

GREAT improves functional interpretation of cis-regula

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Epigenetic signatures distinguish multiple classes of enhancers with distinct cellular functions. <i>Genome Research</i> , 2011, 21, 1273-1283.	2.4	487
2	Three Periods of Regulatory Innovation During Vertebrate Evolution. <i>Science</i> , 2011, 333, 1019-1024.	6.0	127
3	Densely Interconnected Transcriptional Circuits Control Cell States in Human Hematopoiesis. <i>Cell</i> , 2011, 144, 296-309.	13.5	843
4	Control of Embryonic Stem Cell Lineage Commitment by Core Promoter Factor, TAF3. <i>Cell</i> , 2011, 146, 720-731.	13.5	155
5	Lineage Regulators Direct BMP and Wnt Pathways to Cell-Specific Programs during Differentiation and Regeneration. <i>Cell</i> , 2011, 147, 577-589.	13.5	277
6	Genome-wide Analysis of Simultaneous GATA1/2, RUNX1, FLI1, and SCL Binding in Megakaryocytes Identifies Hematopoietic Regulators. <i>Developmental Cell</i> , 2011, 20, 597-609.	3.1	255
7	Genomic Maps of Long Noncoding RNA Occupancy Reveal Principles of RNA-Chromatin Interactions. <i>Molecular Cell</i> , 2011, 44, 667-678.	4.5	1,104
8	5-Hydroxymethylcytosine is associated with enhancers and gene bodies in human embryonic stem cells. <i>Genome Biology</i> , 2011, 12, R54.	13.9	401
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17	Enabling enrichment analysis with the Human Disease Ontology. <i>Journal of Biomedical Informatics</i> , 2011, 44, S31-S38.	2.5	44
18	An integrated ChIP-seq analysis platform with customizable workflows. <i>BMC Bioinformatics</i> , 2011, 12, 277.	1.2	80

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1276	Virtual methylome dissection facilitated by single-cell analyses. <i>Epigenetics and Chromatin</i> , 2019, 12, 66.	1.8	4
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1281	Assisted reproductive technologies are associated with limited epigenetic variation at birth that largely resolves by adulthood. <i>Nature Communications</i> , 2019, 10, 3922.	5.8	94
1282	Maternal vitamin C regulates reprogramming of DNA methylation and germline development. <i>Nature</i> , 2019, 573, 271-275.	13.7	74
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1287	Immediate and deferred epigenomic signatures of in vivo neuronal activation in mouse hippocampus. <i>Nature Neuroscience</i> , 2019, 22, 1718-1730.	7.1	114
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1330	Comparative Analyses of Chromatin Landscape in White Adipose Tissue Suggest Humans May Have Less Beigeing Potential than Other Primates. <i>Genome Biology and Evolution</i> , 2019, 11, 1997-2008.	1.1	23
1331	Association of dietary folate and vitamin B-12 intake with genome-wide DNA methylation in blood: a large-scale epigenome-wide association analysis in 5841 individuals. <i>American Journal of Clinical Nutrition</i> , 2019, 110, 437-450.	2.2	46
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1356	Cardiac Reprogramming Factors Synergistically Activate Genome-wide Cardiogenic Stage-Specific Enhancers. <i>Cell Stem Cell</i> , 2019, 25, 69-86.e5.	5.2	72
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1727	DNA Methylation Signature for EZH2 Functionally Classifies Sequence Variants in Three PRC2 Complex Genes. <i>American Journal of Human Genetics</i> , 2020, 106, 596-610.	2.6	59
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1735	Dynamic chromatin accessibility landscape changes following interleukin-1 stimulation. <i>Epigenetics</i> , 2021, 16, 106-119.	1.3	8

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1743	Aggressive PDACs Show Hypomethylation of Repetitive Elements and the Execution of an Intrinsic IFN Program Linked to a Ductal Cell of Origin. <i>Cancer Discovery</i> , 2021, 11, 638-659.	7.7	65
1744	Diabetes changes gene expression but not DNA methylation in cardiac cells. <i>Journal of Molecular and Cellular Cardiology</i> , 2021, 151, 74-87.	0.9	13
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1746	Genomic characterization of the adolescent idiopathic scoliosis-associated transcriptome and regulome. <i>Human Molecular Genetics</i> , 2021, 29, 3606-3615.	1.4	12
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1751	Modeling Human TBX5 Haploinsufficiency Predicts Regulatory Networks for Congenital Heart Disease. <i>Developmental Cell</i> , 2021, 56, 292-309.e9.	3.1	63
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1753	PPAR β -p53-Mediated Vasculoregenerative Program to Reverse Pulmonary Hypertension. <i>Circulation Research</i> , 2021, 128, 401-418.	2.0	41
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1758	Identification of AR-V7 downstream genes commonly targeted by AR/AR-V7 and specifically targeted by AR-V7 in castration resistant prostate cancer. <i>Translational Oncology</i> , 2021, 14, 1009-15.	1.7	27
1759	Paternal reprogramming-escape histone H3K4me3 marks located within promoters of RNA splicing genes. <i>Bioinformatics</i> , 2021, 37, 1039-1044.	1.8	6
1760	Genome-wide DNA methylation analysis of cognitive function in middle and old-aged Chinese monozygotic twins. <i>Journal of Psychiatric Research</i> , 2021, 136, 571-580.	1.5	13
1761	Sperm DNA methylation changes after short-term nut supplementation in healthy men consuming a Western-style diet. <i>Andrology</i> , 2021, 9, 260-268.	1.9	9
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1773	Editorial: Genomic Colocalization and Enrichment Analyses. <i>Frontiers in Genetics</i> , 2020, 11, 617876.	1.1	0
1774	Three-dimensional interactions between enhancers and promoters during intestinal differentiation depend upon HNF4. <i>Cell Reports</i> , 2021, 34, 108679.	2.9	15
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1776	Identification of DNA methylation signatures associated with poor outcome in lower-risk Stage, Size, Grade and Necrosis (SSIGN) score clear cell renal cell cancer. <i>Clinical Epigenetics</i> , 2021, 13, 12.	1.8	8
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1779	The T-box transcription factor Eomesodermin governs haemogenic competence of yolk sac mesodermal progenitors. <i>Nature Cell Biology</i> , 2021, 23, 61-74.	4.6	10
1780	Ablation of DNA-methyltransferase 3A in skeletal muscle does not affect energy metabolism or exercise capacity. <i>PLoS Genetics</i> , 2021, 17, e1009325.	1.5	7
1781	Age-related and disease locus-specific mechanisms contribute to early remodelling of chromatin structure in Huntington's disease mice. <i>Nature Communications</i> , 2021, 12, 364.	5.8	14
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1809	Immune synapse instructs epigenomic and transcriptomic functional reprogramming in dendritic cells. <i>Science Advances</i> , 2021, 7, .	4.7	10
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1818	Non-CG methylation and multiple histone profiles associate child abuse with immune and small GTPase dysregulation. <i>Nature Communications</i> , 2021, 12, 1132.	5.8	24
1819	A β -catenin-driven switch in TCF/LEF transcription factor binding to DNA target sites promotes commitment of mammalian nephron progenitor cells. <i>ELife</i> , 2021, 10, .	2.8	32
1820	Combinatorial transcription factor activities on open chromatin induce embryonic heterogeneity in vertebrates. <i>EMBO Journal</i> , 2021, 40, e104913.	3.5	23
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1823	Comprehensive analysis of single cell ATAC-seq data with SnapATAC. <i>Nature Communications</i> , 2021, 12, 1337.	5.8	253
1824	Spatially mapped single-cell chromatin accessibility. <i>Nature Communications</i> , 2021, 12, 1274.	5.8	53
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1830	Combined genomic and proteomic approaches reveal DNA binding sites and interaction partners of TBX2 in the developing lung. <i>Respiratory Research</i> , 2021, 22, 85.	1.4	8
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1843	A noncanonical AR addiction drives enzalutamide resistance in prostate cancer. <i>Nature Communications</i> , 2021, 12, 1521.	5.8	43
1844	Prioritization of Osteoporosis-Associated Genome-wide Association Study (<sc>GWAS</sc> Single-Nucleotide Polymorphisms (<sc>SNPs</sc> Using Epigenomics and Transcriptomics. <i>JBMR Plus</i> , 2021, 5, e10481.	1.3	14
1846	Epigenomic tensor predicts disease subtypes and reveals constrained tumor evolution. <i>Cell Reports</i> , 2021, 34, 108927.	2.9	12
1850	Integrative pan cancer analysis reveals epigenomic variation in cancer type and cell specific chromatin domains. <i>Nature Communications</i> , 2021, 12, 1419.	5.8	46
1852	Reprogramming of the FOXA1 cistrome in treatment-emergent neuroendocrine prostate cancer. <i>Nature Communications</i> , 2021, 12, 1979.	5.8	70
1853	An intriguing characteristic of enhancer-promoter interactions. <i>BMC Genomics</i> , 2021, 22, 163.	1.2	3
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1858	Machine learning for deciphering cell heterogeneity and gene regulation. <i>Nature Computational Science</i> , 2021, 1, 183-191.	3.8	14
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1870	How to Get Started with Single Cell RNA Sequencing Data Analysis. <i>Journal of the American Society of Nephrology: JASN</i> , 2021, 32, 1279-1292.	3.0	19
1871	HOXBLOC long non-coding RNA activation promotes leukemogenesis in NPM1-mutant acute myeloid leukemia. <i>Nature Communications</i> , 2021, 12, 1956.	5.8	28
1873	Regulation of B Lymphocyte Development by Histone H2A Deubiquitinase BAP1. <i>Frontiers in Immunology</i> , 2021, 12, 626418.	2.2	8
1875	Single cell regulatory landscape of the mouse kidney highlights cellular differentiation programs and disease targets. <i>Nature Communications</i> , 2021, 12, 2277.	5.8	122
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1884	A compendium and comparative epigenomics analysis of cis-regulatory elements in the pig genome. <i>Nature Communications</i> , 2021, 12, 2217.	5.8	63
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1897	Transient rest restores functionality in exhausted CAR-T cells through epigenetic remodeling. <i>Science</i> , 2021, 372, .	6.0	297
1898	Histone crotonylation promotes mesoendodermal commitment of human embryonic stem cells. <i>Cell Stem Cell</i> , 2021, 28, 748-763.e7.	5.2	59
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1908	Evolution of DNA methylation in the human brain. <i>Nature Communications</i> , 2021, 12, 2021.	5.8	53
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1916	Cell-type-specific effects of genetic variation on chromatin accessibility during human neuronal differentiation. <i>Nature Neuroscience</i> , 2021, 24, 941-953.	7.1	47
1918	Common DNA methylation dynamics in endometrioid adenocarcinoma and glioblastoma suggest universal epigenomic alterations in tumorigenesis. <i>Communications Biology</i> , 2021, 4, 607.	2.0	9
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1926	Epigenetic control of region-specific transcriptional programs in mouse cerebellar and cortical astrocytes. <i>Glia</i> , 2021, 69, 2160-2177.	2.5	13
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1932	Nuclear FGFR1 Regulates Gene Transcription and Promotes Antiestrogen Resistance in ER+ Breast Cancer. <i>Clinical Cancer Research</i> , 2021, 27, 4379-4396.	3.2	30
1934	PKM2-dependent metabolic skewing of hepatic Th17 cells regulates pathogenesis of non-alcoholic fatty liver disease. <i>Cell Metabolism</i> , 2021, 33, 1187-1204.e9.	7.2	60
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1938	Single-PanIN-seq unveils that ARID1A deficiency promotes pancreatic tumorigenesis by attenuating KRAS-induced senescence. <i>ELife</i> , 2021, 10, .	2.8	5
1939	Chromosome-level assembly of southern catfish (<i>Silurus meridionalis</i>) provides insights into visual adaptation to nocturnal and benthic lifestyles. <i>Molecular Ecology Resources</i> , 2021, 21, 1575-1592.	2.2	20
1940	Pathogenic LMNA variants disrupt cardiac lamina-chromatin interactions and de-repress alternative fate genes. <i>Cell Stem Cell</i> , 2021, 28, 938-954.e9.	5.2	61
1941	High-throughput single-cell chromatin accessibility CRISPR screens enable unbiased identification of regulatory networks in cancer. <i>Nature Communications</i> , 2021, 12, 2969.	5.8	73
1942	A meta-analysis of epigenome-wide association studies in Alzheimer's disease highlights novel differentially methylated loci across cortex. <i>Nature Communications</i> , 2021, 12, 3517.	5.8	72
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1944	BCOR modulates transcriptional activity of a subset of glucocorticoid receptor target genes involved in cell growth and mobility. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2021, 210, 105873.	1.2	3
1945	Epigenetic clock and methylation studies in elephants. <i>Aging Cell</i> , 2021, 20, e13414.	3.0	43
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1951	Truncating SRCAP variants outside the Floating-Harbor syndrome locus cause a distinct neurodevelopmental disorder with a specific DNA methylation signature. <i>American Journal of Human Genetics</i> , 2021, 108, 1053-1068.	2.6	31
1955	3D genome alterations associated with dysregulated HOXA13 expression in high-risk T-lineage acute lymphoblastic leukemia. <i>Nature Communications</i> , 2021, 12, 3708.	5.8	24
1956	Breast tumor stiffness instructs bone metastasis via maintenance of mechanical conditioning. <i>Cell Reports</i> , 2021, 35, 109293.	2.9	29
1957	Nuclear ADP-ribosylation drives IFN β -dependent STAT1 enhancer formation in macrophages. <i>Nature Communications</i> , 2021, 12, 3931.	5.8	20
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1963	Evolution of mouse circadian enhancers from transposable elements. Genome Biology, 2021, 22, 193.	3.8	30
1964	Hierarchical reactivation of transcription during mitosis-to-G1 transition by Brn2 and Ascl1 in neural stem cells. Genes and Development, 2021, 35, 1020-1034.	2.7	11
1965	Widespread formation of double-stranded RNAs in testis. Genome Research, 2021, 31, 1174-1186.	2.4	6
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1967	Combined EZH2 Inhibition and IKAROS Degradation Leads to Enhanced Antitumor Activity in Diffuse Large B-cell Lymphoma. Clinical Cancer Research, 2021, 27, 5401-5414.	3.2	16
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1973	Runx1 shapes the chromatin landscape via a cascade of direct and indirect targets. PLoS Genetics, 2021, 17, e1009574.	1.5	19
1974	Krüppel-like factor 6-mediated loss of BCAA catabolism contributes to kidney injury in mice and humans. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	34
1975	Genome-Wide Histone H3K27 Acetylation Profiling Identified Genes Correlated With Prognosis in Papillary Thyroid Carcinoma. Frontiers in Cell and Developmental Biology, 2021, 9, 682561.	1.8	9
1976	MIMIC: an optimization method to identify cell type-specific marker panel for cell sorting. Briefings in Bioinformatics, 2021, 22, .	3.2	1
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1979	Profiling chromatin accessibility responses in human neutrophils with sensitive pathogen detection. Life Science Alliance, 2021, 4, e202000976.	1.3	5
1980	DNA methylation profile of liver of mice conceived by <i>in vitro</i> fertilization. Journal of Developmental Origins of Health and Disease, 2022, 13, 358-366.	0.7	3
1982	Shifting epigenetic contexts influence regulatory variation and disease risk. Aging, 2021, 13, 15699-15749.	1.4	2
1983	Ten-eleven translocation 2 modulates allergic inflammation by 5-hydroxymethylcytosine remodeling of immunologic pathways. Human Molecular Genetics, 2021, 30, 1985-1995.	1.4	2
1984	Analysis of gene network bifurcation during optic cup morphogenesis in zebrafish. Nature Communications, 2021, 12, 3866.	5.8	14
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1989	Structural basis for glucocorticoid receptor recognition of both unmodified and methylated binding sites, precursors of a modern recognition element. <i>Nucleic Acids Research</i> , 2021, 49, 8923-8933.	6.5	3
1990	Single-Cell Epigenomics and Functional Fine-Mapping of Atherosclerosis GWAS Loci. <i>Circulation Research</i> , 2021, 129, 240-258.	2.0	61
1991	Global CpG DNA Methylation Footprint in Kaposi's Sarcoma. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 666143.	1.8	5
1993	Dynamic chromatin regulatory landscape of human CAR T cell exhaustion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	36
1994	Developmental exposure to chlordecone induces transgenerational effects in somatic prostate tissue which are associated with epigenetic histone trimethylation changes. <i>Environment International</i> , 2021, 152, 106472.	4.8	13
1995	Endogenous Retroviruses Drive Lineage-Specific Regulatory Evolution across Primate and Rodent Placentae. <i>Molecular Biology and Evolution</i> , 2021, 38, 4992-5004.	3.5	23
1996	The chromatin, topological and regulatory properties of pluripotency-associated poised enhancers are conserved in vivo. <i>Nature Communications</i> , 2021, 12, 4344.	5.8	50
1997	The long noncoding RNA HOTAIRM1 controlled by AML1 enhances glucocorticoid resistance by activating RHOA/ROCK1 pathway through suppressing ARHGAP18. <i>Cell Death and Disease</i> , 2021, 12, 702.	2.7	8
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2001	Epigenetic scarring of exhausted T cells hinders memory differentiation upon eliminating chronic antigenic stimulation. <i>Nature Immunology</i> , 2021, 22, 1008-1019.	7.0	116
2003	Distinct transcription factor networks control neutrophil-driven inflammation. <i>Nature Immunology</i> , 2021, 22, 1093-1106.	7.0	83
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2007	DNA methylation analysis reveals epimutation hotspots in patients with dilated cardiomyopathy-associated laminopathies. <i>Clinical Epigenetics</i> , 2021, 13, 139.	1.8	5
2010	Whole-genome analysis of TET dioxygenase function in regulatory T cells. <i>EMBO Reports</i> , 2021, 22, e52716.	2.0	19

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2013	Multi-omic profiling of primary mouse neutrophils predicts a pattern of sex- and age-related functional regulation. <i>Nature Aging</i> , 2021, 1, 715-733.	5.3	55
2015	The conserved ASTN2/BRINP1 locus at 9q33.1â€“33.2 is associated with major psychiatric disorders in a large pedigree from Southern Spain. <i>Scientific Reports</i> , 2021, 11, 14529.	1.6	3
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2017	Profiling DNA break sites and transcriptional changes in response to contextual fear learning. <i>PLoS ONE</i> , 2021, 16, e0249691.	1.1	29
2018	BATF regulates progenitor to cytolytic effector CD8+ T cell transition during chronic viral infection. <i>Nature Immunology</i> , 2021, 22, 996-1007.	7.0	78
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2042	Metabolic modeling of single Th17 cells reveals regulators of autoimmunity. Cell, 2021, 184, 4168-4185.e21.	13.5	203
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2057	Epigenome-wide DNA methylation signature of benzo[a]pyrene exposure and their mediation roles in benzo[a]pyrene-associated lung cancer development. Journal of Hazardous Materials, 2021, 416, 125839.	6.5	32
2058	Developmental and evolutionary dynamics of cis-regulatory elements in mouse cerebellar cells. Science, 2021, 373, .	6.0	51
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2068	Epithelial memory of inflammation limits tissue damage while promoting pancreatic tumorigenesis. <i>Science</i> , 2021, 373, eabj0486.	6.0	99
2069	Release of Notch activity coordinated by IL-1 β signalling confers differentiation plasticity of airway progenitors via <i>Fosl2</i> during alveolar regeneration. <i>Nature Cell Biology</i> , 2021, 23, 953-966.	4.6	37
2070	SUPERGNOVA: local genetic correlation analysis reveals heterogeneous etiologic sharing of complex traits. <i>Genome Biology</i> , 2021, 22, 262.	3.8	56
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2077	Chronic stress primes innate immune responses in mice and humans. <i>Cell Reports</i> , 2021, 36, 109595.	2.9	53
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2080	Enhancer recruitment of transcription repressors RUNX1 and TLE3 by mis-expressed FOXC1 blocks differentiation in acute myeloid leukemia. <i>Cell Reports</i> , 2021, 36, 109725.	2.9	15
2082	Single-cell landscape of nuclear configuration and gene expression during stem cell differentiation and X inactivation. <i>Genome Biology</i> , 2021, 22, 279.	3.8	11
2084	Conserved and species-specific chromatin remodeling and regulatory dynamics during mouse and chicken limb bud development. <i>Nature Communications</i> , 2021, 12, 5685.	5.8	6
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2088	JUN promotes hypertrophic skin scarring via CD36 in preclinical in vitro and in vivo models. <i>Science Translational Medicine</i> , 2021, 13, eabb3312.	5.8	32
2089	KDM4B promotes acute myeloid leukemia associated with AML1-ETO by regulating chromatin accessibility. <i>FASEB BioAdvances</i> , 2021, 3, 1020-1033.	1.3	3
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2106	Placental DNA methylation marks are associated with maternal depressive symptoms during early pregnancy. <i>Neurobiology of Stress</i> , 2021, 15, 100374.	1.9	12
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2113	IRF5 regulates airway macrophage metabolic responses. <i>Clinical and Experimental Immunology</i> , 2021, 204, 134-143.	1.1	9
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2126	Considerations on Experimental Design and Data Analysis of Chromatin Immunoprecipitation Experiments. <i>Methods in Molecular Biology</i> , 2018, 1689, 9-28.	0.4	5
2127	Epigenetic Consequences of Low Birth-Weight and Preterm Birth in Adult Twins. , 2017, , 1-13.		1
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2134	BCL9/STAT3 regulation of transcriptional enhancer networks promote DCIS progression. <i>Npj Breast Cancer</i> , 2020, 6, 12.	2.3	10
2135	Global hyperactivation of enhancers stabilizes human and mouse naive pluripotency through inhibition of CDK8/19 Mediator kinases. <i>Nature Cell Biology</i> , 2020, 22, 1223-1238.	4.6	35
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2302	Embryonic Stem Cell (ES)-Specific Enhancers Specify the Expression Potential of ES Genes in Cancer. PLoS Genetics, 2016, 12, e1005840.	1.5	10
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2304	An Integrated Genome-Wide Systems Genetics Screen for Breast Cancer Metastasis Susceptibility Genes. PLoS Genetics, 2016, 12, e1005989.	1.5	19
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3420	Tissue memory relies on stem cell priming in distal undamaged areas. <i>Nature Cell Biology</i> , 2023, 25, 740-753.	4.6	9
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