell Reports, 2021, 34, 108753.	Drosophila	2.9	15
4485	Cell Cycle Regulation of the Pdx1 Transcription Factor in Developing Pancreas and Insu β-Cells. Diabetes, 2021, 70, 903-916.	ılin-Producing	0.3	10
4486	The Histone Modifications of Neuronal Plasticity. Neural Plasticity, 2021, 2021, 1-7.		1.0	27
4487	The Transcriptional Regulatory Network of Corynebacterium pseudotuberculosis. Micr 2021, 9, 415.	oorganisms,	1.6	4
4488	Crosstalk Between mRNA 3'-End Processing and Epigenetics. Frontiers in Genetics, 202	21, 12, 637705.	1.1	13
4489	Targeting EZH2 as cancer therapy. Journal of Biochemistry, 2021, 170, 1-4.		0.9	29
4490	Signalingâ€toâ€chromatin pathways in the immune system. Immunological Reviews, 2	.021, 300, 37-53.	2.8	10
4491	WACS: improving ChIP-seq peak calling by optimally weighting controls. BMC Bioinfor 69.	matics, 2021, 22,	1.2	3
4492	DNA or Protein Methylation-Dependent Regulation of Activator Protein-1 Function. Ce	lls, 2021, 10, 461.	1.8	10
4493	Three-dimensional chromatin in infectious disease—A role for gene regulation and pa PLoS Pathogens, 2021, 17, e1009207.	thogenicity?.	2.1	5
4494	Non-CG methylation and multiple histone profiles associate child abuse with immune a dysregulation. Nature Communications, 2021, 12, 1132.	ind small GTPase	5.8	24
4495	Epigenetic Landscape of Liquid Biopsy in Colorectal Cancer. Frontiers in Cell and Devel Biology, 2021, 9, 622459.	opmental	1.8	31
4496	FAN1, a DNA Repair Nuclease, as a Modifier of Repeat Expansion Disorders. Journal of I Disease, 2021, 10, 95-122.	Huntington's	0.9	34
4497	Targeting Epigenetic Regulators for Endometrial Cancer Therapy: Its Molecular Biology Clinical Applications. International Journal of Molecular Sciences, 2021, 22, 2305.	and Potential	1.8	14
4498	Epigenetic regulation of adipogenesis by histone-modifying enzymes. Epigenomics, 20	21, 13, 235-251.	1.0	17

		TION REPORT	
#	Article	IF	Citations
4499	Combinations of histone post-translational modifications. Biochemical Journal, 2021, 478, 511-532.	1.7	46
4500	RAD: a web application to identify region associated differentially expressed genes. Bioinformatics, 2021, 37, 2741-2743.	1.8	11
4501	<i>Caenorhabditis elegans</i> establishes germline versus soma by balancing inherited histone methylation. Development (Cambridge), 2021, 148, .	1.2	13
4502	Filtering the Junk: Assigning Function to the Mosquito Non-Coding Genome. Insects, 2021, 12, 186.	1.0	7
4504	Annotation of chromatin states in 66 complete mouse epigenomes during development. Communications Biology, 2021, 4, 239.	2.0	34
4505	Multi-Dimensional Gene Regulation in Innate and Adaptive Lymphocytes: A View From Regulomes. Frontiers in Immunology, 2021, 12, 655590.	2.2	12
4506	Dopant-Dependent Toxicity of CeO2 Nanoparticles Is Associated with Dynamic Changes in H3K4me3 an H3K27me3 and Transcriptional Activation of NRF2 Gene in HaCaT Human Keratinocytes. International Journal of Molecular Sciences, 2021, 22, 3087.	nd 1.8	6
4507	Epigenetic evidence of an Ac/Dc axis by VPA and SAHA. Clinical Epigenetics, 2021, 13, 58.	1.8	13
4508	Epigenetic Mechanisms Are Involved in the Oncogenic Properties of ZNF518B in Colorectal Cancer. Cancers, 2021, 13, 1433.	1.7	4
4509	The Cranial Neural Crest in a Multiomics Era. Frontiers in Physiology, 2021, 12, 634440.	1.3	10
4510	The G-Protein-Coupled Estrogen Receptor (GPER) Regulates Trimethylation of Histone H3 at Lysine 4 and Represses Migration and Proliferation of Ovarian Cancer Cells In Vitro. Cells, 2021, 10, 619.	1.8	13
4511	DNA methylation and histone modifications are essential for regulation of stem cell formation and differentiation in zebrafish development. Briefings in Functional Genomics, 2021, , .	1.3	3
4512	Epigenetic Consequences of in Utero Exposure to Rosuvastatin: Alteration of Histone Methylation Patterns in Newborn Rat Brains. International Journal of Molecular Sciences, 2021, 22, 3412.	1.8	4
4514	Runx proteins and transcriptional mechanisms that govern memory CD8 T cell development. Immunological Reviews, 2021, 300, 100-124.	2.8	13
4515	A plug and play microfluidic platform for standardized sensitive low-input chromatin immunoprecipitation. Genome Research, 2021, 31, 919-933.	2.4	4
4516	Pontin Functions as A Transcriptional Co-activator for Retinoic Acid-induced HOX Gene Expression. Journal of Molecular Biology, 2021, 433, 166928.	2.0	1
4517	On the Consistency between Gene Expression and the Gene Regulatory Network of Corynebacterium glutamicum. Network and Systems Medicine, 2021, 4, 51-59.	2.7	7
4519	Epigenetics and microRNAs in cardiovascular diseases. Genomics, 2021, 113, 540-551.	1.3	29

#	Article	IF	CITATIONS
4520	Current paradigms in epigenetic anticancer therapeutics and future challenges. Seminars in Cancer Biology, 2022, 83, 422-440.	4.3	26
4521	Integrative pan cancer analysis reveals epigenomic variation in cancer type and cell specific chromatin domains. Nature Communications, 2021, 12, 1419.	5.8	46
4522	Epigenetic regulation of arginine vasopressin receptor 2 expression by PAX2 and Pax transcription interacting protein. American Journal of Physiology - Renal Physiology, 2021, 320, F404-F417.	1.3	5
4523	Machine learning for deciphering cell heterogeneity and gene regulation. Nature Computational Science, 2021, 1, 183-191.	3.8	14
4524	CD8 ⁺ T-Cell Memory: The Why, the When, and the How. Cold Spring Harbor Perspectives in Biology, 2021, 13, a038661.	2.3	7
4525	The Genome-Wide EMS Mutagenesis Bias Correlates With Sequence Context and Chromatin Structure in Rice. Frontiers in Plant Science, 2021, 12, 579675.	1.7	20
4526	Nutrient regulation of the flow of genetic information by O-GlcNAcylation. Biochemical Society Transactions, 2021, 49, 867-880.	1.6	12
4527	A two-stream convolutional neural network for microRNA transcription start site feature integration and identification. Scientific Reports, 2021, 11, 5625.	1.6	7
4528	Functional annotations of three domestic animal genomes provide vital resources for comparative and agricultural research. Nature Communications, 2021, 12, 1821.	5.8	105
4529	WNT5a in Colorectal Cancer: Research Progress and Challenges. Cancer Management and Research, 2021, Volume 13, 2483-2498.	0.9	6
4530	The Anti-Inflammatory Properties of Phytochemicals and Their Effects on Epigenetic Mechanisms Involved in TLR4/NF-κB-Mediated Inflammation. Frontiers in Immunology, 2021, 12, 606069.	2.2	66
4531	Omics data integration identifiesÂELOVL7ÂandÂMMDÂgene regions as novel loci for adalimumab response in patients with Crohn's disease. Scientific Reports, 2021, 11, 5449.	1.6	8
4532	X chromosome escapee genes are involved in ischemic sexual dimorphism through epigenetic modification of inflammatory signals. Journal of Neuroinflammation, 2021, 18, 70.	3.1	35
4533	Integrative RNA-Seq and H3 Trimethylation ChIP-Seq Analysis of Human Lung Cancer Cells Isolated by Laser-Microdissection. Cancers, 2021, 13, 1719.	1.7	1
4535	Histone Modification: A Mechanism for Regulating Skeletal Muscle Characteristics and Adaptive Changes. Applied Sciences (Switzerland), 2021, 11, 3905.	1.3	5
4536	GS-9822, a Preclinical LEDGIN Candidate, Displays a Block-and-Lock Phenotype in Cell Culture. Antimicrobial Agents and Chemotherapy, 2021, 65, .	1.4	17
4537	The cap-specific m6A methyltransferase, PCIF1/CAPAM, is dynamically recruited to the gene promoter in a transcription-dependent manner. Journal of Biochemistry, 2021, 170, 203-213.	0.9	7
4538	Current Methods of Post-Translational Modification Analysis and Their Applications in Blood Cancers. Cancers, 2021, 13, 1930.	1.7	24

#	Article	IF	CITATIONS
4539	O-GlcNAcylation and O-GlcNAc Cycling Regulate Gene Transcription: Emerging Roles in Cancer. Cancers, 2021, 13, 1666.	1.7	62
4540	Profiling single-cell histone modifications using indexing chromatin immunocleavage sequencing. Genome Research, 2021, 31, 1831-1842.	2.4	17
4541	Control of Breast Cancer Pathogenesis by Histone Methylation and the Hairless Histone Demethylase. Endocrinology, 2021, 162, .	1.4	7
4543	FGF23 ameliorates ischemia-reperfusion induced acute kidney injury via modulation of endothelial progenitor cells: targeting SDF-1/CXCR4 signaling. Cell Death and Disease, 2021, 12, 409.	2.7	12
4544	Nuclear Dishevelled targets gene regulatory regions and promotes tumor growth. EMBO Reports, 2021, 22, e50600.	2.0	15
4545	The Role of Epigenetics in the Progression of Clear Cell Renal Cell Carcinoma and the Basis for Future Epigenetic Treatments. Cancers, 2021, 13, 2071.	1.7	25
4546	Prediction of diseaseâ€associated functional variants in noncoding regions through a comprehensive analysis by integrating datasets and features. Human Mutation, 2021, 42, 667-684.	1.1	0
4547	Histone Methylation Regulation in Neurodegenerative Disorders. International Journal of Molecular Sciences, 2021, 22, 4654.	1.8	40
4548	Notch receptors as a therapeutic target in melanoma: a narrative bibliographic review. Brazilian Journal of Natural Sciences, 2021, 4, 614-628.	0.3	1
4550	Germline variants at SOHLH2 influence multiple myeloma risk. Blood Cancer Journal, 2021, 11, 76.	2.8	6
4551	BARTweb: a web server for transcriptional regulator association analysis. NAR Genomics and Bioinformatics, 2021, 3, lqab022.	1.5	7
4552	Prenatal chlorpyrifos exposure in association with PPAR \hat{i}^3 H3K4me3 and DNA methylation levels and child development. Environmental Pollution, 2021, 274, 116511.	3.7	33
4553	Integrated transcription factor profiling with transcriptome analysis identifies L1PA2 transposons as global regulatory modulators in a breast cancer model. Scientific Reports, 2021, 11, 8083.	1.6	2
4554	Variants That Differentiate Wolf and Dog Populations Are Enriched in Regulatory Elements. Genome Biology and Evolution, 2021, 13, .	1.1	4
4555	BAP1 constrains pervasive H2AK119ub1 to control the transcriptional potential of the genome. Genes and Development, 2021, 35, 749-770.	2.7	38
4556	H3K4me2 ChIP-Seq reveals the epigenetic landscape during mushroom formation and novel developmental regulators of Schizophyllum commune. Scientific Reports, 2021, 11, 8178.	1.6	13
4557	Accurate prediction of <i>cis</i> -regulatory modules reveals a prevalent regulatory genome of humans. NAR Genomics and Bioinformatics, 2021, 3, lqab052.	1.5	21
4558	The histone modification H3K4me3 is altered at the <i>ANK1</i> locus in Alzheimer's disease brain. Future Science OA, 2021, 7, FSO665.	0.9	10

#	Article	IF	CITATIONS
4559	RbAp46/48LIN-53 and HAT-1 are required for initial CENP-AHCP-3 deposition and de novo holocentromere formation on artificial chromosomes in Caenorhabditis elegans embryos. Nucleic Acids Research, 2021, 49, 9154-9173.	6.5	6
4560	Epigenetics in blood–brain barrier disruption. Fluids and Barriers of the CNS, 2021, 18, 17.	2.4	24
4561	Integration of Multiple Resolution Data in 3D Chromatin Reconstruction Using ChromStruct. Biology, 2021, 10, 338.	1.3	1
4562	Cyproheptadine, an epigenetic modifier, exhibits anti-tumor activity by reversing the epigenetic silencing of IRF6 in urothelial carcinoma. Cancer Cell International, 2021, 21, 226.	1.8	2
4563	Key changes in chromatin mark mammalian epidermal differentiation and ageing. Epigenetics, 2022, 17, 444-459.	1.3	5
4564	Histone sumoylation and chromatin dynamics. Nucleic Acids Research, 2021, 49, 6043-6052.	6.5	70
4565	In utero exposure to chlordecone affects histone modifications and activates LINE-1 in cord blood. Life Science Alliance, 2021, 4, e202000944.	1.3	7
4566	Genetic and epigenetic mechanisms in the development of congenital heart diseases. World Journal of Pediatric Surgery, 2021, 4, e000196.	0.2	2
4567	Sodium Valproate-Induced Chromatin Remodeling. Frontiers in Cell and Developmental Biology, 2021, 9, 645518.	1.8	25
4568	Mammalian Germ Cell Development: From Mechanism to InÂVitro Reconstitution. Stem Cell Reports, 2021, 16, 669-680.	2.3	20
4569	Single-suture craniosynostosis and the epigenome: current evidence and a review of epigenetic principles. Neurosurgical Focus, 2021, 50, E10.	1.0	7
4570	Antiretroviral Drugs Regulate Epigenetic Modification of Cardiac Cells Through Modulation of H3K9 and H3K27 Acetylation. Frontiers in Cardiovascular Medicine, 2021, 8, 634774.	1.1	7
4571	Gestational valproic acid exposure induces epigenetic modifications in murine decidua. Placenta, 2021, 107, 31-40.	0.7	6
4572	Epigenetics and Inflammation in Diabetic Nephropathy. Frontiers in Physiology, 2021, 12, 649587.	1.3	28
4574	Chromatin-associated MRN complex protects highly transcribing genes from genomic instability. Science Advances, 2021, 7, .	4.7	18
4575	Structure-Based Design, Docking and Binding Free Energy Calculations of A366 Derivatives as Spindlin1 Inhibitors. International Journal of Molecular Sciences, 2021, 22, 5910.	1.8	5
4576	Chromatin structure-dependent histone incorporation revealed by a genome-wide deposition assay. ELife, 2021, 10, .	2.8	6
4577	Epigenetics and Heart Development. Frontiers in Cell and Developmental Biology, 2021, 9, 637996.	1.8	7

		CITATION REPORT		
#	Article		IF	CITATIONS
4578	Leveraging epigenetics to enhance the efficacy of immunotherapy. Clinical Epigenetics	, 2021, 13, 115.	1.8	24
4579	The role of epigenetic mechanisms in the regulation of gene expression in the cyclical e Clinical Epigenetics, 2021, 13, 116.	ndometrium.	1.8	33
4580	Repression of CTSG, ELANE and PRTN3-mediated histone H3 proteolytic cleavage prom monocyte-to-macrophage differentiation. Nature Immunology, 2021, 22, 711-722.	otes	7.0	36
4582	Characterizing Genetic Regulatory Elements in Ovine Tissues. Frontiers in Genetics, 20.	21, 12, 628849.	1.1	8
4583	G9a/GLP targeting in MM promotes autophagy-associated apoptosis and boosts protection inhibitor–mediated cell death. Blood Advances, 2021, 5, 2325-2338.	asome	2.5	19
4584	Tandem histone methyltransferase upregulation defines a unique aggressive prostate o phenotype. British Journal of Cancer, 2021, 125, 247-254.	ancer	2.9	2
4586	CRED9: a differentially expressed elncRNA regulates expression of transcription factor 2021, 27, 891-906.	CEBPA. Rna,	1.6	5
4587	Postoperative abdominal sepsis induces selective and persistent changes in CTCF bindi MHC-II region of human monocytes. PLoS ONE, 2021, 16, e0250818.	ng within the	1.1	5
4588	Single-cell joint detection of chromatin occupancy and transcriptome enables higher-di epigenomic reconstructions. Nature Methods, 2021, 18, 652-660.	mensional	9.0	57
4589	Ectopic targeting of CG DNA methylation in Arabidopsis with the bacterial SssI methylt Nature Communications, 2021, 12, 3130.	ransferase.	5.8	20
4590	Epithelial-mesenchymal transition: Insights into nickel-induced lung diseases. Seminars Biology, 2021, 76, 99-109.	in Cancer	4.3	40
4591	Hypoxia-inducible factor-1α cooperates with histone Lys methylation to predict prograsquamous cell carcinoma. Biomarkers in Medicine, 2021, 15, 509-522.	osis in esophageal	0.6	1
4592	Role of promoters in regulating alternative splicing. Gene, 2021, 782, 145523.		1.0	9
4593	The Impact of Epigenetic Modifications in Myeloid Malignancies. International Journal of Sciences, 2021, 22, 5013.	f Molecular	1.8	15
4594	Ectopic Overexpression of Histone H3K4 Methyltransferase CsSDG36 from Tea Plant D Hyperosmotic Stress Tolerance in Arabidopsis thaliana. International Journal of Molecul 2021, 22, 5064.		1.8	5
4595	Incorporating K-mers Highly Correlated to Epigenetic Modifications for Bayesian Inferen Interactions. Current Bioinformatics, 2021, 16, 484-492.	nce of Gene	0.7	5
4597	Multiple roles of H2A.Z in regulating promoter chromatin architecture in human cells. N Communications, 2021, 12, 2524.	lature	5.8	22
4598	Multiplexed single-cell profiling of chromatin states at genomic loci by expansion micro Nucleic Acids Research, 2021, 49, e82-e82.	scopy.	6.5	18

#	Article	IF	CITATIONS
4599	Dynamics of broad H3K4me3 domains uncover an epigenetic switch between cell identity and cancer-related genes. Genome Research, 2022, 32, 1328-1342.	2.4	14
4600	SBTD: A Novel Method for Detecting Topological Associated Domains from Hi-C Data. Interdisciplinary Sciences, Computational Life Sciences, 2021, 13, 638-651.	2.2	1
4601	Histone methylation in epigenetic regulation and temperature responses. Current Opinion in Plant Biology, 2021, 61, 102001.	3.5	44
4602	Cancer-epigenetic function of the histone methyltransferase KMT2D and therapeutic opportunities for the treatment of KMT2D-deficient tumors. Oncotarget, 2021, 12, 1296-1308.	0.8	19
4603	Sex dependent alteration of epigenetic marks after chronic morphine treatment in mice organs. Food and Chemical Toxicology, 2021, 152, 112200.	1.8	1
4604	CTCF as a regulator of alternative splicing: new tricks for an old player. Nucleic Acids Research, 2021, 49, 7825-7838.	6.5	31
4605	Islet Epigenetic Impacts on $\hat{I}^2 \hat{a} {\in} \mathbb{C}$ ell Identity and Function. , 2021, 11, 1961-1978.		0
4606	Histone H3K4 Methyltransferases as Targets for Drug-Resistant Cancers. Biology, 2021, 10, 581.	1.3	16
4608	Chromatin accessibility profiling in Neurospora crassa reveals molecular features associated with accessible and inaccessible chromatin. BMC Genomics, 2021, 22, 459.	1.2	13
4609	An Integrated Epigenome and Transcriptome Analysis to Clarify the Effect of Epigenetic Inhibitors on GIST. Anticancer Research, 2021, 41, 2817-2828.	0.5	1
4610	Role of Histone Methylation in Maintenance of Genome Integrity. Genes, 2021, 12, 1000.	1.0	14
4611	A positive-feedback loop between HBx and ALKBH5 promotes hepatocellular carcinogenesis. BMC Cancer, 2021, 21, 686.	1.1	33
4612	A DNA Regulatory Element Haplotype at Zinc Finger Genes Is Associated with Host Resilience to Small Ruminant Lentivirus in Two Sheep Populations. Animals, 2021, 11, 1907.	1.0	1
4613	H3K4 Methyltransferase Smyd3 Mediates Vascular Smooth Muscle Cell Proliferation, Migration, and Neointima Formation. Arteriosclerosis, Thrombosis, and Vascular Biology, 2021, 41, 1901-1914.	1.1	7
4614	Multi-Omics Approaches in Immunological Research. Frontiers in Immunology, 2021, 12, 668045.	2.2	22
4615	Histone tails cooperate to control the breathing of genomic nucleosomes. PLoS Computational Biology, 2021, 17, e1009013.	1.5	21
4618	Contribution of genetic and epigenetic changes to escape from X-chromosome inactivation. Epigenetics and Chromatin, 2021, 14, 30.	1.8	11
4619	Methods of massive parallel reporter assays for investigation of enhancers. Vavilovskii Zhurnal Genetiki I Selektsii, 2021, 25, 344-355.	0.4	2

#	Article	IF	CITATIONS
4620	Liquid–Liquid Phase Separation in Chromatin. Cold Spring Harbor Perspectives in Biology, 2022, 14, a040683.	2.3	80
4621	SpikChIP: a novel computational methodology to compare multiple ChIP-seq using spike-in chromatin. NAR Genomics and Bioinformatics, 2021, 3, Iqab064.	1.5	5
4622	High gestational folic acid supplementation prevents hypoxiaâ€ischemiaâ€induced caspaseâ€3 augmenting without changing synapsin and H3 methylation levels in the rat hippocampus. International Journal of Developmental Neuroscience, 2021, 81, 510-519.	0.7	3
4623	Regulation of RNA polymerase II activity is essential for terminal erythroid maturation. Blood, 2021, 138, 1740-1756.	0.6	20
4625	Putative Causal Variants Are Enriched in Annotated Functional Regions From Six Bovine Tissues. Frontiers in Genetics, 2021, 12, 664379.	1.1	20
4626	Association of medically assisted reproduction with offspring cord blood DNA methylation across cohorts. Human Reproduction, 2021, 36, 2403-2413.	0.4	17
4627	BET Protein-Mediated Transcriptional Regulation in Heart Failure. International Journal of Molecular Sciences, 2021, 22, 6059.	1.8	5
4628	DOT1L complex regulates transcriptional initiation in human erythroleukemic cells. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	26
4629	Potentially functional variants of HBEGF and ITPR3 in GnRH signaling pathway genes predict survival of non-small cell lung cancer patients. Translational Research, 2021, 233, 92-103.	2.2	14
4631	Multiomics metabolic and epigenetics regulatory network in cancer: A systems biology perspective. Journal of Genetics and Genomics, 2021, 48, 520-530.	1.7	6
4632	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
4633	Core promoter activity contributes to chromatin-based regulation of internal cryptic promoters. Nucleic Acids Research, 2021, 49, 8097-8109.	6.5	4
4634	The dynamic broad epigenetic (H3K4me3, H3K27ac) domain as a mark of essential genes. Clinical Epigenetics, 2021, 13, 138.	1.8	84
4635	The Effects of Interferons on Allogeneic T Cell Response in GVHD: The Multifaced Biology and Epigenetic Regulations. Frontiers in Immunology, 2021, 12, 717540.	2.2	5
4637	A plate-based single-cell ATAC-seq workflow for fast and robust profiling of chromatin accessibility. Nature Protocols, 2021, 16, 4084-4107.	5.5	40
4638	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
4639	Ethanol-Induced Cell Damage Can Result in the Development of Oral Tumors. Cancers, 2021, 13, 3846.	1.7	7
4641	Structure, Activity and Function of the Suv39h1 and Suv39h2 Protein Lysine Methyltransferases. Life, 2021, 11, 703.	1.1	17

#	Article	IF	CITATIONS
4642	HERON: A Novel Tool Enables Identification of Long, Weakly Enriched Genomic Domains in ChIP-seq Data. International Journal of Molecular Sciences, 2021, 22, 8123.	1.8	0
4643	Set1 Targets Genes with Essential Identity and Tumor-Suppressing Functions in Planarian Stem Cells. Genes, 2021, 12, 1182.	1.0	3
4644	Dysregulation of Synaptic Signaling Genes Is Involved in Biology of Uterine Leiomyoma. Genes, 2021, 12, 1179.	1.0	2
4645	The Updating of Biological Functions of Methyltransferase SETDB1 and Its Relevance in Lung Cancer and Mesothelioma. International Journal of Molecular Sciences, 2021, 22, 7416.	1.8	4
4646	Exploring epigenetic and microRNA approaches for γ-globin gene regulation. Experimental Biology and Medicine, 2021, 246, 2347-2357.	1.1	5
4647	Chromatin Profiling Techniques: Exploring the Chromatin Environment and Its Contributions to Complex Traits. International Journal of Molecular Sciences, 2021, 22, 7612.	1.8	6
4648	Transcriptional Regulation of RUNX1: An Informatics Analysis. Genes, 2021, 12, 1175.	1.0	4
4649	Epigenetic regulation of reproduction in human and in animal models. Molecular Human Reproduction, 2021, 27, .	1.3	3
4651	Epigenetic Regulation of Cardiomyocyte Differentiation from Embryonic and Induced Pluripotent Stem Cells. International Journal of Molecular Sciences, 2021, 22, 8599.	1.8	5
4652	Bidirectional promoters: an enigmatic genome architecture and their roles in cancers. Molecular Biology Reports, 2021, 48, 6637-6644.	1.0	0
4653	Transcriptional enhancers and their communication with gene promoters. Cellular and Molecular Life Sciences, 2021, 78, 6453-6485.	2.4	25
4654	Identification of Novel IncRNA and Differentially Expressed Genes (DEGs) of Testicular Tissues among Cattle, Yak, and Cattle-Yak Associated with Male Infertility. Animals, 2021, 11, 2420.	1.0	11
4656	Epigenetic Deregulation of the Histone Methyltransferase KMT5B Contributes to Malignant Transformation in Glioblastoma. Frontiers in Cell and Developmental Biology, 2021, 9, 671838.	1.8	6
4657	The molecular principles of gene regulation by Polycomb repressive complexes. Nature Reviews Molecular Cell Biology, 2021, 22, 815-833.	16.1	207
4658	Expression pattern and regulatory effect of lysine-specific demethylase 2A gene in clear cell renal cell carcinoma. BMC Urology, 2021, 21, 108.	0.6	1
4659	Opportunity knocks for uncovering the new function of an understudied nucleosome remodeling complex member, the bromodomain PHD finger transcription factor, BPTF. Current Opinion in Chemical Biology, 2021, 63, 57-67.	2.8	11
4660	Chromatin-mediated epigenetic regulation of HSV-1 transcription as a potential target in antiviral therapy. Antiviral Research, 2021, 192, 105103.	1.9	9
4661	The Nuclear Lamina. Cold Spring Harbor Perspectives in Biology, 2022, 14, a040113.	2.3	28

#	Article	IF	CITATIONS
4662	Emerging Single-Cell Technological Approaches to Investigate Chromatin Dynamics and Centromere Regulation in Human Health and Disease. International Journal of Molecular Sciences, 2021, 22, 8809.	1.8	7
4663	A CpG island promoter drives the CXXC5 gene expression. Scientific Reports, 2021, 11, 15655.	1.6	2
4664	Genetic and epigenetic orchestration of Gfi1aa-Lsd1- <i>cebpα</i> in zebrafish neutrophil development. Development (Cambridge), 2021, 148, .	1.2	3
4665	Alcohol-abuse drug disulfiram targets pediatric glioma via MLL degradation. Cell Death and Disease, 2021, 12, 785.	2.7	11
4666	Building Pluripotency Identity in the Early Embryo and Derived Stem Cells. Cells, 2021, 10, 2049.	1.8	6
4667	Emerging Roles of Posttranslational Modifications in Plant-Pathogenic Fungi and Bacteria. Annual Review of Phytopathology, 2021, 59, 99-124.	3.5	14
4668	Bivalent Regulation and Related Mechanisms of H3K4/27/9me3 in Stem Cells. Stem Cell Reviews and Reports, 2022, 18, 165-178.	1.7	8
4669	Chromatin Alterations in Neurological Disorders and Strategies of (Epi)Genome Rescue. Pharmaceuticals, 2021, 14, 765.	1.7	3
4670	CHIPIN: ChIP-seq inter-sample normalization based on signal invariance across transcriptionally constant genes. BMC Bioinformatics, 2021, 22, 407.	1.2	8
4671	Histone H4 lysine 20 mono-methylation directly facilitates chromatin openness and promotes transcription of housekeeping genes. Nature Communications, 2021, 12, 4800.	5.8	56
4672	Gravitational Force—Induced 3D Chromosomal Conformational Changes Are Associated with Rapid Transcriptional Response in Human T Cells. International Journal of Molecular Sciences, 2021, 22, 9426.	1.8	17
4673	D-2-Hydroxyglutarate in Glioma Biology. Cells, 2021, 10, 2345.	1.8	26
4674	Targeting Histone Modifications in Breast Cancer: A Precise Weapon on the Way. Frontiers in Cell and Developmental Biology, 2021, 9, 736935.	1.8	18
4675	Multi-Omics Approach to Dissect the Mechanisms of Rexinoid Signaling in Myoblast Differentiation. Frontiers in Pharmacology, 2021, 12, 746513.	1.6	3
4678	Phospho-Tau and Chromatin Landscapes in Early and Late Alzheimer's Disease. International Journal of Molecular Sciences, 2021, 22, 10283.	1.8	8
4679	Histone deacetylase HDA-4-mediated epigenetic regulation in space-flown C. elegans. Npj Microgravity, 2021, 7, 33.	1.9	7
4681	Combination LSD1 and HOTAIR-EZH2 inhibition disrupts cell cycle processes and induces apoptosis in glioblastoma cells. Pharmacological Research, 2021, 171, 105764.	3.1	30
4682	Somaâ€ŧoâ€germline transformation in chromatinâ€ŀinked neurodevelopmental disorders?. FEBS Journal, 2022, 289, 2301-2317.	2.2	6

#	Article	IF	CITATIONS
4683	Epigenetic treatment of behavioral and physiological deficits in a tauopathy mouse model. Aging Cell, 2021, 20, e13456.	3.0	15
4684	An integrated analysis of DNA promoter methylation, microRNA regulation, and gene expression in gastric adenocarcinoma. Annals of Translational Medicine, 2021, 9, 1414-1414.	0.7	1
4685	Differential contribution to gene expression prediction of histone modifications at enhancers or promoters. PLoS Computational Biology, 2021, 17, e1009368.	1.5	9
4687	Epigenetic Alterations in Pediatric Sleep Apnea. International Journal of Molecular Sciences, 2021, 22, 9523.	1.8	2
4688	Enhancer decommissioning imposes an epigenetic barrier to sensory hair cell regeneration. Developmental Cell, 2021, 56, 2471-2485.e5.	3.1	37
4689	High frequency of intron retention and clustered H3K4me3-marked nucleosomes in short first introns of human long non-coding RNAs. Epigenetics and Chromatin, 2021, 14, 45.	1.8	6
4690	Hybrid Stomach-Intestinal Chromatin States Underlie Human Barrett's Metaplasia. Gastroenterology, 2021, 161, 924-939.e11.	0.6	18
4691	Dynamic alterations of H3K4me3 and H3K27me3 at <i>ADAM17</i> and <i>Jagged†</i> gene promoters cause an inflammatory switch of endothelial cells. Journal of Cellular Physiology, 2022, 237, 992-1012.	2.0	8
4692	Rational Design and Development of HDAC Inhibitors for Breast Cancer Treatment. Current Pharmaceutical Design, 2021, 27, 4610-4629.	0.9	9
4693	Global chromatin relabeling accompanies spatial inversion of chromatin in rod photoreceptors. Science Advances, 2021, 7, eabj3035.	4.7	16
4694	Function of histone methylation and acetylation modifiers in cardiac hypertrophy. Journal of Molecular and Cellular Cardiology, 2021, 159, 120-129.	0.9	22
4695	Histone lysine modifying enzymes and their critical roles in DNA double-strand break repair. DNA Repair, 2021, 107, 103206.	1.3	6
4696	Histone deacetylase 4 deletion broadly affects cardiac epigenetic repression and regulates transcriptional susceptibility via H3K9 methylation. Journal of Molecular and Cellular Cardiology, 2022, 162, 119-129.	0.9	3
4697	Epigenetic heterogeneity in primary bone cancers. , 2022, , 431-445.		0
4698	Rice protein-binding microarrays: a tool to detect cis-acting elements near promoter regions in rice. Planta, 2021, 253, 40.	1.6	1
4699	Region-Specific Network Analysis Reveals That Epigenetic Modifications Outside Transcriptional Start Sites Are Tightly Linked to mRNA. IEEE Access, 2021, 9, 17041-17048.	2.6	0
4700	Chromatin accessibility profiling methods. Nature Reviews Methods Primers, 2021, 1, .	11.8	95
4701	The N-Terminal Tail of Histone H3 Regulates Copper Homeostasis in <i>Saccharomyces cerevisiae</i> . Molecular and Cellular Biology, 2021, 41, .	1.1	5

#	Article	IF	CITATIONS
4702	Nanomaterials as Source of Environmental Contaminants: From Exposure to Preventive Interventions. Emerging Contaminants and Associated Treatment Technologies, 2021, , 355-400.	0.4	2
4703	JAZF1, A Novel p400/TIP60/NuA4 Complex Member, Regulates H2A.Z Acetylation at Regulatory Regions. International Journal of Molecular Sciences, 2021, 22, 678.	1.8	16
4704	Genome-wide analysis of primary microRNA expression using H3K36me3 ChIP-seq data. Computational and Structural Biotechnology Journal, 2021, 19, 1944-1955.	1.9	3
4705	Perinatal stress and epigenetics. Handbook of Clinical Neurology / Edited By P J Vinken and G W Bruyn, 2021, 180, 125-148.	1.0	14
4706	Targeted attenuation of elevated histone marks at <i>SNCA</i> alleviates αâ€synuclein in Parkinson's disease. EMBO Molecular Medicine, 2021, 13, e12188.	3.3	43
4709	The Role of H3K4 Trimethylation in CpG Islands Hypermethylation in Cancer. Biomolecules, 2021, 11, 143.	1.8	11
4710	ATACgraph: Profiling Genome-Wide Chromatin Accessibility From ATAC-seq. Frontiers in Genetics, 2020, 11, 618478.	1.1	8
4711	AddictGene: An integrated knowledge base for differentially expressed genes associated with addictive substance. Computational and Structural Biotechnology Journal, 2021, 19, 2416-2422.	1.9	3
4712	Other omics approaches to the study of rare diseases. , 2021, , 229-262.		0
4713	A Comprehensive Toolbox to Analyze Enhancer–Promoter Functions. Methods in Molecular Biology, 2021, 2351, 3-22.	0.4	2
4714	Epigenetic Alterations in Renal Cell Cancer With TKIs Resistance: From Mechanisms to Clinical Applications. Frontiers in Genetics, 2020, 11, 562868.	1.1	10
4716	Histone methylation modifiers in medical therapeutics. , 2021, , 693-720.		0
4719	Multiplex Sequencing of Paired End Ditags for Transcriptome and Genome Analysis. , 0, , 165-182.		2
4720	Direct Sequencing by TEM ofZ-Substituted DNA Molecules. , 0, , 103-116.		2
4721	Retina Development in Vertebrates: Systems Biology Approaches to Understanding Genetic Programs. BioEssays, 2020, 42, e1900187.	1.2	17
4722	Topâ€down characterization of mouse core histones. Journal of Mass Spectrometry, 2019, 54, 258-265.	0.7	4
4723	Chemical and biochemical approaches in the study of histone methylation and demethylation. Medicinal Research Reviews, 2010, 32, n/a-n/a.	5.0	3
4724	Chromatin Remodeling and Androgen Receptor-Mediated Transcription. , 2009, , 405-424.		1

#	Article	IF	CITATIONS
4725	Transposon Resources for Forward and Reverse Genetics in Maize. , 2009, , 561-584.		29
4726	The Analysis of MicroRNAs in Stem Cells. , 2008, , 141-167.		1
4727	Genomic Imprinting – A Model for Roles of Histone Modifications in Epigenetic Control. , 2009, , 235-258.		5
4728	Sequencing the Epigenome. , 2009, , 19-35.		2
4729	Cancer Epigenomics. , 2009, , 385-395.		1
4730	Epigenetic Profiling of Histone Variants. , 2009, , 101-118.		2
4731	Interplay Between Cyclin-Dependent Kinases and E2F-Dependent Transcription. , 2010, , 23-41.		6
4732	Complexity and High-End Computing in Biology and Medicine. Advances in Experimental Medicine and Biology, 2011, 696, 377-384.	0.8	4
4733	Gene Regulatory Elements. , 2012, , 1-17.		1
4734	Epigenetics and Human Disease. , 2012, , 253-279.		2
4735	The Role of DNMT3B Mutations in the Pathogenesis of ICF Syndrome. , 2012, , 15-41.		5
4736	Epigenetic Control of Germline Development. Advances in Experimental Medicine and Biology, 2013, 757, 373-403.	0.8	4
4737	Next-Generation Sequencing in Cancer Epigenomics and Potential Clinical Applications. , 2013, , 31-53.		2
4738	Impact of the Early-Life Environment on the Epigenome and Behavioral Development. , 2013, , 179-207.		1
4739	Transcription Through Chromatin. , 2014, , 427-489.		2
4740	Regulating Chromatin by Histone Acetylation. , 2014, , 147-212.		38
4741	Histone Methylation in Chromatin Signaling. , 2014, , 213-256.		4
4742	Use Model-Based Analysis of ChIP-Seq (MACS) to Analyze Short Reads Generated by Sequencing Protein–DNA Interactions in Embryonic Stem Cells. Methods in Molecular Biology, 2014, 1150, 81-95.	0.4	222

#	Article	IF	CITATIONS
4743	Spatial Clustering for Identification of ChIP-Enriched Regions (SICER) to Map Regions of Histone Methylation Patterns in Embryonic Stem Cells. Methods in Molecular Biology, 2014, 1150, 97-111.	0.4	206
4744	Methodological Approaches for Understanding the Epigenetic Landscape of the Human Breast and Its Implications in Cancer and Prevention. , 2014, , 253-283.		1
4745	Chromatin Immunoprecipitation and Chromatin Immunoprecipitation with Massively Parallel Sequencing on Mouse Embryonic Tissue. Methods in Molecular Biology, 2014, 1196, 231-239.	0.4	5
4746	Polarized Activation of Macrophages. , 2014, , 37-57.		3
4747	Mapping the Genomic Binding Sites of the Activated Retinoid X Receptor in Murine Bone Marrow-Derived Macrophages Using Chromatin Immunoprecipitation Sequencing. Methods in Molecular Biology, 2014, 1204, 15-24.	0.4	18
4748	Techniques to Study Epigenetic Control and the Epigenome in Parasites. Methods in Molecular Biology, 2015, 1201, 177-191.	0.4	6
4749	Purification of Specific Chromatin Loci for Proteomic Analysis. Methods in Molecular Biology, 2015, 1228, 83-92.	0.4	9
4750	Chromatin Immunoprecipitation (ChIP) Assay in Candida albicans. Methods in Molecular Biology, 2016, 1356, 43-57.	0.4	6
4751	Long Non-coding RNA. , 2015, , 83-108.		4
4752	ChlPseq in Yeast Species: From Chromatin Immunoprecipitation to High-Throughput Sequencing and Bioinformatics Data Analyses. Methods in Molecular Biology, 2016, 1361, 185-202.	0.4	7
4753	Chromatin Immunoprecipitation Assay to Identify Genomic Binding Sites of Regulatory Factors. Methods in Molecular Biology, 2016, 1366, 53-65.	0.4	3
4754	Considerations on Experimental Design and Data Analysis of Chromatin Immunoprecipitation Experiments. Methods in Molecular Biology, 2018, 1689, 9-28.	0.4	5
4755	Global Proteomic Analysis of Saccharomyces cerevisiae Identifies Molecular Pathways of Histone Modifications. Methods in Molecular Biology, 2009, 548, 175-186.	0.4	1
4756	Polycomb Group Protein Homeostasis in Stem Cell Identity – A Hypothetical Appraisal. , 2009, , 285-290.		1
4757	Chromatin Immunoprecipitation (ChIP) Methodology and Readouts. Methods in Molecular Biology, 2009, 505, 123-137.	0.4	12
4758	Relative Avidity, Specificity, and Sensitivity of Transcription Factor–DNA Binding in Genome-Scale Experiments. Methods in Molecular Biology, 2009, 563, 15-50.	0.4	5
4759	Genome-Wide Approaches to Studying Yeast Chromatin Modifications. Methods in Molecular Biology, 2011, 759, 61-71.	0.4	4
4760	Genome-Wide Epigenetic Analysis of Human Pluripotent Stem Cells by ChIP and ChIP-Seq. Methods in Molecular Biology, 2011, 767, 253-267.	0.4	16

#	Article	IF	CITATIONS
4761	Making Reporter Gene Constructs to Analyze Cis-regulatory Elements. Methods in Molecular Biology, 2012, 772, 397-408.	0.4	5
4762	Using ChIP-Seq Technology to Generate High-Resolution Profiles of Histone Modifications. Methods in Molecular Biology, 2011, 791, 265-286.	0.4	119
4763	Computational Methods for Epigenetic Analysis: The Protocol of Computational Analysis for Modified Methylation-Specific Digital Karyotyping Based on Massively Parallel Sequencing. Methods in Molecular Biology, 2011, 791, 313-328.	0.4	2
4764	Methylated DNA Immunoprecipitation Genome-Wide Analysis. Methods in Molecular Biology, 2011, 791, 113-123.	0.4	2
4765	Genome-Wide In Vivo Cross-linking of Sequence-Specific Transcription Factors. Methods in Molecular Biology, 2012, 809, 3-26.	0.4	6
4766	Using ChIPMotifs for De Novo Motif Discovery of OCT4 and ZNF263 Based on ChIP-Based High-Throughput Experiments. Methods in Molecular Biology, 2012, 802, 323-334.	0.4	4
4767	Strain Construction and Screening Methods for a Yeast Histone H3/H4 Mutant Library. Methods in Molecular Biology, 2012, 833, 1-14.	0.4	2
4768	DNA Methylation and Histone Modifications in Breast Cancer. Methods in Molecular Biology, 2012, 863, 35-45.	0.4	15
4769	Breast Cancer Epigenetics: Biomarkers and Therapeutic Potential. , 2013, , 211-259.		1
4770	Quantitatively Profiling Genome-Wide Patterns of Histone Modifications in Arabidopsis thaliana Using ChIP-seq. Methods in Molecular Biology, 2014, 1112, 177-193.	0.4	12
4771	Histone Methylome of the Human Parasite Schistosoma Mansoni. RNA Technologies, 2019, , 607-624.	0.2	5
4772	Role of Next-Generation Sequencing Technologies in Personalized Medicine. , 2020, , 125-154.		13
4773	Epigenetic Regulation of Chromatin in Prostate Cancer. Advances in Experimental Medicine and Biology, 2019, 1210, 379-407.	0.8	10
4774	Epigenetic Control Using Small Molecules in Cancer. Human Perspectives in Health Sciences and Technology, 2020, , 111-148.	0.2	2
4775	Pituitary Development and Organogenesis: Transcription Factors in Development and Disease. Masterclass in Neuroendocrinology, 2020, , 129-177.	0.1	4
4776	Epigenetics and Ageing. , 2020, , 141-166.		1
4777	Advances in Diagnostic Procedures and Their Applications in the Era of Cancer Immunotherapy. Advances in Experimental Medicine and Biology, 2020, 1244, 37-50.	0.8	2
4778	DAMP-Promoted Efferent Innate Immune Responses in Human Diseases: Inflammation. , 2020, , 151-209.		1

#	Article	IF	CITATIONS
4779	MOSAiCS-HMM: A Model-Based Approach for Detecting Regions of Histone Modifications from ChIP-Seq Data. , 2014, , 277-295.		3
4781	Maternal Energetics and the Developmental Origins of Prostate Cancer in Offspring. Energy Balance and Cancer, 2015, , 217-246.	0.2	1
4782	Epigenetic Regulation of Gammaherpesviruses: A Focus on Kaposi's Sarcoma-Associated Herpesvirus (KSHV/HHV-8). Epigenetics and Human Health, 2017, , 15-46.	0.2	2
4783	Epigenetic Regulation of Intestinal Fibrosis. , 2018, , 39-58.		2
4784	mpscan: Fast Localisation of Multiple Reads in Genomes. Lecture Notes in Computer Science, 2009, , 246-260.	1.0	11
4785	The Intersection of Genetics and Epigenetics: Reactivation of Mammalian LINE-1 Retrotransposons by Environmental Injury. Epigenetics and Human Health, 2013, , 127-160.	0.2	4
4786	Prediction of Transcription Factor Binding Sites by Integrating DNase Digestion and Histone Modification. Lecture Notes in Computer Science, 2012, , 109-119.	1.0	1
4787	Phylogenetic Analysis of Cell Types Using Histone Modifications. Lecture Notes in Computer Science, 2013, , 326-337.	1.0	1
4788	The Epigenomics of Cancer. , 2010, , 51-67.		3
4789	Centromeres: Assembling and Propagating Epigenetic Function. Sub-Cellular Biochemistry, 2010, 50, 223-249.	1.0	9
4790	Function and Evolution of C2H2 Zinc Finger Arrays. Sub-Cellular Biochemistry, 2011, 52, 75-94.	1.0	37
4791	Chromatin Organization and the Mammalian Nucleolus. , 2013, , 119-148.		5
4792	Methylation in Colorectal Cancer. , 2015, , 373-455.		1
4793	miRNA-Mediated RNA Activation in Mammalian Cells. Advances in Experimental Medicine and Biology, 2017, 983, 81-89.	0.8	43
4794	Plant Genetic Engineering and GM Crops: Merits and Demerits. , 2019, , 155-229.		4
4795	The Role of Nucleosomes in Epigenetic Gene Regulation. , 2019, , 87-117.		3
4796	Overview of Histone Modification. Advances in Experimental Medicine and Biology, 2021, 1283, 1-16.	0.8	186
4797	Introduction to Epigenetic Mechanisms. , 2016, , 49-62.		2

# 4798	ARTICLE Learning Rule-Based Models - The Rough Set Approach. , 2014, , 19-39.	IF	CITATIONS
4799	Lamin B2 promotes the malignant phenotype of non-small cell lung cancer cells by upregulating dimethylation of histone 3 lysine 9. Experimental Cell Research, 2020, 393, 112090.	1.2	12
4800	Proteasome inhibition creates a chromatin landscape favorable to RNA Pol II processivity. Journal of Biological Chemistry, 2020, 295, 1271-1287.	1.6	9
4801	Genomic Studies and Computational Predictions of Nucleosome Positions and Formation Energies. Advances in Protein Chemistry and Structural Biology, 2010, 79, 1-57.	1.0	17
4802	A lasting marriage: histones and DNA tie a knot that is here to stay. Nature Reviews Genetics, 2007, 8, S23-S23.	7.7	2
4803	Perfecting DNA double-strand break repair on transcribed chromatin. Essays in Biochemistry, 2020, 64, 705-719.	2.1	10
4804	AtINO80 represses photomorphogenesis by modulating nucleosome density and H2A.Z incorporation in light-related genes. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 33679-33688.	3.3	22
4805	Neuronal Lhx1 expression is regulated by DNMT1-dependent modulation of histone marks. Epigenetics, 2020, 15, 1259-1274.	1.3	29
4807	Epigenetics and Trained Immunity. Antioxidants and Redox Signaling, 2018, 29, 1023-1040.	2.5	176
4808	ChIP-seq and Functional Analysis of the SOX2 Gene in Colorectal Cancers. OMICS A Journal of Integrative Biology, 2010, , 121207092956007.	1.0	1
4809	Prediction of histone post-translational modifications using deep learning. Bioinformatics, 2021, 36, 5610-5617.	1.8	7
4810	Histone methyltransferase Dot1L is a coactivator for thyroid hormone receptor during Xenopus development. FASEB Journal, 2017, 31, 4821-4831.	0.2	13
4811	Crystal structures of heterotypic nucleosomes containing histones H2A.Z and H2A. Open Biology, 2016, 6, 160127.	1.5	27
4868	Mechanisms Underlying the Selection and Function of Macrophage-Specific Enhancers. Cold Spring Harbor Symposia on Quantitative Biology, 2015, 80, 213-221.	2.0	22
4869	Investigation of Interactions between DNA and Nuclear Receptors: A Review of the Most Used Methods. Nuclear Receptor Research, 2014, 1, 1-20.	2.5	2
4870	Epigenetic reprogramming of immune cells in injury, repair, and resolution. Journal of Clinical Investigation, 2019, 129, 2994-3005.	3.9	55
4871	JMJD3 regulates CD4+ T cell trafficking by targeting actin cytoskeleton regulatory gene Pdlim4. Journal of Clinical Investigation, 2019, 129, 4745-4757.	3.9	13
4872	CD19-targeting CAR T cell immunotherapy outcomes correlate with genomic modification by vector integration. Journal of Clinical Investigation, 2019, 130, 673-685.	3.9	78

#	Article	IF	CITATIONS
4873	The histone trimethyllysine demethylase JMJD2A promotes cardiac hypertrophy in response to hypertrophic stimuli in mice. Journal of Clinical Investigation, 2011, 121, 2447-2456.	3.9	185
4874	GATA3 controls Foxp3+ regulatory T cell fate during inflammation in mice. Journal of Clinical Investigation, 2011, 121, 4503-4515.	3.9	462
4875	HDAC4 controls histone methylation in response to elevated cardiac load. Journal of Clinical Investigation, 2013, 123, 1359-1370.	3.9	157
4876	Cigarette smoke mediates epigenetic repression of miR-487b during pulmonary carcinogenesis. Journal of Clinical Investigation, 2013, 123, 1241-1261.	3.9	124
4877	KDM2A promotes lung tumorigenesis by epigenetically enhancing ERK1/2 signaling. Journal of Clinical Investigation, 2013, 123, 5231-5246.	3.9	164
4878	UTX demethylase activity is required for satellite cell–mediated muscle regeneration. Journal of Clinical Investigation, 2016, 126, 1555-1565.	3.9	74
4879	Epigenetic silencing of tumor suppressor Par-4 promotes chemoresistance in recurrent breast cancer. Journal of Clinical Investigation, 2018, 128, 4413-4428.	3.9	44
4880	Mitochondrial carrier homolog 2 is necessary for AML survival. Blood, 2020, 136, 81-92.	0.6	19
4881	Cfp1 is required for gene expression dependent H3K4me3 and H3K9 acetylation in embryonic stem cells. Genome Biology, 2014, 15, 451.	13.9	1
4882	intePareto: an R package for integrative analyses of RNA-Seq and ChIP-Seq data. BMC Genomics, 2020, 21, 802.	1.2	11
4883	Personalized and graph genomes reveal missing signal in epigenomic data. Genome Biology, 2020, 21, 124.	3.8	29
4884	Influence of Alcohol on Folate Status and Methionine Metabolism in Relation to Alcoholic Liver Disease. , 2009, , 429-448.		4
4885	The Sound of Silence: RNAi in Poly (ADP-Ribose) Research. , 2013, , 225-256.		1
4886	A ChIP on the shoulder? Chromatin immunoprecipitation and validation strategies for ChIP antibodies. F1000Research, 2015, 4, 235.	0.8	17
4887	Chromas from chromatin: sonification of the epigenome. F1000Research, 2016, 5, 274.	0.8	3
4888	Histone modifications and a choice of variant: a language that helps the genome express itself. F1000prime Reports, 2014, 6, 76.	5.9	42
4890	Epigenomic Consequences of Immortalized Plant Cell Suspension Culture. PLoS Biology, 2008, 6, e302.	2.6	179
4891	PcG Proteins, DNA Methylation, and Gene Repression by Chromatin Looping. PLoS Biology, 2008, 6, e306.	2.6	179

#	Article	IF	Citations
4892	Perm-seq: Mapping Protein-DNA Interactions in Segmental Duplication and Highly Repetitive Regions of Genomes with Prior-Enhanced Read Mapping. PLoS Computational Biology, 2015, 11, e1004491.	1.5	11
4893	The Role of Genome Accessibility in Transcription Factor Binding in Bacteria. PLoS Computational Biology, 2016, 12, e1004891.	1.5	17
4894	Integration and Fixation Preferences of Human and Mouse Endogenous Retroviruses Uncovered with Functional Data Analysis. PLoS Computational Biology, 2016, 12, e1004956.	1.5	41
4895	CHD7 Targets Active Gene Enhancer Elements to Modulate ES Cell-Specific Gene Expression. PLoS Genetics, 2010, 6, e1001023.	1.5	213
4896	A Single cis Element Maintains Repression of the Key Developmental Regulator Gata2. PLoS Genetics, 2010, 6, e1001103.	1.5	48
4897	Epigenetics in Cancer: A Hematological Perspective. PLoS Genetics, 2016, 12, e1006193.	1.5	77
4898	Convergence of Mutation and Epigenetic Alterations Identifies Common Genes in Cancer That Predict for Poor Prognosis. PLoS Medicine, 2008, 5, e114.	3.9	141
4899	Identification of Novel Tumor Markers in Prostate, Colon and Breast Cancer by Unbiased Methylation Profiling. PLoS ONE, 2008, 3, e2079.	1.1	110
4900	Genome-Scale Validation of Deep-Sequencing Libraries. PLoS ONE, 2008, 3, e3713.	1.1	17
4901	High-Resolution Analysis of the 5′-End Transcriptome Using a Next Generation DNA Sequencer. PLoS ONE, 2009, 4, e4108.	1.1	42
4902	A Histone Map of Human Chromosome 20q13.12. PLoS ONE, 2009, 4, e4479.	1.1	7
4903	Genome-Wide Profiling of Histone H3 Lysine 4 and Lysine 27 Trimethylation Reveals an Epigenetic Signature in Prostate Carcinogenesis. PLoS ONE, 2009, 4, e4687.	1.1	130
4904	An Integrated Approach to Identifying Cis-Regulatory Modules in the Human Genome. PLoS ONE, 2009, 4, e5501.	1.1	17
4905	Polycomb Mediated Epigenetic Silencing and Replication Timing at the INK4a/ARF Locus during Senescence. PLoS ONE, 2009, 4, e5622.	1.1	117
4906	Integrated Expression Profiling and ChIP-seq Analyses of the Growth Inhibition Response Program of the Androgen Receptor. PLoS ONE, 2009, 4, e6589.	1.1	77
4907	In Vivo Expression of MHC Class I Genes Depends on the Presence of a Downstream Barrier Element. PLoS ONE, 2009, 4, e6748.	1.1	4
4908	Epigenetic Signatures Associated with Different Levels of Differentiation Potential in Human Stem Cells. PLoS ONE, 2009, 4, e7809.	1.1	96
4909	Genome-Wide Analysis of Immune Activation in Human T and B Cells Reveals Distinct Classes of Alternatively Spliced Genes. PLoS ONE, 2009, 4, e7906.	1.1	35

#	Article	IF	CITATIONS
4910	ChIP-Chip Designs to Interrogate the Genome of Xenopus Embryos for Transcription Factor Binding and Epigenetic Regulation. PLoS ONE, 2010, 5, e8820.	1.1	10
4911	Genomic Approaches Uncover Increasing Complexities in the Regulatory Landscape at the Human SCL (TAL1) Locus. PLoS ONE, 2010, 5, e9059.	1.1	15
4912	Histone H3 Lysine 27 Methylation Asymmetry on Developmentally-Regulated Promoters Distinguish the First Two Lineages in Mouse Preimplantation Embryos. PLoS ONE, 2010, 5, e9150.	1.1	91
4913	Lsh Mediated RNA Polymerase II Stalling at HoxC6 and HoxC8 Involves DNA Methylation. PLoS ONE, 2010, 5, e9163.	1.1	39
4914	Whole Methylome Analysis by Ultra-Deep Sequencing Using Two-Base Encoding. PLoS ONE, 2010, 5, e9320.	1.1	52
4915	A Moonlighting Function of Plasmodium falciparum Histone 3, Mono-Methylated at Lysine 9?. PLoS ONE, 2010, 5, e10252.	1.1	14
4916	Tissue-Specific and Ubiquitous Expression Patterns from Alternative Promoters of Human Genes. PLoS ONE, 2010, 5, e12274.	1.1	30
4917	Complete Biallelic Insulation at the H19/Igf2 Imprinting Control Region Position Results in Fetal Growth Retardation and Perinatal Lethality. PLoS ONE, 2010, 5, e12630.	1.1	12
4918	Defining Hypo-Methylated Regions of Stem Cell-Specific Promoters in Human iPS Cells Derived from Extra-Embryonic Amnions and Lung Fibroblasts. PLoS ONE, 2010, 5, e13017.	1.1	51
4919	Polycomb CBX7 Directly Controls Trimethylation of Histone H3 at Lysine 9 at the p16 Locus. PLoS ONE, 2010, 5, e13732.	1.1	53
4920	RNA Polymerase II Binding Patterns Reveal Genomic Regions Involved in MicroRNA Gene Regulation. PLoS ONE, 2010, 5, e13798.	1.1	49
4921	Discovering Cooperative Relationships of Chromatin Modifications in Human T Cells Based on a Proposed Closeness Measure. PLoS ONE, 2010, 5, e14219.	1.1	8
4922	High-Definition Mapping of Retroviral Integration Sites Defines the Fate of Allogeneic T Cells After Donor Lymphocyte Infusion. PLoS ONE, 2010, 5, e15688.	1.1	39
4923	Detection and Removal of Biases in the Analysis of Next-Generation Sequencing Reads. PLoS ONE, 2011, 6, e16685.	1.1	81
4924	NF-Y Recruits Ash2L to Impart H3K4 Trimethylation on CCAAT Promoters. PLoS ONE, 2011, 6, e17220.	1.1	22
4925	Effects of Nickel Treatment on H3K4 Trimethylation and Gene Expression. PLoS ONE, 2011, 6, e17728.	1.1	37
4926	Histone Demethylase JMJD2B Functions as a Co-Factor of Estrogen Receptor in Breast Cancer Proliferation and Mammary Gland Development. PLoS ONE, 2011, 6, e17830.	1.1	166
4927	Abnormal Dosage Compensation of Reporter Genes Driven by the Drosophila Glass Multiple Reporter (GMR) Enhancer-Promoter. PLoS ONE, 2011, 6, e20455.	1.1	8

#	Article	IF	CITATIONS
4929	ChIP-seq Defined Genome-Wide Map of TGFβ/SMAD4 Targets: Implications with Clinical Outcome of Ovarian Cancer. PLoS ONE, 2011, 6, e22606.	1.1	27
4930	Co-Regulation of Histone-Modifying Enzymes in Cancer. PLoS ONE, 2011, 6, e24023.	1.1	13
4931	DNA Methylation Profiling of Embryonic Stem Cell Differentiation into the Three Germ Layers. PLoS ONE, 2011, 6, e26052.	1.1	41
4932	Next-Generation Sequencing of Apoptotic DNA Breakpoints Reveals Association with Actively Transcribed Genes and Gene Translocations. PLoS ONE, 2011, 6, e26054.	1.1	11
4933	Occupancy Classification of Position Weight Matrix-Inferred Transcription Factor Binding Sites. PLoS ONE, 2011, 6, e26160.	1.1	2
4934	CATCHprofiles: Clustering and Alignment Tool for ChIP Profiles. PLoS ONE, 2012, 7, e28272.	1.1	10
4935	Chromatin States Accurately Classify Cell Differentiation Stages. PLoS ONE, 2012, 7, e31414.	1.1	13
4936	CTCF Mediates the Cell-Type Specific Spatial Organization of the Kcnq5 Locus and the Local Gene Regulation. PLoS ONE, 2012, 7, e31416.	1.1	15
4937	PRC1 and PRC2 Are Not Required for Targeting of H2A.Z to Developmental Genes in Embryonic Stem Cells. PLoS ONE, 2012, 7, e34848.	1.1	40
4938	Loss of Maternal CTCF Is Associated with Peri-Implantation Lethality of Ctcf Null Embryos. PLoS ONE, 2012, 7, e34915.	1.1	106
4939	Linking the Epigenome to the Genome: Correlation of Different Features to DNA Methylation of CpG Islands. PLoS ONE, 2012, 7, e35327.	1.1	29
4940	Multiple Histone Methyl and Acetyltransferase Complex Components Bind the HLA-DRA Gene. PLoS ONE, 2012, 7, e37554.	1.1	17
4941	An Interferon-Related Signature in the Transcriptional Core Response of Human Macrophages to Mycobacterium tuberculosis Infection. PLoS ONE, 2012, 7, e38367.	1.1	29
4942	Genome-Wide Bovine H3K27me3 Modifications and the Regulatory Effects on Genes Expressions in Peripheral Blood Lymphocytes. PLoS ONE, 2012, 7, e39094.	1.1	16
4943	ChIPnorm: A Statistical Method for Normalizing and Identifying Differential Regions in Histone Modification ChIP-seq Libraries. PLoS ONE, 2012, 7, e39573.	1.1	32
4944	Genome-Wide Detection of Genes Targeted by Non-Ig Somatic Hypermutation in Lymphoma. PLoS ONE, 2012, 7, e40332.	1.1	44
4945	Comprehensive Identification and Annotation of Cell Type-Specific and Ubiquitous CTCF-Binding Sites in the Human Genome. PLoS ONE, 2012, 7, e41374.	1.1	119
4946	Histone Methylation Analysis and Pathway Predictions in Chickens after MDV Infection. PLoS ONE, 2012, 7, e41849.	1.1	21

#	Article	IF	CITATIONS
4947	Stage and Gene Specific Signatures Defined by Histones H3K4me2 and H3K27me3 Accompany Mammalian Retina Maturation In Vivo. PLoS ONE, 2012, 7, e46867.		47
4948	Systematic Determination of Replication Activity Type Highlights Interconnections between Replication, Chromatin Structure and Nuclear Localization. PLoS ONE, 2012, 7, e48986.	1.1	13
4949	Epigenetic Regulation of Myogenic Gene Expression by Heterochromatin Protein 1 Alpha. PLoS ONE, 2013, 8, e58319.	1.1	19
4950	The Patterns of Histone Modifications in the Vicinity of Transcription Factor Binding Sites in Human Lymphoblastoid Cell Lines. PLoS ONE, 2013, 8, e60002.	1.1	18
4951	Utx Is Required for Proper Induction of Ectoderm and Mesoderm during Differentiation of Embryonic Stem Cells. PLoS ONE, 2013, 8, e60020.	1.1	81
4952	diffReps: Detecting Differential Chromatin Modification Sites from ChIP-seq Data with Biological Replicates. PLoS ONE, 2013, 8, e65598.	1.1	355
4953	Suppression of Gluconeogenic Gene Expression by LSD1-Mediated Histone Demethylation. PLoS ONE, 2013, 8, e66294.	1.1	48
4954	Genome-Wide Identification of Chromatin Transitional Regions Reveals Diverse Mechanisms Defining the Boundary of Facultative Heterochromatin. PLoS ONE, 2013, 8, e67156.	1.1	11
4955	Modeling Exon Expression Using Histone Modifications. PLoS ONE, 2013, 8, e67448.	1.1	13
4956	DNA Methylation of Alternative Promoters Directs Tissue Specific Expression of Epac2 Isoforms. PLoS ONE, 2013, 8, e67925.	1.1	47
4957	Systemic Lupus Erythematosus Patients Contain Significantly Less IgM against Mono-Methylated Lysine than Healthy Subjects. PLoS ONE, 2013, 8, e68520.	1.1	10
4958	A Computational Model for Histone Mark Propagation Reproduces the Distribution of Heterochromatin in Different Human Cell Types. PLoS ONE, 2013, 8, e73818.	1.1	7
4959	Structural Variation-Associated Expression Changes Are Paralleled by Chromatin Architecture Modifications. PLoS ONE, 2013, 8, e79973.	1.1	27
4960	Peg3 Mutational Effects on Reproduction and Placenta-Specific Gene Families. PLoS ONE, 2013, 8, e83359.	1.1	63
4961	A New Exhaustive Method and Strategy for Finding Motifs in ChIP-Enriched Regions. PLoS ONE, 2014, 9, e86044.	1.1	34
4962	Transcription Factor Binding Sites Prediction Based on Modified Nucleosomes. PLoS ONE, 2014, 9, e89226.	1.1	12
4963	ZBED6 Modulates the Transcription of Myogenic Genes in Mouse Myoblast Cells. PLoS ONE, 2014, 9, e94187.	1.1	19
4964	Genome-Wide Quantitative Analysis of Histone H3 Lysine 4 Trimethylation in Wild House Mouse Liver: Environmental Change Causes Epigenetic Plasticity. PLoS ONE, 2014, 9, e97568.	1.1	12

\sim			DEDO	DT
ι.		ON	REPC	ו או
<u> </u>	/			

#	Article	IF	CITATIONS
4965	Changes in Histone H3 Lysine 36 Methylation in Porcine Oocytes and Preimplantation Embryos. PLoS ONE, 2014, 9, e100205.	1.1	14
4966	Genome-Wide H3K4me3 Analysis in Angus Cattle with Divergent Tenderness. PLoS ONE, 2015, 10, e0115358.	1.1	40
4967	A Non-Parametric Peak Calling Algorithm for DamID-Seq. PLoS ONE, 2015, 10, e0117415.	1.1	5
4968	DELTA: A Distal Enhancer Locating Tool Based on AdaBoost Algorithm and Shape Features of Chromatin Modifications. PLoS ONE, 2015, 10, e0130622.	1.1	57
4969	Smooth Muscle Cell Genome Browser: Enabling the Identification of Novel Serum Response Factor Target Genes. PLoS ONE, 2015, 10, e0133751.	1.1	48
4970	The Role of H3K4me3 in Transcriptional Regulation Is Altered in Huntington's Disease. PLoS ONE, 2015, 10, e0144398.	1.1	47
4971	DNA-Binding Motif of the Imprinted Transcription Factor PEG3. PLoS ONE, 2015, 10, e0145531.	1.1	24
4972	Differential Roles for DUSP Family Members in Epithelial-to-Mesenchymal Transition and Cancer Stem Cell Regulation in Breast Cancer. PLoS ONE, 2016, 11, e0148065.	1.1	48
4973	Alteration of Gene Expression, DNA Methylation, and Histone Methylation in Free Radical Scavenging Networks in Adult Mouse Hippocampus following Fetal Alcohol Exposure. PLoS ONE, 2016, 11, e0154836.	1.1	51
4974	Epigenetic Repeat-Induced Gene Silencing in the Chromosomal and Extrachromosomal Contexts in Human Cells. PLoS ONE, 2016, 11, e0161288.	1.1	18
4975	Transcriptional Activation of Pericentromeric Satellite Repeats and Disruption of Centromeric Clustering upon Proteasome Inhibition. PLoS ONE, 2016, 11, e0165873.	1.1	6
4976	Genome-wide mapping of histone H3K9me2 in acute myeloid leukemia reveals large chromosomal domains associated with massive gene silencing and sites of genome instability. PLoS ONE, 2017, 12, e0173723.	1.1	29
4977	HPV16 Down-Regulates the Insulin-Like Growth Factor Binding Protein 2 to Promote Epithelial Invasion in Organotypic Cultures. PLoS Pathogens, 2015, 11, e1004988.	2.1	20
4978	Epigenetic modification in congenital heart diseases by using stem cell technologies. Stem Cell Epigenetics, 0, , .	2.0	1
4979	Androgen receptor enhancer usage and the chromatin regulatory landscape in human prostate cancers. Endocrine-Related Cancer, 2019, 26, R267-R285.	1.6	22
4980	Computational Biology of Genome Expression and Regulation—A Review of Microarray Bioinformatics. Journal of Environmental Pathology, Toxicology and Oncology, 2008, 27, 157-179.	0.6	22
4981	PRMT6 mediates inflammation via activation of the NF- $\hat{I}^{o}B/p65$ pathway on a cigarette smoke extract-induced murine emphysema model. Tobacco Induced Diseases, 2020, 18, 8.	0.3	14
4982	Histone Code and Higher-Order Chromatin Folding: A Hypothesis. Genomics and Computational Biology, 2017, 3, 41.	0.7	18

#	Article	IF	CITATIONS
4983	Smyd3-PARP16 axis accelerates unfolded protein response and vascular aging. Aging, 2020, 12, 21423-21445.	1.4	12
4984	The apoptosis associated tyrosine kinase gene is frequently hypermethylated in human cancer and is regulated by epigenetic mechanisms. Genes and Cancer, 2014, 5, 365-374.	0.6	25
4985	A novel MeCP2 acetylation site regulates interaction with ATRX and HDAC1. Genes and Cancer, 2015, 6, 408-421.	0.6	34
4986	Identification and validation of regulatory SNPs that modulate transcription factor chromatin binding and gene expression in prostate cancer. Oncotarget, 2016, 7, 54616-54626.	0.8	41
4987	Differential effects of histone deacetylase inhibitors on cellular drug transporters and their implications for using epigenetic modifiers in combination chemotherapy. Oncotarget, 2016, 7, 63829-63838.	0.8	16
4988	The JAZF1-SUZ12 fusion protein disrupts PRC2 complexes and impairs chromatin repression during human endometrial stromal tumorogenesis. Oncotarget, 2017, 8, 4062-4078.	0.8	50
4989	An annotated list of bivalent chromatin regions in human ES cells: a new tool for cancer epigenetic research. Oncotarget, 2017, 8, 4110-4124.	0.8	43
4990	Histone demethylase lysine demethylase 5B in development and cancer. Oncotarget, 2017, 8, 8980-8991.	0.8	61
4991	The crosstalk between lncRNA and microRNA in cancer metastasis: orchestrating the epithelial-mesenchymal plasticity. Oncotarget, 2017, 8, 12472-12483.	0.8	148
4992	Histone demethylase JMJD3 regulates CD11a expression through changes in histone H3K27 tri-methylation levels in CD4+ T cells of patients with systemic lupus erythematosus. Oncotarget, 2017, 8, 48938-48947.	0.8	25
4993	BMI-1 is a potential therapeutic target in diffuse intrinsic pontine glioma. Oncotarget, 2017, 8, 62962-62975.	0.8	46
4994	CTCF promotes epithelial ovarian cancer metastasis by broadly controlling the expression of metastasis-associated genes. Oncotarget, 2017, 8, 62217-62230.	0.8	15
4995	Histone modification alteration coordinated with acquisition of promoter DNA methylation during Epstein-Barr virus infection. Oncotarget, 2017, 8, 55265-55279.	0.8	25
4996	Evidence for the association of chromatin and microRNA regulation in the human genome. Oncotarget, 2017, 8, 70958-70966.	0.8	18
4997	TGFBR-IDH1-Cav1 axis promotes TGF-β signalling in cancer-associated fibroblast. Oncotarget, 2017, 8, 83962-83974.	0.8	11
4998	Epigenetic landscape change analysis during human EMT sheds light on a key EMT mediator TRIM29. Oncotarget, 2017, 8, 98322-98335.	0.8	13
4999	Distinct histone modifications denote early stress-induced drug tolerance in cancer. Oncotarget, 2018, 9, 8206-8222.	0.8	54
5000	Prominent role of histone lysine demethylases in cancer epigenetics and therapy. Oncotarget, 2018, 9, 34429-34448.	0.8	15

#	Article	IF	CITATIONS
5001	Region-specific alteration of histone modification by LSD1 inhibitor conjugated with pyrrole-imidazole polyamide. Oncotarget, 2018, 9, 29316-29335.	0.8	6
5002	Metformin alters H2A.Z dynamics and regulates androgen dependent prostate cancer progression. Oncotarget, 2018, 9, 37054-37068.	0.8	14
5003	Inhibition of mutant IDH1 decreases D-2-HG levels without affecting tumorigenic properties of chondrosarcoma cell lines. Oncotarget, 2015, 6, 12505-12519.	0.8	81
5004	DNA methylation and cognitive aging. Oncotarget, 2015, 6, 13922-13932.	0.8	55
5005	On the presence and role of human gene-body DNA methylation. Oncotarget, 2012, 3, 462-474.	0.8	409
5006	The transcription factor c-Fos coordinates with histone lysine-specific demethylase 2A to activate the expression of <i>cyclooxygenase-2</i> . Oncotarget, 2015, 6, 34704-34717.	0.8	8
5007	Therapeutic opportunities in Ewing sarcoma: EWS-FLI inhibition <i>via</i> LSD1 targeting. Oncotarget, 2016, 7, 17616-17630.	0.8	62
5008	P300 acetyltransferase regulates fatty acid synthase expression, lipid metabolism and prostate cancer growth. Oncotarget, 2016, 7, 15135-15149.	0.8	45
5009	LTR12 promoter activation in a broad range of human tumor cells by HDAC inhibition. Oncotarget, 2016, 7, 33484-33497.	0.8	30
5010	SETD2: an epigenetic modifier with tumor suppressor functionality. Oncotarget, 2016, 7, 50719-50734.	0.8	136
5011	DNA damage-induced nuclear factor-kappa B activation and its roles in cancer progression. Journal of Cancer Metastasis and Treatment, 2017, 3, 45.	0.5	71
5012	DNA methylation, environmental exposures and early embryo development. Animal Reproduction, 2019, 16, 465-474.	0.4	41
5013	Imaging Epigenetics in Alzheimer's Disease. Current Pharmaceutical Design, 2013, 19, 6393-6415.	0.9	33
5014	Inhibitors of DNA Methylation and Histone Deacetylation as Epigenetically Active Drugs for Anticancer Therapy. Current Pharmaceutical Design, 2019, 25, 635-641.	0.9	12
5015	Vertebrate Protein CTCF and its Multiple Roles in a Large-Scale Regulation of Genome Activity. Current Genomics, 2009, 10, 294-302.	0.7	29
5016	Anticancer Natural Compounds as Epigenetic Modulators of Gene Expression. Current Genomics, 2017, 18, 175-205.	0.7	42
5017	Recurrent Rearrangements in Prostate Cancer: Causes and Therapeutic Potential. Current Drug Targets, 2013, 14, 450-459.	1.0	18
5018	Epigenetic Regulation of Myocardial Homeostasis, Self-Regeneration and Senescence. Current Drug Targets, 2015, 16, 827-842.	1.0	8

#	Article	IF	CITATIONS
5019	Methods for Activity Analysis of the Proteins that Regulate Histone Methylation. Current Chemical Genomics, 2011, 5, 95-105.	2.0	13
5020	Epigenetic Modulation of Myocardial Angiogenic Balance: An Emerging Therapeutic Perspective for Adult Failing Heart. Current Angiogenesis, 2014, 3, 3-10.	0.1	2
5021	Genome- and epigenome-wide analysis of endothelial cell activation and inflammation. Inflammation and Regeneration, 2014, 34, 094-102.	1.5	1
5022	Regulating Methylation at H3K27: A Trick or Treat for Cancer Cell Plasticity. Cancers, 2020, 12, 2792.	1.7	26
5023	Regulation of Expression and Latency in BLV and HTLV. Viruses, 2020, 12, 1079.	1.5	16
5024	The application of massively parallel sequencing technologies in diagnostics. F1000 Biology Reports, 2010, 2, 59.	4.0	5
5025	How do RNA sequence, DNA sequence, and chromatin properties regulate splicing?. F1000 Biology Reports, 2010, 2, 74.	4.0	5
5027	Progress of Bioinformatics Study in DNA Methylation*. Progress in Biochemistry and Biophysics, 2009, 2009, 143-150.	0.3	5
5028	Current trends in the development and application of molecular technologies for cancer epigenetics. World Journal of Gastroenterology, 2013, 19, 1030.	1.4	9
5029	Epigenetic silencing during early lineage commitment. Stembook, 2009, , .	0.3	8
5030	The chromatin signature of pluripotent cells. Stembook, 2009, , .	0.3	11
5031	General mechanism of JQ1 in inhibiting various types of cancer. Molecular Medicine Reports, 2020, 21, 1021-1034.	1.1	22
5032	Increased expression of EHMT2 associated with H3K9me2 level contributes to the poor prognosis of gastric cancer. Oncology Letters, 2020, 20, 1734-1742.	0.8	5
5033	Comparative epigenomics: an emerging field with breakthrough potential to understand evolution of epigenetic regulation. AIMS Genetics, 2014, 01, 034-054.	1.9	7
5034	Androgen receptor genomic regulation. Translational Andrology and Urology, 2013, 2, 157-177.	0.6	63
5035	Prediction of Epigenetic Target Sites by Using Genomic DNA Sequence. , 2011, , 187-201.		2
5036	Regulation of neuronal survival by DNA methyltransferases. Neural Regeneration Research, 2017, 12, 1768.	1.6	37
5037	Increased brain-derived neurotrophic factor exon IV histone 3 lysine 9 dimethylation in patients with schizophrenia. Taiwanese Journal of Psychiatry, 2019, 33, 99.	0.1	2

#	Article	IF	CITATIONS
5038	The Roles of CCR7 for the Homing of Memory CD8+ T Cells into Their Survival Niches. Immune Network, 2020, 20, e20.	1.6	30
5039	Positive-Negative Feedback Loop between Mir-197 and IL-17A Signaling in Human Keratinocytes. Immunome Research, 2016, 12, .	0.1	5
5040	Identification of Histone Epigenetic Modifications with Chromatin Immunoprecipitation PCR Array in Chronic Lymphocytic Leukemia Specimens. Journal of Cancer Science & Therapy, 2014, 06, .	1.7	1
5041	The Contribution of Next Generation Sequencing Technologies to Epigenome Research of Stem Cell and Tumorigenesis. , 2013, 01, .		4
5042	TALEN-Mediated FLAG-Tagging of Endogenous Histone Methyltransferase DOT1L. Advances in Bioscience and Biotechnology (Print), 2017, 08, 311-323.	0.3	1
5043	Analysis of the Hox epigenetic code. World Journal of Clinical Oncology, 2012, 3, 48.	0.9	3
5044	Methyltransferase and demethylase profiling studies during brown adipocyte differentiation. BMB Reports, 2016, 49, 388-393.	1.1	14
5045	Epigenetic memory in gene regulation and immune response. BMB Reports, 2019, 52, 127-132.	1.1	9
5046	Analysis of opposing histone modifications H3K4me3 and H3K27me3 reveals candidate diagnostic biomarkers for TNBC and gene set prediction combination. BMB Reports, 2020, 53, 266-271.	1.1	5
5047	Detection and characterization of regulatory elements using probabilistic conditional random field and hidden Markov models. Chinese Journal of Cancer, 2013, 32, 186-194.	4.9	4
5048	Fun with Microarrays Part III: Integration and the End of Microarrays as We Know Them. Hypothesis (University of Toronto Dept of Medical Biophysics), 2008, 6, .	1.1	1
5049	Characterization of Chromatin Structure-associated Histone Modifications in Breast Cancer Cells. Genomics and Informatics, 2012, 10, 145.	0.4	18
5050	Regulation and Function of the Peg3 Imprinted Domain. Genomics and Informatics, 2014, 12, 105.	0.4	37
5051	Comparative analysis of commonly used peak calling programs for ChIP-Seq analysis. Genomics and Informatics, 2020, 18, e42.	0.4	15
5052	Computational Epigenetics: the new scientific paradigm. Bioinformation, 2010, 4, 331-337.	0.2	36
5053	The activity-dependent histone variant H2BE modulates the life span of olfactory neurons. ELife, 2012, 1, e00070.	2.8	93
5054	Chromatin signature of widespread monoallelic expression. ELife, 2013, 2, e01256.	2.8	71
5055	p50-associated COX-2 extragenic RNA (PACER) activates COX-2 gene expression by occluding repressive NF-I® complexes. ELife, 2014, 3, e01776.	2.8	285

#	ARTICLE Mof-associated complexes have overlapping and unique roles in regulating pluripotency in embryonic	IF	Citations
5056	stem cells and during differentiation. ELife, 2014, 3, .	2.8	43
5057	The zinc finger proteins ZNF644 and WIZ regulate the G9a/GLP complex for gene repression. ELife, 2015, 4, .	2.8	40
5058	Genome-wide errant targeting by Hairy. ELife, 2015, 4, .	2.8	13
5059	H2A histone-fold and DNA elements in nucleosome activate SWR1-mediated H2A.Z replacement in budding yeast. ELife, 2015, 4, e06845.	2.8	48
5060	Wiz binds active promoters and CTCF-binding sites and is required for normal behaviour in the mouse. ELife, 2016, 5, .	2.8	20
5061	Regulation of alternative polyadenylation by Nkx2-5 and Xrn2 during mouse heart development. ELife, 2016, 5, .	2.8	18
5062	Satb2 determines miRNA expression and long-term memory in the adult central nervous system. ELife, 2016, 5, .	2.8	68
5063	Landscape of histone modifications in a sponge reveals the origin of animal cis-regulatory complexity. ELife, 2017, 6, .	2.8	51
5064	Tri-methylation of histone H3 lysine 4 facilitates gene expression in ageing cells. ELife, 2018, 7, .	2.8	69
5065	VivosX, a disulfide crosslinking method to capture site-specific, protein-protein interactions in yeast and human cells. ELife, 2018, 7, .	2.8	11
5066	Multiple tumor suppressors regulate a HIF-dependent negative feedback loop via ISGF3 in human clear cell renal cancer. ELife, 2018, 7, .	2.8	25
5067	Structural basis for COMPASS recognition of an H2B-ubiquitinated nucleosome. ELife, 2020, 9, .	2.8	79
5068	Integrated analysis of H2A.Z isoforms function reveals a complex interplay in gene regulation. ELife, 2020, 9, .	2.8	35
5069	ZCWPW1 is recruited to recombination hotspots by PRDM9 and is essential for meiotic double strand break repair. ELife, 2020, 9, .	2.8	31
5070	Cancer systems immunology. ELife, 2020, 9, .	2.8	14
5071	Cell-specific exon methylation and CTCF binding in neurons regulate calcium ion channel splicing and function. ELife, 2020, 9, .	2.8	25
5072	A machine learning framework for the prediction of chromatin folding in <i>Drosophila</i> using epigenetic features. PeerJ Computer Science, 2020, 6, e307.	2.7	11
5073	Oxytetracycline induces DNA damage and epigenetic changes: a possible risk for human and animal health?. PeerJ, 2017, 5, e3236.	0.9	24

#	Article		CITATIONS
5074	Transcriptional regulation of metabolism in disease: From transcription factors to epigenetics. PeerJ, 2018, 6, e5062.	0.9	9
5075	Gosling: A Grammar-based Toolkit for Scalable and Interactive Genomics Data Visualization. IEEE Transactions on Visualization and Computer Graphics, 2022, 28, 140-150.	2.9	24
5076	Over-methylation of Histone H3 Lysines Is a Common Molecular Change Among the Three Major Types of Soft-tissue Sarcoma in Patient-derived Xenograft (PDX) Mouse Models. Cancer Genomics and Proteomics, 2021, 18, 715-721.	1.0	8
5077	Gene bookmarking by the heat shock transcription factor programs the insulin-like signaling pathway. Molecular Cell, 2021, 81, 4843-4860.e8.	4.5	16
5078	Segmentation and genome annotation algorithms for identifying chromatin state and other genomic patterns. PLoS Computational Biology, 2021, 17, e1009423.	1.5	21
5079	Dynamic changes of histone methylation in mammalian oocytes and early embryos. Histochemistry and Cell Biology, 2022, 157, 7-25.	0.8	14
5080	The H2A.Z-nucleosome code in mammals: emerging functions. Trends in Genetics, 2022, 38, 273-289.	2.9	23
5081	SETD2-mediated epigenetic regulation of noncanonical Wnt5A during osteoclastogenesis. Clinical Epigenetics, 2021, 13, 192.	1.8	5
5082	Dual detection of chromatin accessibility and DNA methylation using ATAC-Me. Nature Protocols, 2021, 16, 5377-5397.	5.5	10
5083	Searching for methyllysine-binding aromatic cages. Biochemical Journal, 2021, 478, 3613-3619.	1.7	3
5084	Characterizing batch effects and binding site-specific variability in ChIP-seq data. NAR Genomics and Bioinformatics, 2021, 3, Iqab098.	1.5	3
5085	Role of Enhancers in Development and Diseases. Epigenomes, 2021, 5, 21.	0.8	8
5086	ldentification 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
5087	Decoding the function of bivalent chromatin in development and cancer. Genome Research, 2021, 31, 2170-2184.	2.4	48
5088	Comprehensive Analysis of Genes Associated With Sudden Infant Death Syndrome. Frontiers in Pediatrics, 2021, 9, 742225.	0.9	3
5089	G9a: An Emerging Epigenetic Target for Melanoma Therapy. Epigenomes, 2021, 5, 23.	0.8	8
5090	Transcriptomics of the depressed and PTSD brain. Neurobiology of Stress, 2021, 15, 100408.	1.9	8
5091	MULTI-SCALE CORRELATIONS IN CONTINUOUS GENOMIC DATA. , 2007, , 201-15.		1

#	Article	IF	CITATIONS
5094	Diagnosing Cancer Using Histone Modification Analysis. , 2008, , 347-357.		0
5095	DNA Methylation and the Epigenetic Program in Stem Cells. , 2009, , 277-284.		1
5096	Stem Cell Epigenetics. , 2009, , 235-246.		1
5097	Modeling and Visualizing Heterogeneity of Spatial Patterns of Protein-DNA Interaction from High-Density Chromatin Precipitation Mapping Data. Lecture Notes in Computer Science, 2009, , 236-247.	1.0	0
5098	Stem Cell Chromatin Patterns and DNA Hypermethylation. , 2009, , 85-97.		0
5099	Mapping the Androgen Receptor Cistrome. , 2009, , 663-680.		0
5100	Molecular Regulation of the State of Embryonic Stem Cells. , 2009, , 33-60.		0
5101	Applications of high-throughput sequencing to chromatin structure and function in mammals. F1000 Biology Reports, 2009, 1, 32.	4.0	0
5102	Chromatin Structure in Senescent Cells. , 2010, , 125-174.		0
5103	Insulators: linking genome architecture to gene regulation. F1000 Biology Reports, 2009, 1, 92.	4.0	0
5104	Nuclear Receptor Coactivators. , 2010, , 1999-2004.		0
5106	Examining DNA–Protein Interactions with Genome-Wide Chromatin Immunoprecipitation Analysis. , 2010, , 33-45.		0
5107	Predicting Nucleosome Positioning Using Multiple Evidence Tracks. Lecture Notes in Computer Science, 2010, , 441-455.	1.0	1
5108	Diversity of Vitamin D Target Genes. , 2010, , 255-274.		0
5113	Epigenetic Mechanisms of Mental Retardation. , 2011, 67, 125-146.		8
5114	High Throughput Sequencing Methods and Applications of Read Mapping Algorithm. Hans Journal of Biomedicine, 2011, 01, 1-5.	0.0	0
5115	Personal Genomes: A New Frontier in Database Research. Lecture Notes in Computer Science, 2011, , 78-88.	1.0	0
5116	Regulation of the Transcription of G Protein-Coupled Receptor Genes. Neuromethods, 2011, , 49-69.	0.2	Ο

		CITATION R	EPORT	
#	Article		IF	CITATIONS
5117	Stem Cells: Epigenetic Basis of Differentiation. Open Stem Cell Journal, 2011, 3, 28-33.		2.0	0
5118	Histone H3K27 Modifications and Gene Transcription. Journal of Life Science, 2011, 21,	, 616-620.	0.2	0
5120	Histone Modification Research Methods. Materials and Methods, 0, 1, .		0.0	1
5121	Generation of Functional Long Noncoding RNA Through Transcription and Natural Select 151-174.	ction. , 2012, ,		0
5122	Data Mining as a Discovery Tool for Imprinted Genes. Methods in Molecular Biology, 20	12, 925, 89-134.	0.4	0
5123	Analyse der Genregulation. , 2012, , 467-499.			0
5124	High-Throughput Computational Approaches to Analyzing Histone Modification Next-G Sequencing Data. Computational Molecular Biology, 0, , .	eneration	0.0	0
5126	Human Cancer Epigenetics. Epigenetics and Human Health, 2013, , 269-293.		0.2	0
5127	Immunological Analysis of Chromatin and Epigenetic Modifications. Materials and Meth	10ds, 0, 3, .	0.0	0
5128	Epigenetic Reprogramming in the Mammalian Germline. , 2013, , 3-34.			0
5129	Establishment of Tissue-Specific Epigenetic States During Development. , 2013, , 35-62			0
5130	Chromatin Switching and Gene Dynamics Associated with Type 2 Diabetes. Epigenetics Health, 2013, , 219-233.	and Human	0.2	0
5131	Inheritance of Stress-Induced Epigenetic Changes Mediated by the ATF-2 Family of Tran Factors. , 2013, , 103-118.	scription		0
5132	Epigenomic and Noncoding RNA Regulation in Addictive Processes. Epigenetics and Hu , 115-165.	man Health, 2013,	0.2	0
5133	Epigenetic Signatures of Breast Cancer Genes. , 2013, , 167-202.			0
5135	Application of Next-Generation Sequencing to Analysis of TGF ${\rm \widehat{I}^2}/{\rm SMAD4}$ Targets in Oval , 119-135.	ian Cancer. , 2013,		0
5136	The Fundamental Role of Epigenetic Regulation in Normal and Disturbed Cell Growth, D and Stemness. , 2014, , 1-41.	Vifferentiation,		0
5139	Epigenetics of Host-Pathogen Interactions. , 2013, , 1-22.			0

		CITATION RE	PORT	
# 5140	ARTICLE Aberrant Epigenetic Silencing is Triggered by a Transient Reduction in Gene Expression	n. , 2013, , 197-224.	IF	CITATIONS
5141	The Macrophage Epigenome and the Control of Inflammatory Gene Expression. Epigen Health, 2014, , 383-398.	etics and Human	0.2	0
5142	Genetics and epigenetics in human cancer. Cancer Genetics and Epigenetics, 0, , .		0.0	0
5144	Network Biology Empowering Detection and Understanding of Interactions Between C in Development of Complex Phenotypes. , 2014, , 175-194.	Genetic Factors		0
5145	Employing Genetic Algorithm to Construct Epigenetic Tree-Based Features for Enhance Prediction. Lecture Notes in Computer Science, 2014, , 390-397.	er Region	1.0	1
5146	Regulation of Pancreatic Islet Formation. , 2014, , 1-19.			0
5147	Epigenomics of Breast Cancer. , 2014, , 105-126.			0
5148	The Control of Gene Expression in Macrophages. , 2014, , 519-543.			0
5149	MOLECULAR MECHANISMS OF EPIGENETIC VARIATION IN PLANTS. , 2014, , 357-386.			0
5152	Theoretical Estimation of Nucleosome Density for Gene Sequences of Different Orthole Euchromatic and Heterochromatic Locations. Mathematical Biology and Bioinformatic 273-285.		0.1	0
5154	Enzyme and Protein Families that Regulate Histone Modifications and Crosstalk. RSC E Series, 2015, , 20-46.)rug Discovery	0.2	0
5155	Exploring function of conserved non-coding DNA in its chromosomal context. AIMS Bio 2, 773-793.	ophysics, 2015,	0.3	1
5156	High-Throughput Technologies: DNA and RNA Sequencing Strategies and Potential. , 2	015, , 47-68.		1
5157	QBioDiff: a web-based tool for quantification and interpretation of biological dif-ference multiple samples. Cancer Genetics and Epigenetics, 0, , .	es among	0.0	0
5160	The Analyses of Clobal Gene Expression and Transcription Factor Regulation. Translatic Bioinformatics, 2016, , 1-35.	onal	0.0	2
5161	The Effects of Pueraria and Rehmannia Clutinosa Intake and Exercise on Epigenetic Mo Ovariectomized Rat Skeletal Muscle. Journal of Life Science, 2015, 25, 1214-1222.	dification in	0.2	0
5164	Codon Usage Bias is not Significantly Different between the High and the Low Express Human. International Journal of Molecular Genetics and Gene Therapy, 2016, 1, .	ion Genes in	0.1	1
5165	Crosstalk Between DNA Methylation andÂChromatin Structure. , 2016, , 257-270.			0

# 5166	ARTICLE Epigenetic Mechanism in Breast Cancer. , 2016, , 329-344.	IF	Citations 0
5167	Acute Promyelocytic Leukaemia: Epigenetic Function of the PML-RARα Oncogene. , 2016, , 71-98.		0
5168	Lymphocyte Identity and Genomic Switches. Epigenetics and Human Health, 2016, , 41-52.	0.2	0
5171	Silicon Era of Carbon-Based Life: Application of Genomics and Bioinformatics in Crop Stress Research. , 2016, , 137-165.		0
5174	CENP Antibodies Used Additionally to FISH. Springer Protocols, 2017, , 347-351.	0.1	0
5180	Multilocus Methylation Assays in Epigenetics. , 2017, , 1-22.		0
5181	Epigenetics of Malaria Parasites. Epigenetics and Human Health, 2017, , 243-264.	0.2	0
5183	A Condensed History of Chromatin Research. Springer Theses, 2017, , 1-24.	0.0	0
5184	Periodic and Symmetric Organisation of Meiotic Chromosomes. Springer Theses, 2017, , 105-133.	0.0	1
5185	Forward and Reverse Epigenomics in Embryonic Stem Cells. , 2017, , 1-20.		0
5187	THERAPEUTIC TARGETING OF TUMORIGENESIS AND TUMOR DISEASE -FOR CLINICAL ANALYSIS OF EPIGENETICS AND EPIGENOME. International Journal of Hematology & Therapy, 2017, 3, 1-12.	0.1	0
5188	An Overview of Next Generation Sequencing and its Application in Neurodegenerative Diseases. International Journal of Engineering Research & Technology, 2017, V6, .	0.2	0
5191	3 Genetic and Epigenetic Considerations in iPSC Technology. , 2017, , 51-86.		0
5200	Finding commonality between the pattern of histone modifications across normal and cancer cell types dictated by DNA sequence features. Canadian Journal of Biotechnology, 2017, 1, 43-43.	0.3	0
5206	TET-Catalyzed 5-Carboxylcytosine Promotes CTCF Binding to Suboptimal Sequences Genome-Wide. SSRN Electronic Journal, 0, , .	0.4	0
5207	Epigenetic Changes and Epigenetic Targets in Head and Neck Cancer. Current Cancer Research, 2018, , 327-352.	0.2	Ο
5208	OBSOLETE: Epigenomics. , 2018, , .		0
5209	The Molecular and Functional Foundations of Conducive Somatic Cell Reprogramming to Ground State Pluripotency. SSRN Electronic Journal, 0, , .	0.4	0

#	Article	IF	CITATIONS
5210	Super-Resolution Imaging of Higher-Order Chromatin Structures at Different Epigenetic States in Single Mammalian Cells. SSRN Electronic Journal, 0, , .	0.4	2
5217	Sexual Differentiation, Gonadal Development, and Development of the External Genitalia. , 0, , 1-33.		0
5226	Defining CBX7-Dependent Chromatin Architecture with Rapid Small-Molecule Inhibition. SSRN Electronic Journal, 0, , .	0.4	0
5227	Systems biology in inflammatory bowel diseases: on the way to precision medicine. Annals of Gastroenterology, 2019, 32, 233-246.	0.4	7
5228	ModHMM: A Modular Supra-Bayesian Genome Segmentation Method. Lecture Notes in Computer Science, 2019, , 35-50.	1.0	2
5229	The DNA Methylation Machinery. , 2019, , 47-64.		1
5231	Chromatin Epigenomics in Muscle Development and Disease. , 2019, , 31-44.		0
5232	The Role of Histone Variants in Cancer. , 2019, , 133-151.		2
5233	Dysregulation of Cis-Regulatory Elements in Cancer. , 2019, , 173-192.		1
5239	Transcriptome and Genome Characterization Using Massively Parallel Paired End Tag (PET) Sequencing Analysis. , 2019, , 41-60.		0
5249	Genome-Wide Profiling of Histone Modifications with ChIP-Seq. Methods in Molecular Biology, 2020, 2072, 101-117.	0.4	5
5259	Modulating Epigenetic Modification Enzymes Through Relevant Epidrugs as a Timely Strategy in Anticancer Therapy. , 2020, , 137-157.		0
5269	Unified Analysis of Multiple ChIP-Seq Datasets. Methods in Molecular Biology, 2021, 2198, 451-465.	0.4	2
5271	A Semiautomated ChIP-Seq Procedure for Large-scale Epigenetic Studies. Journal of Visualized Experiments, 2020, , .	0.2	1
5273	DNA methyltransferases hitchhiking on chromatin. Swiss Medical Weekly, 2020, 150, w20329.	0.8	6
5274	Decoding the Equine Genome: Lessons from ENCODE. Genes, 2021, 12, 1707.	1.0	5
5275	KDM5D predicts response to docetaxel chemotherapy in metastatic castration resistant prostate cancer patients. Translational Andrology and Urology, 2021, 10, 3946-3952.	0.6	5
5277	ls There a Histone Code for Cellular Quiescence?. Frontiers in Cell and Developmental Biology, 2021, 9, 739780.	1.8	13

<u> </u>			<u> </u>	
(15	ГАТ	ON	REPC	TDT
			NLFC	ואנ

#	Article	IF	CITATIONS
5279	Alternative Lengthening of Telomeres: Lessons to Be Learned from Telomeric DNA Double-Strand Break Repair. Genes, 2021, 12, 1734.	1.0	7
5280	Cul4A-DDB1–mediated monoubiquitination of phosphoglycerate dehydrogenase promotes colorectal cancer metastasis via increased S-adenosylmethionine. Journal of Clinical Investigation, 2021, 131, .	3.9	36
5281	Global DNA methylation: role, status and genome-wide approaches to study epigenetic mark in cloned embryos. The Applied Biology & Chemistry Journal, 0, , 41-59.	0.0	0
5282	ChIP-Seq Assays from Mammalian and. Methods in Molecular Biology, 2021, 2245, 167-178.	0.4	1
5283	Epigenetic Analysis in Ewing Sarcoma. Methods in Molecular Biology, 2021, 2226, 285-302.	0.4	1
5285	User-Friendly and Interactive Analysis of ChIP-Seq Data Using EaSeq. Methods in Molecular Biology, 2020, 2117, 35-63.	0.4	4
5289	Genomics of Visceral Pain. , 2020, , 111-130.		0
5290	Transcription for Protein Biosynthesis. Biological and Medical Physics Series, 2020, , 477-508.	0.3	0
5291	Chapter 2. Epigenetic Reprogramming by Endocrine Disrupting Chemicals. Issues in Toxicology, 2020, , 25-66.	0.2	0
5295	Targeting DOT1L for mixed-lineage rearranged leukemia. , 2020, , 81-99.		2
5301	Systematic overview on the most widespread techniques for inducing and visualizing the DNA double-strand breaks. Mutation Research - Reviews in Mutation Research, 2021, 788, 108397.	2.4	5
5303	Bend family proteins mark chromatin boundaries and synergistically promote early germ cell differentiation. Protein and Cell, 2022, 13, 721-741.	4.8	6
5304	Identification of high-confidence human poly(A) RNA isoform scaffolds using nanopore sequencing. Rna, 2022, 28, 162-176.	1.6	12
5305	Genome-Wide Analysis of H3K27me3 in Porcine Embryonic Muscle Development. Frontiers in Cell and Developmental Biology, 2021, 9, 739321.	1.8	5
5307	Recent Progress of Small Molecule Menin–MLL Interaction Inhibitors as Therapeutic Agents for Acute Leukemia. Journal of Medicinal Chemistry, 2021, 64, 15519-15533.	2.9	11
5308	Prediction of Epigenetic Target Sites by Using Genomic DNA Sequence. , 0, , 498-512.		0
5309	Sequencing Genes and Gene Islands by Gene Enrichment. , 2009, , 673-689.		1
5310	Integrating the Genome and Epigenome in Human Disease. , 2009, , 343-368.		0

ARTICLE IF CITATIONS A Changing Epigenome in Health and Disease., 2009, , 369-384. 0 5311 Visualising the Epigenome., 2009, , 55-66. Generation of Functional Long Noncoding RNA Through Transcription and Natural Selection., 2012,, 5313 0 151-174. Tracking in and Low-Input Samples Using Ultrasensitive STAR. Methods in Molecular Biology, 2021, 0.4 2214, 241-252. Fast detection of differential chromatin domains with SCIDDO. Bioinformatics, 2021, 37, 1198-1205. 5320 1.8 6 Evidence for context-dependent functions of KDM5B in prostate development and prostate cancer. Oncotarget, 2020, 11, 4243-4252. 0.8 Dynamic nature of transcriptional regulation of nuclear receptor target genes in the context of 5323 1.9 2 chromatin organization. Dermato-Endocrinology, 2011, 3, 125-9. Regulatory genomics: Insights from the zebrafish. Current Topics in Genetics, 2012, 5, 1-10. 0.0 Novel Gene Discovery in the Human Malaria Parasite using Nucleosome Positioning Data. 5329 Computational Systems Bioinformatics / Life Sciences Society Computational Systems Bioinformatics 0.4 0 Conference, 2010, 9, 124-135. Knockdown of protein tyrosine phosphatase receptor U inhibits growth and motility of gastric cancer cells. International Journal of Clinical and Experimental Pathology, 2014, 7, 5750-61. Genetic alterations of KDM4 subfamily and therapeutic effect of novel demethylase inhibitor in breast 5331 30 1.4 cancer. American Journal of Cancer Research, 2015, 5, 1519-30. Epigenetic: A missing paradigm in cellular and molecular pathways of sulfur mustard lung: a 1.0 prospective and comparative study. Iranian Journal of Basic Medical Sciences, 2015, 18, 723-36. The histone methyltransferase DOT1L: regulatory functions and a cancer therapy target. American 5334 1.4 27 Journal of Cancer Research, 2015, 5, 2823-37. DNA Hypomethylation in Intragenic and Intergenic Enhancer Chromatin of Muscle-Specific Genes 0.2 Usually Correlates with their Expression. Yale Journal of Biology and Medicine, 2016, 89, 441-455. From Genotype to Phenotype: A Primer on the Functional Follow-up of Genome-Wide Association 5337 5 1.6 Studies in Cardiovascular Disease. Circulation Genomic and Precision Medicine, 2018, 11, . H3K27 trimethylation and H3K9 dimethylation as poor prognostic markers for patients with esophageal squamous cell carcinoma. International Journal of Clinical and Experimental Pathology, 5338 2019, 12, 2657-2664. Understanding Transcriptional Networks Regulating Initiation of Cutaneous Wound Healing. Yale 5339 0.2 5 Journal of Biology and Medicine, 2020, 93, 161-173. 5340 Network biology and applications. , 2022, , 381-407.

#	Article	IF	CITATIONS
5341	Dysregulation of Transglutaminase type 2 through GATA3 defines aggressiveness and Doxorubicin sensitivity in breast cancer. International Journal of Biological Sciences, 2022, 18, 1-14.	2.6	6
5342	Epigenetics and tissue immunity—Translating environmental cues into functional adaptations*. Immunological Reviews, 2022, 305, 111-136.	2.8	6
5343	Emerging role of G9a in cancer stemness and promises as a therapeutic target. Oncogenesis, 2021, 10, 76.	2.1	18
5344	BAF complexes drive proliferation and block myogenic differentiation in fusion-positive rhabdomyosarcoma. Nature Communications, 2021, 12, 6924.	5.8	25
5346	Histone 3 Lysine 27 Trimethylation Signature in Breast Cancer. International Journal of Molecular Sciences, 2021, 22, 12853.	1.8	9
5347	Deficiency of autism risk factor ASH1L in prefrontal cortex induces epigenetic aberrations and seizures. Nature Communications, 2021, 12, 6589.	5.8	30
5349	EZH2-mediated suppression of CLDN1 leads to barrier dysfunction in PPI-refractory gastroesophageal reflux disease. Digestive and Liver Disease, 2022, 54, 776-783.	0.4	2
5350	Novel role of prostate cancer risk variant rs7247241 on <i>PPP1R14A</i> isoform transition through allelic TF binding and CpG methylation. Human Molecular Genetics, 2022, 31, 1610-1621.	1.4	5
5351	Persistence and plasticity in bacterial gene regulation. Nature Methods, 2021, 18, 1499-1505.	9.0	23
5352	Yersinia remodels epigenetic histone modifications in human macrophages. PLoS Pathogens, 2021, 17, e1010074.	2.1	3
5353	Trans-tail regulation-mediated suppression of cryptic transcription. Experimental and Molecular Medicine, 2021, 53, 1683-1688.	3.2	6
5354	Histone Methyltransferase Dot1L Contributes to RIPK1 Kinaseâ€Dependent Apoptosis in Cerebral Ischemia/Reperfusion. Journal of the American Heart Association, 2021, 10, e022791.	1.6	8
5355	Fast alignment and preprocessing of chromatin profiles with Chromap. Nature Communications, 2021, 12, 6566.	5.8	39
5356	Concurrent mapping of multiple epigenetic marks and co-occupancy using ACT2-seq. Cell and Bioscience, 2021, 11, 198.	2.1	2
5357	Epigenetics in Food Allergy and Immunomodulation. Nutrients, 2021, 13, 4345.	1.7	17
5359	A Review on CRISPR-mediated Epigenome Editing: A Future Directive for Therapeutic Management of Cancer. Current Drug Targets, 2022, 23, 836-853.	1.0	7
5360	KAS-seq: genome-wide sequencing of single-stranded DNA by N3-kethoxal–assisted labeling. Nature Protocols, 2022, 17, 402-420.	5.5	16
5361	The histone methyltransferase DOT1L is a new epigenetic regulator of pulmonary fibrosis. Cell Death and Disease, 2022, 13, 60.	2.7	14

#	Article	IF	CITATIONS
5362	LncRNA IPW inhibits growth of ductal carcinoma in situ by downregulating ID2 through miR-29c. Breast Cancer Research, 2022, 24, 6.	2.2	6
5363	Noncoding RNAs in patients with colorectal cancer. , 2022, , 65-95.		0
5364	Epigenomics analysis of miRNA cis-regulatory elements in pig muscle and fat tissues. Genomics, 2022, 114, 110276.	1.3	7
5365	Cisâ€regulation of antisense nonâ€coding RNA at the <i>JAZF1</i> locus in type 2 diabetes. Journal of Gene Medicine, 2022, 24, e3407.	1.4	3
5366	Securin overexpression correlates with the activated Rb/E2F1 pathway and histone H3 epigenetic modifications in raw areca nut-induced carcinogenesis in mice. Cancer Cell International, 2022, 22, 30.	1.8	5
5367	Histone Methylation Regulates Gene Expression in the Round Spermatids to Set the RNA Payloads of Sperm. Reproductive Sciences, 2022, 29, 857-882.	1.1	7
5368	The roles of transcription, chromatin organisation and chromosomal processes in holocentromere establishment and maintenance. Seminars in Cell and Developmental Biology, 2022, , .	2.3	4
5369	Universal annotation of the human genome through integration of over a thousand epigenomic datasets. Genome Biology, 2022, 23, 9.	3.8	39
5370	Targeting Epigenetic Mechanisms in Vascular Aging. Frontiers in Cardiovascular Medicine, 2021, 8, 806988.	1.1	10
5373	Cell-type-specific epigenomic variations associated with <i>BRCA1</i> mutation in pre-cancer human breast tissues. NAR Genomics and Bioinformatics, 2022, 4, Iqac006.	1.5	2
5374	Deconstructing a Syndrome: Genomic Insights Into PCOS Causal Mechanisms and Classification. Endocrine Reviews, 2022, 43, 927-965.	8.9	75
5375	The histone demethylase Kdm6b regulates the maturation and cytotoxicity of TCRαβ+CD8αα+ intestinal intraepithelial lymphocytes. Cell Death and Differentiation, 2022, 29, 1349-1363.	5.0	6
5376	Kynurenic Acid and Its Analog SZR104 Exhibit Strong Antiinflammatory Effects and Alter the Intracellular Distribution and Methylation Patterns of H3 Histones in Immunochallenged Microglia-Enriched Cultures of Newborn Rat Brains. International Journal of Molecular Sciences, 2022, 23, 1079.	1.8	7
5377	The Current State of Chromatin Immunoprecipitation (ChIP) from FFPE Tissues. International Journal of Molecular Sciences, 2022, 23, 1103.	1.8	7
5378	Experimental methods to study proteinâ \in "nucleic acid interactions. , 2022, , 137-161.		0
5380	Epigenomic and enhancer dysregulation in uterine leiomyomas. Human Reproduction Update, 2022, 28, 518-547.	5.2	15
5382	Aggressive variants of prostate cancer: underlying mechanisms of neuroendocrine transdifferentiation. Journal of Experimental and Clinical Cancer Research, 2022, 41, 46.	3.5	43
5384	Functions, mechanisms, and therapeutic implications of METTL14 in human cancer. Journal of Hematology and Oncology, 2022, 15, 13.	6.9	34

#	Article	IF	CITATIONS
5385	Enhanced Generation of Human Induced Pluripotent Stem Cells from Peripheral Blood and Using Their Mesoderm Differentiation Ability to Regenerate Infarcted Myocardium. Stem Cells International, 2022, 2022, 1-19.	1.2	0
5386	Wild epigenetics: insights from epigenetic studies on natural populations. Proceedings of the Royal Society B: Biological Sciences, 2022, 289, 20211633.	1.2	18
5390	Contributions of epigenetic inheritance to the predisposition of major psychiatric disorders: Theoretical framework, evidence, and implications. Neuroscience and Biobehavioral Reviews, 2022, 135, 104579.	2.9	8
5391	Cis-regulatory sequences in plants: Their importance, discovery, and future challenges. Plant Cell, 2022, 34, 718-741.	3.1	125
5393	Regulation of epigenetic state by non-histone chromatin proteins and transcription factors: Implications in disease. Journal of Biosciences, 2020, 45, .	0.5	2
5395	Integration with systems biology approaches and -omics data to characterize risk variation. , 2022, , 289-315.		4
5396	Proteome-wide identification of non-histone lysine methylation in tomato during fruit ripening. Journal of Advanced Research, 2022, 42, 177-188.	4.4	5
5397	New Developments in T Cell Immunometabolism and Implications for Cancer Immunotherapy. Cells, 2022, 11, 708.	1.8	8
5398	Whole-genome methods to define DNA and histone accessibility and long-range interactions in chromatin. Biochemical Society Transactions, 2022, 50, 199-212.	1.6	2
5399	NUT Carcinoma: Clinicopathologic Features, Molecular Genetics and Epigenetics. Frontiers in Oncology, 2022, 12, 860830.	1.3	17
5400	Experimental development of the epigenomic library construction method to elucidate the epigenetic diversity and causal relationship between epigenome and transcriptome at a single-cell level. Genomics and Informatics, 2022, 20, e2.	0.4	0
5401	The BTB transcription factors ZBTB11 and ZFP131 maintain pluripotency by repressing pro-differentiation genes. Cell Reports, 2022, 38, 110524.	2.9	7
5402	Histone methylation-mediated microRNA-32-5p down-regulation in sensory neurons regulates pain behaviors via targeting Cav3.2 channels. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2117209119.	3.3	16
5403	Nascent transcription as a predictor and driver of histone modifications. Nature Genetics, 2022, 54, 223-224.	9.4	2
5404	Sodium Valproate Modulates the Methylation Status of Lysine Residues 4, 9 and 27 in Histone H3 of HeLa Cells. Current Molecular Pharmacology, 2023, 16, 197-210.	0.7	5
5405	Epigenetic Factors as Etiological Agents, Diagnostic Markers, and Therapeutic Targets for Luminal Breast Cancer. Biomedicines, 2022, 10, 748.	1.4	0
5407	Methylation of Subtelomeric Chromatin Modifies the Expression of the IncRNA TERRA, Disturbing Telomere Homeostasis. International Journal of Molecular Sciences, 2022, 23, 3271.	1.8	1
5408	Recruitment of DNA to tumor-derived microvesicles. Cell Reports, 2022, 38, 110443.	2.9	18

#	Article	IF	CITATIONS
5409	Inhibition of Histone H3 Lysine-27 Demethylase Activity Relieves Rheumatoid Arthritis Symptoms via Repression of IL6 Transcription in Macrophages. Frontiers in Immunology, 2022, 13, 818070.	2.2	7
5410	SWI/SNF Antagonism of PRC2 Mediates Estrogen-Induced Progesterone Receptor Expression. Cells, 2022, 11, 1000.	1.8	12
5411	An optimized ChIP‣eq framework for profiling histone modifications in <i>Chromochloris zofingiensis</i> . Plant Direct, 2022, 6, e392.	0.8	0
5412	Downregulation of the endothelial histone demethylase JMJD3 is associated with neointimal hyperplasia of arteriovenous fistulas in kidney failure. Journal of Biological Chemistry, 2022, 298, 101816.	1.6	2
5413	Histone Acetylation and Methylation Underlie Oligodendroglial and Myelin Susceptibility in Schizophrenia. Frontiers in Cellular Neuroscience, 2022, 16, 823708.	1.8	4
5414	Structure–function relationship of long noncoding <scp>RNAs</scp> : Advances and challenges. Wiley Interdisciplinary Reviews: Computational Molecular Science, 2022, 12, .	6.2	0
5415	Prediction of histone post-translational modification patterns based on nascent transcription data. Nature Genetics, 2022, 54, 295-305.	9.4	53
5416	Cell type–specific mechanism of Setd1a heterozygosity in schizophrenia pathogenesis. Science Advances, 2022, 8, eabm1077.	4.7	16
5418	KDM5-mediated redistribution of H3K4me3 is required for oocyte-to-embryonic transition in cattle. Biology of Reproduction, 2022, , .	1.2	1
5419	Histone post-translational modifications — cause and consequence of genome function. Nature Reviews Genetics, 2022, 23, 563-580.	7.7	253
5420	Chromatin Structure and Dynamics: Focus on Neuronal Differentiation and Pathological Implication. Genes, 2022, 13, 639.	1.0	8
5421	Exploring Methods of Targeting Histone Methyltransferases and Their Applications in Cancer Therapeutics. ACS Chemical Biology, 2022, 17, 744-755.	1.6	14
5422	Epigenomic alterations in cancer: mechanisms and therapeutic potential. Clinical Science, 2022, 136, 473-492.	1.8	4
5423	DiMeLo-seq: a long-read, single-molecule method for mapping protein–DNA interactions genome wide. Nature Methods, 2022, 19, 711-723.	9.0	45
5424	Jumonji Domain–containing Protein-3 (JMJD3/Kdm6b) Is Critical for Normal Ovarian Function and Female Fertility. Endocrinology, 2022, 163, .	1.4	4
5425	Metaboloepigenetics in cancer, immunity, and cardiovascular disease. Cardiovascular Research, 2023, 119, 357-370.	1.8	5
5426	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
5427	Divergent Effects of EZH1 and EZH2 Protein Expression on the Prognosis of Patients with T-Cell Lymphomas. Biomedicines, 2021, 9, 1842.	1.4	6

#	Article	IF	CITATIONS
5428	Chromatin Profiling of Human NaÃ⁻ve Pluripotent Stem Cells. Methods in Molecular Biology, 2022, 2416, 181-200.	0.4	0
5430	LSD1-directed therapy affects glioblastoma tumorigenicity by deregulating the protective ATF4-dependent integrated stress response. Science Translational Medicine, 2021, 13, eabf7036.	5.8	18
5431	ChIP-AP: an integrated analysis pipeline for unbiased ChIP-seq analysis. Briefings in Bioinformatics, 2022, 23, .	3.2	6
5432	cLoops2: a full-stack comprehensive analytical tool for chromatin interactions. Nucleic Acids Research, 2022, 50, 57-71.	6.5	24
5433	Muscles in Winter: The Epigenetics of Metabolic Arrest. Epigenomes, 2021, 5, 28.	0.8	5
5434	Chromatin Landscape Dynamics in the Early Development of the Plant Parasitic Nematode Meloidogyne incognita. Frontiers in Cell and Developmental Biology, 2021, 9, 765690.	1.8	2
5435	The H2A N-terminal tail is required to alleviate copper-induced stress in <i>Saccharomyces cerevisiae</i> . FEMS Yeast Research, 2021, 21, .	1.1	0
5436	GraphTGI: an attention-based graph embedding model for predicting TF-target gene interactions. Briefings in Bioinformatics, 2022, 23, .	3.2	7
5437	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
5438	METTL3 promotes prostate cancer progression by regulating miRâ€182 maturation in m6Aâ€dependent manner. Andrologia, 2022, 54, 1581-1591.	1.0	10
5439	H3K4 demethylase KDM5B regulates cancer cell identity and epigenetic plasticity. Oncogene, 2022, 41, 2958-2972.	2.6	8
5440	Smarcb1 Loss Results in a Deregulation of esBAF Binding and Impacts the Expression of Neurodevelopmental Genes. Cells, 2022, 11, 1354.	1.8	2
5441	Pleiotropic <i>MLLT10</i> variation confers risk of meningioma and estrogen-mediated cancers. Neuro-Oncology Advances, 2022, 4, .	0.4	4
5442	Histone H3K4me3 breadth in hypoxia reveals endometrial core functions and stress adaptation linked to endometriosis. IScience, 2022, 25, 104235.	1.9	4
5443	Natural Bioactive Compounds Targeting Histone Deacetylases in Human Cancers: Recent Updates. Molecules, 2022, 27, 2568.	1.7	12
5444	An alternative CYB5A transcript is expressed in aneuploid ALL and enriched in relapse. BMC Genomic Data, 2022, 23, 30.	0.7	1
5445	Systems biology approaches bring new insights in the understanding of global gene regulatory mechanisms and their deregulation in cancer. , 0, , 56-69.		0
5446	Epigenomic code. , 0, , 113-133.		0

#	ARTICLE
#	

ç"²åŸºè½¬ç§»é...¶SETDå®¶æ—ë,Žå¿fè;€ç®jå&,²å'Œç–¾ç—...çš"ç"究进展. Zhejiang Da Xue Xue Bao Yi Xue Ban = Journal of Zhejian 1-10.

5546	CUT&RUN Profiling of the Budding Yeast Epigenome. Methods in Molecular Biology, 2022, 2477, 129-147.	0.4	4
5547	Contribution of the histone variant H2A.Z to expression of responsive genes in plants. Seminars in Cell and Developmental Biology, 2022, , .	2.3	7
5548	The intrinsic and microenvironmental features of diffuse midline glioma: Implications for the development of effective immunotherapeutic treatment strategies. Neuro-Oncology, 2022, 24, 1408-1422.	0.6	27
5550	Development, regeneration and tumorigenesis of the urothelium. Development (Cambridge), 2022, 149, .	1.2	6
5552	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
5553	Protein Methylation in Diabetic Kidney Disease. Frontiers in Medicine, 2022, 9, .	1.2	5
5554	Functional Characterization of Genetic Variant Effects on Expression. Annual Review of Biomedical Data Science, 2022, 5, 119-139.	2.8	7
5555	High Dietary Salt Intake Is Associated With Histone Methylation in Salt-Sensitive Individuals. Frontiers in Nutrition, 2022, 9, 857562.	1.6	1
5556	Identification of EPZ004777 and FG2216 as inhibitors of TGF-β1 induced Treg cells by screening a library of epigenetic compounds. Life Sciences, 2022, 301, 120643.	2.0	0
5557	Folic acid intervention during pregnancy alters DNA methylation, affecting neural target genes through two distinct mechanisms. Clinical Epigenetics, 2022, 14, 63.	1.8	17
5558	Mitotically heritable, RNA polymerase II-independent H3K4 dimethylation stimulates INO1 transcriptional memory. ELife, 2022, 11, .	2.8	14
5559	Structural and functional specificity of H3K36 methylation. Epigenetics and Chromatin, 2022, 15, 17.	1.8	20
5560	Early Steps of Resistance to Targeted Therapies in Non-Small-Cell Lung Cancer. Cancers, 2022, 14, 2613.	1.7	8
5564	ePeak: from replicated chromatin profiling data to epigenomic dynamics. NAR Genomics and Bioinformatics, 2022, 4, .	1.5	1
5565	The Lysine Demethylases KdmA and KdmB Differently Regulate Asexual Development, Stress Response, and Virulence in Aspergillus fumigatus. Journal of Fungi (Basel, Switzerland), 2022, 8, 590.	1.5	2
5566	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
5568	Epigenetic regulation of T cell exhaustion. Nature Immunology, 2022, 23, 848-860.	7.0	82

#	Article	IF	CITATIONS
5570	Zinc finger protein 280C contributes to colorectal tumorigenesis by maintaining epigenetic repression at H3K27me3-marked loci. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	5
5571	H2A.Z's â€~social' network: functional partners of an enigmatic histone variant. Trends in Biochemical Sciences, 2022, 47, 909-920.	3.7	8
5572	Mammalian PERIOD2 regulates H2A.Z incorporation in chromatin to orchestrate circadian negative feedback. Nature Structural and Molecular Biology, 2022, 29, 549-562.	3.6	4
5574	The Intricate Epigenetic and Transcriptional Alterations in Pediatric High-Grade Cliomas: Targeting the Crosstalk as the Oncogenic Achilles' Heel. Biomedicines, 2022, 10, 1311.	1.4	3
5575	Epigenetic Signatures of Centrosomes Are Novel Targets in Cancer Diagnosis: Insights from an Analysis of the Cancer Genome Atlas. Epigenomes, 2022, 6, 14.	0.8	1
5582	Exerciseâ€induced histone H3 trimethylation at lysine 27 facilitates the adaptation of skeletal muscle to exercise in mice. Journal of Physiology, 2022, 600, 3331-3353.	1.3	11
5583	Time makes histone H3 modifications drift in mouse liver. Aging, 2022, 14, 4959-4975.	1.4	1
5584	Somatic point mutations are enriched in non-coding RNAs with possible regulatory function in breast cancer. Communications Biology, 2022, 5, .	2.0	5
5585	ChIP-Hub provides an integrative platform for exploring plant regulome. Nature Communications, 2022, 13, .	5.8	35
5586	H3K4me3 CUT&Tag and Transcriptome Analysis Reveal the Epigenetic Regulatory Landscape in Gill Tissue of Large Yellow Croaker (Larimichthys crocea) Under Low Salinity Stress. Frontiers in Marine Science, 0, 9, .	1.2	0
5587	Identification of essential element determining fruit-specific transcriptional activity in the tomato HISTIDINE DECARBOXYLASE A gene promoter. Plant Cell Reports, 0, , .	2.8	0
5588	Early in an SV40 infection, histone modifications correlate with the presence or absence of RNAPII and direction of transcription. Virology, 2022, 573, 59-71.	1.1	0
5589	Epigenetic Aspects and Prospects in Autoimmune Hepatitis. Frontiers in Immunology, 0, 13, .	2.2	6
5590	GoPeaks: histone modification peak calling for CUT&Tag. Genome Biology, 2022, 23, .	3.8	9
5591	TP53-Status-Dependent Oncogenic EZH2 Activity in Pancreatic Cancer. Cancers, 2022, 14, 3451.	1.7	5
5592	Epigenetics of the frozen brain: roles for lysine methylation in hypometabolism. FEBS Letters, 0, , .	1.3	2
5593	Catching Nucleosome by Its Decorated Tails Determines Its Functional States. Frontiers in Genetics, 0, 13, .	1.1	0
5594	Epigenetic Memories in Hematopoietic Stem and Progenitor Cells. Cells, 2022, 11, 2187.	1.8	3

#	Article	IF	CITATIONS
5595	Targeting histone demethylases as a potential cancer therapy (Review). International Journal of Oncology, 2022, 61, .	1.4	6
5598	Characterization of a Novel Heterochromatin Protein 1 Homolog "HP1c―in the Silkworm, Bombyx mori. Insects, 2022, 13, 631.	1.0	0
5599	Studying Epigenetics of Cardiovascular Diseases on Chip Guide. Neurology International, 2022, 12, 218-234.	0.2	0
5600	Application of Small Molecules in the Central Nervous System Direct Neuronal Reprogramming. Frontiers in Bioengineering and Biotechnology, 0, 10, .	2.0	5
5601	Characterizing cis-regulatory elements using single-cell epigenomics. Nature Reviews Genetics, 2023, 24, 21-43.	7.7	72
5602	Applications of singleâ€cell multiâ€omics sequencing in deep understanding of brain diseases. Clinical and Translational Discovery, 2022, 2, .	0.2	Ο
5603	Efficacy of Vafidemstat in Experimental Autoimmune Encephalomyelitis Highlights the KDM1A/RCOR1/HDAC Epigenetic Axis in Multiple Sclerosis. Pharmaceutics, 2022, 14, 1420.	2.0	3
5605	SOX2 transcription factor binding and function. Development (Cambridge), 2022, 149, .	1.2	1
5606	HDAC1 and PRC2 mediate combinatorial control in SPI1/PU.1-dependent gene repression in murine erythroleukaemia. Nucleic Acids Research, 2022, 50, 7938-7958.	6.5	12
5608	Epigenetics of Breast Cancer. , 2022, , 139-170.		0
5608 5609	Epigenetics of Breast Cancer., 2022, , 139-170. Epigenetic Regulation of Stem Cells., 2022, , .		0
		1.3	
5609	Epigenetic Regulation of Stem Cells. , 2022, , . Tracing the Origin of Cell-Free DNA Molecules through Tissue-Specific Epigenetic Signatures.	1.3	0
5609 5610	Epigenetic Regulation of Stem Cells. , 2022, , . Tracing the Origin of Cell-Free DNA Molecules through Tissue-Specific Epigenetic Signatures. Diagnostics, 2022, 12, 1834. The shaping of cancer genomes with the regional impact of mutation processes. Experimental and		0
5609 5610 5611	 Epigenetic Regulation of Stem Cells. , 2022, , . Tracing the Origin of Cell-Free DNA Molecules through Tissue-Specific Epigenetic Signatures. Diagnostics, 2022, 12, 1834. The shaping of cancer genomes with the regional impact of mutation processes. Experimental and Molecular Medicine, 2022, 54, 1049-1060. Functional genomic tools for emerging model species. Trends in Ecology and Evolution, 2022, 37, 	3.2	0 14 3
5609 5610 5611 5612	 Epigenetic Regulation of Stem Cells. , 2022, , . Tracing the Origin of Cell-Free DNA Molecules through Tissue-Specific Epigenetic Signatures. Diagnostics, 2022, 12, 1834. The shaping of cancer genomes with the regional impact of mutation processes. Experimental and Molecular Medicine, 2022, 54, 1049-1060. Functional genomic tools for emerging model species. Trends in Ecology and Evolution, 2022, 37, 1104-1115. X, but not Y, Chromosomal Complement Contributes to Stroke Sensitivity in Aged Animals. 	3.2 4.2	0 14 3 13
5609 5610 5611 5612 5613	 Epigenetic Regulation of Stem Cells. , 2022, , . Tracing the Origin of Cell-Free DNA Molecules through Tissue-Specific Epigenetic Signatures. Diagnostics, 2022, 12, 1834. The shaping of cancer genomes with the regional impact of mutation processes. Experimental and Molecular Medicine, 2022, 54, 1049-1060. Functional genomic tools for emerging model species. Trends in Ecology and Evolution, 2022, 37, 1104-1115. X, but not Y, Chromosomal Complement Contributes to Stroke Sensitivity in Aged Animals. Translational Stroke Research, 2023, 14, 776-789. Loss of TIP60 (KAT5) abolishes H2AZ lysine 7 acetylation and causes p53, INK4A, and ARF-independent cell 	3.2 4.2 2.3	0 14 3 13 6

#	Article	IF	CITATIONS
5618	Regulation, functions and transmission of bivalent chromatin during mammalian development. Nature Reviews Molecular Cell Biology, 2023, 24, 6-26.	16.1	51
5619	Transcription-coupled and epigenome-encoded mechanisms direct H3K4 methylation. Nature Communications, 2022, 13, .	5.8	17
5621	The Roles of Histone Post-Translational Modifications in the Formation and Function of a Mitotic Chromosome. International Journal of Molecular Sciences, 2022, 23, 8704.	1.8	3
5622	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
5623	Elevated levels of the methyltransferase SETD2 causes transcription and alternative splicing changes resulting in oncogenic phenotypes. Frontiers in Cell and Developmental Biology, 0, 10, .	1.8	4
5624	Structural insight into ASH1L PHD finger recognizing methylated histone H3K4 and promoting cell growth in prostate cancer. Frontiers in Oncology, 0, 12, .	1.3	6
5625	Histone Acid Extraction and High Throughput Mass Spectrometry to Profile Histone Modifications in <i>Arabidopsis thaliana</i> . Current Protocols, 2022, 2, .	1.3	3
5626	De Novo Polycomb Recruitment and Repressive Domain Formation. Epigenomes, 2022, 6, 25.	0.8	5
5628	A widespread length-dependent splicing dysregulation in cancer. Science Advances, 2022, 8, .	4.7	7
5629	A brief history of epigenetics. Immunology Letters, 2022, 249, 1-4.	1.1	5
5630	Gut Microbiome Influence on Human Epigenetics, Health, and Disease. , 2023, , 669-686.		1
5631	Mechanisms of Histone Modifications. , 2023, , 27-54.		1
5632	Epigenetic regulation of post-transcriptional machinery. , 2022, , 69-88.		0
5633	Regeneration and Developmental Enhancers are Differentially Compatible with Minimal Promoters. SSRN Electronic Journal, 0, , .	0.4	0
5634	Higher-order Chromatin Organization in Diseases, from Chromosomal Position Effect to Phenotype Variegation. , 2023, , 89-110.		0
5635	Chromatin Variants Reveal the Genetic Determinants of Oncogenesis in Breast Cancer. Cold Spring Harbor Perspectives in Medicine, 2022, 12, a041322.	2.9	1
5636	RNA helicase-dependent gene looping impacts messenger RNA processing. Nucleic Acids Research, 2022, 50, 9226-9246.	6.5	10
5637	Protein Lysine Methyltransferases Inhibitors. Current Medicinal Chemistry, 2023, 30, 3060-3089.	1.2	Ο

#	Article	IF	CITATIONS
5638	Changes in chromatin accessibility are not concordant with transcriptional changes for singleâ€factor perturbations. Molecular Systems Biology, 2022, 18, .	3.2	22
5639	Function and mechanism of histone \hat{l}^2 -hydroxybutyrylation in health and disease. Frontiers in Immunology, 0, 13, .	2.2	19
5640	Epigenetic modifications: Critical participants of the PD‑L1 regulatory mechanism in solid tumors (Review). International Journal of Oncology, 2022, 61, .	1.4	3
5641	Structural basis for product specificities of MLL family methyltransferases. Molecular Cell, 2022, 82, 3810-3825.e8.	4.5	4
5642	Histone methyltransferase GLP epigenetically activates GPCPD1 to sustain cancer cell metastasis and invasion. Genome Instability & Disease, 2023, 4, 21-37.	0.5	1
5643	Genome-Wide Study of Colocalization between Genomic Stretches: A Method and Applications to the Regulation of Gene Expression. Biology, 2022, 11, 1422.	1.3	0
5644	Building integrative functional maps of gene regulation. Human Molecular Genetics, 0, , .	1.4	2
5645	Targeting epigenetic alterations in cancer stem cells. Frontiers in Molecular Medicine, 0, 2, .	0.6	3
5646	Genomeâ€wide analysis of bivalent histone modifications during <i>Drosophila</i> embryogenesis. Genesis, 0, , .	0.8	0
5647	In situ tools for chromatin structural epigenomics. Protein Science, 2022, 31, .	3.1	5
5648	Multiplexed, single-molecule, epigenetic analysis of plasma-isolated nucleosomes for cancer diagnostics. Nature Biotechnology, 2023, 41, 212-221.	9.4	24
5649	The Histone Demethylase HR Suppresses Breast Cancer Development through Enhanced CELF2 Tumor Suppressor Activity. Cancers, 2022, 14, 4648.	1.7	1
5650	KDOAM-25 Overcomes Resistance to MEK Inhibitors by Targeting KDM5B in Uveal Melanoma. BioMed Research International, 2022, 2022, 1-9.	0.9	3
5652	<i>LncRNA-Smad7</i> mediates cross-talk between Nodal/TGF-β and BMP signaling to regulate cell fate determination of pluripotent and multipotent cells. Nucleic Acids Research, 2022, 50, 10526-10543.	6.5	2
5653	Distinct histone H3 modification profiles correlate with aggressive characteristics of salivary gland neoplasms. Scientific Reports, 2022, 12, .	1.6	6
5654	Dynamic and aberrant patterns of H3K4me3, H3K9me3, and H3K27me3 during early zygotic genome activation in cloned mouse embryos. Zygote, 2022, 30, 903-909.	0.5	2
5655	Epigenetics and environment in breast cancer: New paradigms for anti-cancer therapies. Frontiers in Oncology, 0, 12, .	1.3	9
5656	Thyroid Hormone–mediated Histone Modification Protects Cortical Neurons From the Toxic Effects of Hypoxic Injury. Journal of the Endocrine Society, 2022, 6, .	0.1	2

CITATION REPORT ARTICLE IF CITATIONS Super-enhancers conserved within placental mammals maintain stem cell pluripotency. Proceedings of 3.3 11 the National Academy of Sciences of the United States of America, 2022, 119, . Chromatin Immunoprecipitation Sequencing (ChIP-seq) for Detecting Histone Modifications and Modifiers. Methods in Molecular Biology, 2023, , 55-64. 0.4 Omics and Multi-Omics Analysis for the Early Identification and Improved Outcome of Patients with 1.4 13 Psoriatic Arthritis. Biomedicines, 2022, 10, 2387. MLL regulates the actin cytoskeleton and cell migration by stabilising Rho GTPases via the expression 1.2 of RhoĞDI1. Journal of Cell Science, 2022, 135, . Histone modification and histone modification-targeted anti-cancer drugs in breast cancer: 1.6 9 Fundamentals and beyond. Frontiers in Pharmacology, 0, 13, . Epigenetic modifications and targeted therapy in pediatric acute myeloid leukemia. Frontiers in Pediatrics, 0, 10, . p300/CBP sustains Polycomb silencing by non-enzymatic functions. Molecular Cell, 2022, 82, 4.5 9 3580-3597.e9. Celastrol inhibits lung cancer growth by triggering histone acetylation and acting synergically with 9 3.1HDAC inhibitors. Pharmacological Research, 2022, 185, 106487. Protocol to use RNaseH1-based CRISPR to modulate locus-associated R-loops. STAR Protocols, 2022, 3, 0.5 2 101734. Regeneration and developmental enhancers are differentially compatible with minimal promoters. Developmental Biology, 2022, 492, 47-58. Epigenetics and the Extreme Stress Response., 2022, , 177-213. 0 Ovarian Cancer Biomarkers., 2022, , 27-42. TCA-phospholipid-glycolysis targeted triple therapy effectively suppresses ATP production and tumor 4.6 8 growth in glioblastoma. Theranostics, 2022, 12, 7032-7050. The Histone Methyltransferase SETD8 Regulates the Expression of Tumor Suppressor Genes via H4K20 1.7 Methylation and the p53 Signaling Pathway in Endometrial Cancer Cells. Cancers, 2022, 14, 5367. Deep mendelian randomization: Investigating the causal knowledge of genomic deep learning models. 2 1.5 PLoS Computational Biology, 2022, 18, e1009880. Lysine Methyltransferase NSD1 and Cancers: Any Role in Melanoma?. Cancers, 2022, 14, 4865.

5679Multifactorial profiling of epigenetic landscapes at single-cell resolution using MulTI-Tag. Nature9.427Biotechnology, 2023, 41, 708-716.

1.6

4

Biological and therapeutic role of LSD1 in Alzheimer's diseases. Frontiers in Pharmacology, 0, 13, .

#

5657

5658

5659

5661

5662

5664

5666

5667

5668

5669

5670

5671

5672

5673

5674

#	Article	IF	CITATIONS
5681	Trained Immunity Provides Long-Term Protection against Bacterial Infections in Channel Catfish. Pathogens, 2022, 11, 1140.	1.2	2
5682	Hippo-Yap Signaling Maintains Sinoatrial Node Homeostasis. Circulation, 2022, 146, 1694-1711.	1.6	8
5683	Current and Emerging Technologies for the Analysis of the Genome-Wide and Locus-Specific DNA Methylation Patterns. Advances in Experimental Medicine and Biology, 2022, , 395-469.	0.8	2
5684	Enzymology of Mammalian DNA Methyltransferases. Advances in Experimental Medicine and Biology, 2022, , 69-110.	0.8	3
5685	Effective Quality Breeding Directions—Comparison and Conservative Analysis of Hepatic Super-Enhancers between Chinese and Western Pig Breeds. Biology, 2022, 11, 1631.	1.3	2
5686	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
5687	Sequencing Illumina libraries at high accuracy on the ONT MinION using R2C2. Genome Research, 2022, 32, 2092-2106.	2.4	6
5688	ÂCommercial ChIP-Seq Library Preparation Kits Performed Differently for Different Classes of Protein Targets. , 2022, 33, .		0
5689	Epigenetic insight into effects of prenatal alcohol exposure on stress axis development: Systematic review with metaâ€analytic approaches. Alcoholism: Clinical and Experimental Research, 2023, 47, 18-35.	1.4	2
5690	Repression of DERL3 via DNA methylation by Epstein-Barr virus latent membrane protein 1 in nasopharyngeal carcinoma. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2023, 1869, 166598.	1.8	4
5691	Nickel-induced alterations to chromatin structure and function. Toxicology and Applied Pharmacology, 2022, 457, 116317.	1.3	2
5692	Oncogenic Roles of Polycomb Repressive Complex 2 in Bladder Cancer and Upper Tract Urothelial Carcinoma. Biomedicines, 2022, 10, 2925.	1.4	0
5693	A framework for group-wise summarization and comparison of chromatin state annotations. Bioinformatics, 2023, 39, .	1.8	2
5694	Trained Immunity as a Prospective Tool against Emerging Respiratory Pathogens. Vaccines, 2022, 10, 1932.	2.1	1
5695	FRET-FISH probes chromatin compaction at individual genomic loci in single cells. Nature Communications, 2022, 13, .	5.8	4
5696	H2A.Z deposition by SWR1C involves multiple ATP-dependent steps. Nature Communications, 2022, 13, .	5.8	6
5697	Molecular responses to acute exercise and their relevance for adaptations in skeletal muscle to exercise training. Physiological Reviews, 2023, 103, 2057-2170.	13.1	51
5700	A novel small molecule glycolysis inhibitor WZ35 exerts anti-cancer effect via metabolic reprogramming. Journal of Translational Medicine, 2022, 20, .	1.8	2

		CITATION REPORT		
#	Article		IF	CITATIONS
5702	Role of primary aging hallmarks in Alzheimer´s disease. Theranostics, 2023, 13, 197-2	30.	4.6	8
5703	Discovery of cysteine-targeting covalent histone methyltransferase inhibitors. Europea Medicinal Chemistry, 2023, 246, 115028.	n Journal of	2.6	2
5704	Epigenetic drug library screening reveals targeting DOT1L abrogates NAD+ synthesis b H3K79 methylation in uveal melanoma. Journal of Pharmaceutical Analysis, 2023, 13, 2	y reprogramming .4-38.	2.4	4
5705	Novel insights into histone lysine methyltransferases in cancer therapy: From epigeneti to selective drugs. Journal of Pharmaceutical Analysis, 2023, 13, 127-141.	c regulation	2.4	6
5706	In Situ Hybridization as a Method to Examine Gene Regulatory Activity In Vivo. Method Biology, 2023, , 241-254.	s in Molecular	0.4	0
5708	Microâ€Topographies Induce Epigenetic Reprogramming and Quiescence in Human Mo Cells. Advanced Science, 2023, 10, .	esenchymal Stem	5.6	4
5710	Epigenetic regulation of radioresistance: insights from preclinical and clinical studies. E Opinion on Investigational Drugs, 0, , 1-17.	xpert	1.9	0
5713	Histone variants and modifications during abiotic stress response. Frontiers in Plant Sc	ience, 0, 13, .	1.7	9
5714	Chromatin modules and their implication in genomic organization and gene regulation Genetics, 2023, 39, 140-153.	. Trends in	2.9	9
5716	An Evidence Theory and Fuzzy Logic Combined Approach for the Prediction of Potentia Genes in Quinoa. Plants, 2023, 12, 71.	l ARF-Regulated	1.6	2
5718	DNA methylation episignatures: insight into copy number variation. Epigenomics, 2022	2, 14, 1373-1388.	1.0	7
5719	Histone modifications and DNA methylation act cooperatively in regulating symbiosis g anemone Aiptasia. BMC Biology, 2022, 20, .	genes in the sea	1.7	3
5720	Strategies for activity analysis of single nucleotide polymorphisms associated with hun Clinical Genetics, 2023, 103, 392-400.	ıan diseases.	1.0	3
5721	Tip60-mediated H2A.Z acetylation promotes neuronal fate specification and bivalent g Molecular Cell, 2022, 82, 4627-4646.e14.	ene activation.	4.5	11
5722	Developmental phenomics suggests that H3K4 monomethylation confers multi-level pl robustness. Cell Reports, 2022, 41, 111832.	nenotypic	2.9	5
5723	Mass-Cytometry-Based Quantification of Global Histone Post-Translational Modificatio Single-Cell Resolution Across Peripheral Immune Cells in IBD. Journal of Crohn's and Co 804-815.	ns at litis, 2023, 17,	0.6	3
5724	Epigenetic regulation of mesenchymal stem cell aging through histone modifications. Diseases, 2022, , .	Genes and	1.5	2
5725	Shaking up the silence: consequences of HMGN1 antagonizing PRC2 in the Down sync Epigenetics and Chromatin, 2022, 15, .	rome brain.	1.8	2

#	Article	IF	CITATIONS
5726	Whole-genome functional characterization of RE1 silencers using a modified massively parallel reporter assay. Cell Genomics, 2023, 3, 100234.	3.0	0
5727	Recent advances in understanding of the epigenetic regulation of plant regeneration. ABIOTECH, 2023, 4, 31-46.	1.8	6
5728	The chromatin determinants and Ph1 gene effect at wheat sites with contrasting recombination frequency. Journal of Advanced Research, 2023, , .	4.4	0
5729	Dual-specificity RNA aptamers enable manipulation of target-specific O-GlcNAcylation and unveil functions of O-GlcNAc on β-catenin. Cell, 2023, 186, 428-445.e27.	13.5	27
5730	Practical application of massively parallel reporter assay in biotechnology and medicine. Journal of Clinical Practice, 2023, 13, 74-87.	0.2	0
5731	<scp>PRMT3</scp> regulates the progression of invasive micropapillary carcinoma of the breast. Cancer Science, 2023, 114, 1912-1928.	1.7	6
5732	Inflammation and histone modification in chronic pain. Frontiers in Immunology, 0, 13, .	2.2	5
5733	Characterizing crosstalk in epigenetic signaling to understand disease physiology. Biochemical Journal, 2023, 480, 57-85.	1.7	4
5734	Targeting the epigenome of cancer stem cells in pediatric nervous system tumors. Molecular and Cellular Biochemistry, 2023, 478, 2241-2255.	1.4	3
5735	PfSET2 Is Involved in Genome Organization of <i>Var</i> Gene Family in Plasmodium falciparum. Microbiology Spectrum, 2023, 11, .	1.2	2
5736	Behavior, BDNF and epigenetic mechanisms in response to social isolation and social support in middle aged rats exposed to chronic stress. Behavioural Brain Research, 2023, 441, 114303.	1.2	3
5737	Chromatin mutations in pediatric high grade gliomas. Frontiers in Oncology, 0, 12, .	1.3	1
5739	Molecular basis of locus-specific H3K9 methylation catalyzed by SUVH6 in plants. Proceedings of the National Academy of Sciences of the United States of America, 2023, 120, .	3.3	3
5740	Sperm Energy Restriction and Recovery (SER) Alters Epigenetic Marks during the First Cell Cycle of Development in Mice. International Journal of Molecular Sciences, 2023, 24, 640.	1.8	2
5741	A Green Light to Switch on Genes: Revisiting Trithorax on Plants. Plants, 2023, 12, 75.	1.6	0
5743	Epigenetic regulation of cis-regulatory elements and transcription factors during development. , 2023, , 71-113.		1
5744	Beyond expression: role of phosphorylated residues of EZH2 in lineage plasticity in prostate cancer. Endocrinology, 0, , .	1.4	0
5745	Evolution of genome wide approaches to unveil transcriptional networks. , 2024, , 36-45.		Ο

#	Article	IF	CITATIONS
5746	Chromatin and noncoding RNA-mediated mechanisms of gastric tumorigenesis. Experimental and Molecular Medicine, 2023, 55, 22-31.	3.2	6
5747	Epigenetic signatures that maintain stemness in pluripotent and mesenchymal stem cells. , 2023, , 99-122.		0
5748	Quantitative Comparison of Multiple Chromatin Immunoprecipitation-Sequencing (ChIP-seq) Experiments with spikChIP. Methods in Molecular Biology, 2023, , 55-72.	0.4	0
5749	Epigenetic modifications and alternative pre-mRNA splicing in cancer. , 2023, , 123-146.		0
5750	Auxin-inducible degron 2 system deciphers functions of CTCF domains in transcriptional regulation. Genome Biology, 2023, 24, .	3.8	4
5751	Enhancers for Selective Targeting. Neuromethods, 2023, , 169-184.	0.2	0
5752	Epigenetic regulation of gene expression: an overview of classical and recently discovered novel players. , 2023, , 3-45.		0
5753	HDAC inhibition in cancer. , 2023, , 63-97.		0
5754	H3K4me3 mediates uterine leiomyoma pathogenesis via neuronal processes, synapsis components, proliferation, and Wnt/β-catenin and TGF-β pathways. Reproductive Biology and Endocrinology, 2023, 21, .	1.4	3
5756	SPR-1/CoREST facilitates the maternal epigenetic reprogramming of the histone demethylase SPR-5/LSD1. Genetics, 0, , .	1.2	0
5757	Epigenetic Reprogramming and Somatic Cell Nuclear Transfer. Methods in Molecular Biology, 2023, , 37-58.	0.4	0
5758	Analytical and therapeutic profiles of DNA methylation alterations in cancer; an overview of changes in chromatin arrangement and alterations in histone surfaces. Hormone Molecular Biology and Clinical Investigation, 2022, .	0.3	0
5760	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
5761	Selenium nanoparticles modulate histone methylation via lysine methyltransferase activity and S-adenosylhomocysteine depletion. Redox Biology, 2023, 61, 102641.	3.9	3
5762	Design, synthesis and in vitro/in vivo anticancer activity of tranylcypromine-based triazolopyrimidine analogs as novel LSD1 inhibitors. European Journal of Medicinal Chemistry, 2023, 253, 115321.	2.6	1
5763	Prolonged activity of the transposase helper may raise safety concerns during DNA transposon-based gene therapy. Molecular Therapy - Methods and Clinical Development, 2023, 29, 145-159.	1.8	1
5764	The role of lamin B2 in human diseases. Gene, 2023, 870, 147423.	1.0	0
5765	Epigenetic Mechanisms Governing Female and Male Germline Development in Mammals. Sexual Development, 2022, 16, 365-387.	1.1	3

#	Article	IF	CITATIONS
5766	A truncated and catalytically inactive isoform of KDM5B histone demethylase accumulates in breast cancer cells and regulates H3K4 tri-methylation and gene expression. Cancer Gene Therapy, 2023, 30, 822-832.	2.2	3
5767	Threeâ€dimensional chromatin reâ€organization during muscle stem cell aging. Aging Cell, 2023, 22, .	3.0	5
5768	New approaches to targeted therapy for metastatic melanoma in the presence of rare genetic changes in the tumor. Onkologiya Zhurnal Imeni P A Gertsena, 2023, 12, 65.	0.0	0
5770	Transient high salt intake causes epigenetic changes and leads to persistent inflammatory activation to produce "salt memoryâ€. Journal of Nutritional Biochemistry, 2023, 115, 109281.	1.9	1
5771	The role of histone methyltransferases in neurocognitive disorders associated with brain size abnormalities. Frontiers in Neuroscience, 0, 17, .	1.4	2
5772	High-Speed Atomic Force Microscopy Reveals Spontaneous Nucleosome Sliding of H2A.Z at the Subsecond Time Scale. Nano Letters, 2023, 23, 1696-1704.	4.5	1
5773	High-throughput Sequencing Technology and Its Application in Epigenetics Studies. SHS Web of Conferences, 2023, 158, 01005.	0.1	1
5775	Leveraging massively parallel reporter assays for evolutionary questions. Genome Biology, 2023, 24, .	3.8	10
5776	Targeting epigenetic regulation for cancer therapy using small molecule inhibitors. Advances in Cancer Research, 2023, , 73-161.	1.9	5
5777	Characterization of Histone Modifications in Late-Stage Rotator Cuff Tendinopathy. Genes, 2023, 14, 496.	1.0	1
5778	Epigenetic regulation in hematopoiesis and its implications in the targeted therapy of hematologic malignancies. Signal Transduction and Targeted Therapy, 2023, 8, .	7.1	20
5779	Detailed molecular and epigenetic characterization of the pig IPEC-J2 and chicken SL-29 cell lines. IScience, 2023, 26, 106252.	1.9	1
5780	Retinoblastoma-Binding Protein 5 Regulates H3K4 Methylation Modification to Inhibit the Proliferation of Melanoma Cells by Inactivating the Wnt/l²-Catenin and Epithelial-Mesenchymal Transition Pathways. Journal of Oncology, 2023, 2023, 1-19.	0.6	2
5781	The Histone Variant H2A.Z C-Terminal Domain Has Locus-Specific Differential Effects on H2A.Z Occupancy and Nucleosome Localization. Microbiology Spectrum, 2023, 11, .	1.2	0
5782	CHIP-seq: The evolution of genome-wide approaches to unveil the transcriptional network. , 2023, , .		0
5783	A promising new cancer marker: Long noncoding RNA EGFR-AS1. Frontiers in Oncology, 0, 13, .	1.3	3
5786	Effects of Histone H2B Ubiquitylations and H3K79me ₃ on Transcription Elongation. ACS Chemical Biology, 2023, 18, 537-548.	1.6	3
5787	Using QTL to Identify Genes and Pathways Underlying the Regulation and Production of Milk Components in Cattle. Animals, 2023, 13, 911.	1.0	1

		CITATION REPORT		
#	Article		IF	CITATIONS
5788	Epigenetics as a versatile regulator of fibrosis. Journal of Translational Medicine, 2023,	21,.	1.8	8
5789	Epigenetic Regulations in Mammalian Cells: Roles and Profiling Techniques. Molecules 46, 86-98.	and Cells, 2023,	1.0	5
5790	Systematic characterization of chromodomain proteins reveals an H3K9me1/2 reader in C. elegans. Nature Communications, 2023, 14, .	regulating aging	5.8	1
5791	Mechanistic aspects of reversible methylation modifications of arginine and lysine of n histones and their roles in human colon cancer. Progress in Molecular Biology and Trar Science, 2023, , 261-302.		0.9	3
5792	The TUDOR domain of SMN is an H3K79 ^{me1} histone mark reader. Life Sci 6, e202201752.	ence Alliance, 2023,	1.3	0
5793	Actin-related protein 6 facilitates proneural protein-induced gene activation for rapid n differentiation. Development (Cambridge), 2023, 150, .	eural	1.2	0
5795	Phenotypic dimorphism between honeybee queen and worker is regulated by complications. IScience, 2023, 26, 106308.	ated epigenetic	1.9	0
5797	Statistical Analysis in ChIP-seq-Related Applications. Methods in Molecular Biology, 20	23, , 169-181.	0.4	0
5798	SETD8 inhibits ferroptosis in pancreatic cancer by inhibiting the expression of RRAD. C International, 2023, 23, .	ancer Cell	1.8	1
5799	Epigenetic and epitranscriptomic regulation of axon regeneration. Molecular Psychiatr 1440-1450.	y, 2023, 28,	4.1	3
5800	BIND&MODIFY: a long-range method for single-molecule mapping of chromatin meukaryotes. Genome Biology, 2023, 24, .	nodifications in	3.8	5
5801	H3K27me3-H3K4me1 transition at bivalent promoters instructs lineage specification in Cell and Bioscience, 2023, 13, .	n development.	2.1	6
5804	Single-cell protein-DNA interactomics and multiomics tools for deciphering genome re- 2023, , 20220057.	gulation. ,		0
5805	Nuclei on the Rise: When Nuclei-Based Methods Meet Next-Generation Sequencing. Co	ells, 2023, 12, 1051.	1.8	1
5806	Titration-based normalization of antibody amount improves consistency of ChIP-seq ex Genomics, 2023, 24, .	operiments. BMC	1.2	0
5807	Esearch3D: propagating gene expression in chromatin networks to illuminate active er Nucleic Acids Research, 0, , .	ihancers.	6.5	1
5808	Changes in nascent chromatin structure regulate activation of the pro-fibrotic transcri myofibroblast emergence in organ fibrosis. IScience, 2023, 26, 106570.	ptome and	1.9	2
5809	Restraint of IFN-γ expression through a distal silencer CNS–28 for tissue homeostas 56, 944-958.e6.	is. Immunity, 2023,	6.6	3

#	ARTICLE Elevated enhancer-oncogene contacts and higher oncogene expression levels by recurrent CTCF	IF 2.9	CITATIONS 3
5812	inactivating mutations in acute TÂcell leukemia. Cell Reports, 2023, 42, 112373. HMGXB4 Targets Sleeping Beauty Transposition to Germinal Stem Cells. International Journal of Molecular Sciences, 2023, 24, 7283.	1.8	0
5815	The histone demethylase Utx controls <scp>CD8</scp> ⁺ Tâ€cellâ€dependent antitumor immunity via epigenetic regulation of the effector function. Cancer Science, 2023, 114, 2787-2797.	1.7	0
5816	Experimental Validation and Prediction of Super-Enhancers: Advances and Challenges. Cells, 2023, 12, 1191.	1.8	1
5818	The NPAC-LSD2 complex in nucleosome demethylation. The Enzymes, 2023, , .	0.7	0
5819	CRISPR technology and its potential role in treating rare imprinting diseases. , 2023, , 273-300.		0
5825	DNA and RNA Sequencing. , 2022, , 324-349.		0
5838	New genetic and epigenetic insights into the chemokine system: the latest discoveries aiding progression toward precision medicine. , 2023, 20, 739-776.		5
5840	Pathophysiological mechanisms and therapeutic approaches in obstructive sleep apnea syndrome. Signal Transduction and Targeted Therapy, 2023, 8, .	7.1	29
5868	Epigenetic regulation in the tumor microenvironment: molecular mechanisms and therapeutic targets. Signal Transduction and Targeted Therapy, 2023, 8, .	7.1	30
5877	Probiotics as Potential Remedy for Restoration of Gut Microbiome and Mitigation of Polycystic Ovarian Syndrome. , 2023, , 1-33.		0
5878	Centromeric and pericentric transcription and transcripts: their intricate relationships, regulation, and functions. Chromosoma, 2023, 132, 211-230.	1.0	3
5890	Chemical probes and methods for the study of protein arginine methylation. RSC Chemical Biology, 2023, 4, 647-669.	2.0	1
5907	Mapping epigenetic modifications by sequencing technologies. Cell Death and Differentiation, 0, , .	5.0	2
5909	Epigenetic control of pancreatic cancer metastasis. Cancer and Metastasis Reviews, 2023, 42, 1113-1131.	2.7	2
5912	KDM5 Lysine Demethylases in Pathogenesis, from Basic Science Discovery to the Clinic. Advances in Experimental Medicine and Biology, 2023, , 113-137.	0.8	0
5915	The chemistry of next-generation sequencing. Nature Biotechnology, 2023, 41, 1709-1715.	9.4	4
5918	Profiling histone posttranslational modifications and chromatin-modifying proteins by high-throughput reverse phase protein array. , 2024, , 13-35.		0

#	Article	IF	CITATIONS
5919	Alterations of histone modifications in cancer. , 2024, , 85-172.		0
5920	CHROMO domain readers: A rainbow of opportunities. , 2024, , 99-193.		0
5933	Epigenetic regulation: Histone modifying enzymes as targets for novel therapeutics. , 2024, , 430-452.		0
5938	CUT&RUN and CUT&Tag: Low-input methods for genome-wide mapping of chromatin proteins. , 2024, , 371-385.		0
5949	Bioinformatics of epigenetic data generated from next-generation sequencing. , 2024, , 37-82.		0
5950	Therapy of infectious diseases using epigenetic approaches. , 2024, , 853-882.		0
5951	Emerging role of epigenetics in human neurodevelopmental disorders. , 2024, , 285-331.		0
5952	Therapeutic approaches to imprinting diseases. , 2024, , 1077-1112.		0
5957	Interrogating epigenetic mechanisms with chemically customized chromatin. Nature Reviews Genetics, 2024, 25, 255-271.	7.7	1
5964	Epigenetic Modification in Ferroptosis. , 2023, , 241-261.		0
5972	Childhood Separation Anxiety: Human and Preclinical Studies. , 2023, , 5-28.		0
5988	Epigenetic (De)regulation in Prostate Cancer. Cancer Treatment and Research, 2023, , 321-360.	0.2	0
5991	The role of H3K27me3 methylation in cancer development. Genome Instability & Disease, 2024, 5, 17-34.	0.5	0
6001	Roles and Regulation of H3K4 Methylation During Mammalian Early Embryogenesis and Embryonic Stem Cell Differentiation. Advances in Experimental Medicine and Biology, 2024, , .	0.8	0
6002	Infection and Autoimmune Thyroid Diseases. , 2024, , 877-908.		0
6004	Best practices for ChIP-seq and its data analysis. , 2024, , 319-341.		0