

The Encyclopedia of DNA elements (ENCODE): data por

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Developing DNA methylation-based diagnostic biomarkers. <i>Journal of Genetics and Genomics</i> , 2018, 45, 87-97.	1.7	41
2	Genomic and Functional Fidelity of Small Cell Lung Cancer Patient-Derived Xenografts. <i>Cancer Discovery</i> , 2018, 8, 600-615.	7.7	157
3	The next generation of melanocyte data: Genetic, epigenetic, and transcriptional resource datasets and analysis tools. <i>Pigment Cell and Melanoma Research</i> , 2018, 31, 442-447.	1.5	3
4	The 2018 Nucleic Acids Research database issue and the online molecular biology database collection. <i>Nucleic Acids Research</i> , 2018, 46, D1-D7.	6.5	106
5	CRISPR-mediated deletion of prostate cancer risk-associated CTCF loop anchors identifies repressive chromatin loops. <i>Genome Biology</i> , 2018, 19, 160.	3.8	60
6	The Cellosaurus, a Cell-Line Knowledge Resource. <i>Journal of Biomolecular Techniques</i> , 2018, 29, 25-38.	0.8	437
7	Decoding the non-coding genome: Opportunities and challenges of genomic and epigenomic consortium data. <i>Current Opinion in Systems Biology</i> , 2018, 11, 82-90.	1.3	4
8	Developmental Chromatin Restriction of Proliferation Gene Networks Acts as an Epigenetic Barrier to Axon Regeneration in Cortical Neurons. <i>Developmental Neurobiology</i> , 2018, 78, 960-977.	1.5	29
9	GWAS4D: multidimensional analysis of context-specific regulatory variant for human complex diseases and traits. <i>Nucleic Acids Research</i> , 2018, 46, W114-W120.	6.5	69
10	KLF6 and STAT3 co-occupy regulatory DNA and functionally synergize to promote axon growth in CNS neurons. <i>Scientific Reports</i> , 2018, 8, 12565.	1.6	34
11	Patterns and mechanisms of structural variations in human cancer. <i>Experimental and Molecular Medicine</i> , 2018, 50, 1-11.	3.2	73
12	Non-coding genetic variation shaping mental health. <i>Current Opinion in Psychology</i> , 2019, 27, 18-24.	2.5	14
13	Glial response to hypoxia in mutants of NPAS1/3 homolog Trachealess through Wg signaling to modulate synaptic bouton organization. <i>PLoS Genetics</i> , 2019, 15, e1007980.	1.5	8
14	Genome-Wide Association Study of Metabolic Syndrome Reveals Primary Genetic Variants at CETP Locus in Indians. <i>Biomolecules</i> , 2019, 9, 321.	1.8	16
15	EpiFIT: functional interpretation of transcription factors based on combination of sequence and epigenetic information. <i>Quantitative Biology</i> , 2019, 7, 233-243.	0.3	4
16	Disruption of chromatin organisation causes MEF2C gene overexpression in intellectual disability: a case report. <i>BMC Medical Genomics</i> , 2019, 12, 116.	0.7	10
17	The lncRNA Locus Handsdown Regulates Cardiac Gene Programs and Is Essential for Early Mouse Development. <i>Developmental Cell</i> , 2019, 50, 644-657.e8.	3.1	66
18	Over 1000 genetic loci influencing blood pressure with multiple systems and tissues implicated. <i>Human Molecular Genetics</i> , 2019, 28, R151-R161.	1.4	39

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19	Replication timing networks reveal a link between transcription regulatory circuits and replication timing control. <i>Genome Research</i> , 2019, 29, 1415-1428.	2.4	12
20	Hidden Markov models lead to higher resolution maps of mutation signature activity in cancer. <i>Genome Medicine</i> , 2019, 11, 49.	3.6	22
21	Securing the future of research computing in the biosciences. <i>PLoS Computational Biology</i> , 2019, 15, e1006958.	1.5	6
22	Identification of important invasion and proliferation related genes in adrenocortical carcinoma. <i>Medical Oncology</i> , 2019, 36, 73.	1.2	19
23	coMethDMR: accurate identification of co-methylated and differentially methylated regions in epigenome-wide association studies with continuous phenotypes. <i>Nucleic Acids Research</i> , 2019, 47, e98-e98.	6.5	28
24	Lung Cancer Risk in Never-Smokers of European Descent is Associated With Genetic Variation in the 5p15.33 TERT-CLPTM1L1 Region. <i>Journal of Thoracic Oncology</i> , 2019, 14, 1360-1369.	0.5	27
25	Connectivity Mapping: Methods and Applications. <i>Annual Review of Biomedical Data Science</i> , 2019, 2, 69-92.	2.8	39
26	Mapping cis-regulatory chromatin contacts in neural cells links neuropsychiatric disorder risk variants to target genes. <i>Nature Genetics</i> , 2019, 51, 1252-1262.	9.4	139
27	Hit and Run Transcriptional Repressors Are Difficult to Catch in the Act. <i>BioEssays</i> , 2019, 41, 1900041.	1.2	8
28	Reversible Regulation of Polyubiquitin Gene UBC via Modified Inducible CRISPR/Cas9 System. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3168.	1.8	4
29	Integrating proteomics and transcriptomics for the identification of potential targets in early colorectal cancer. <i>International Journal of Oncology</i> , 2019, 55, 439-450.	1.4	15
30	Association study identified biologically relevant receptor genes with synergistic functions in celiac disease. <i>Scientific Reports</i> , 2019, 9, 13811.	1.6	2
31	Differential chamber-specific expression and regulation of long non-coding RNAs during cardiac development. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2019, 1862, 194435.	0.9	19
32	Electroconvulsive seizures induce autophagy by activating the AMPK signaling pathway in the rat frontal cortex. <i>International Journal of Neuropsychopharmacology</i> , 2020, 23, 42-52.	1.0	7
33	ReMap 2020: a database of regulatory regions from an integrative analysis of Human and Arabidopsis DNA-binding sequencing experiments. <i>Nucleic Acids Research</i> , 2020, 48, D180-D188.	6.5	95
34	MaGenDB: a functional genomics hub for Malvaceae plants. <i>Nucleic Acids Research</i> , 2020, 48, D1076-D1084.	6.5	23
35	TSEA-DB: a trait-tissue association map for human complex traits and diseases. <i>Nucleic Acids Research</i> , 2019, 48, D1022-D1030.	6.5	23
36	U2 <i>scf</i> AF <i>scf</i> ⁶⁵ assemblies drive sequence-specific splice site recognition. <i>EMBO Reports</i> , 2019, 20, e47604.	2.0	21

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37	The Role of MicroRNAs in Diabetes-Related Oxidative Stress. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5423.	1.8	19
38	Xenbase: deep integration of GEO & SRA RNA-seq and ChIP-seq data in a model organism database. <i>Nucleic Acids Research</i> , 2020, 48, D776-D782.	6.5	47
39	7C:ÂComputational Chromosome Conformation Capture by Correlation of ChIP-seq at CTCF motifs. <i>BMC Genomics</i> , 2019, 20, 777.	1.2	10
40	The TargetMine Data Warehouse: Enhancement and Updates. <i>Frontiers in Genetics</i> , 2019, 10, 934.	1.1	21
41	A Pan-cancer Transcriptome Analysis Reveals Pervasive Regulation through Alternative Promoters. <i>Cell</i> , 2019, 178, 1465-1477.e17.	13.5	144
42	LncRNA SATB2-AS1 inhibits tumor metastasis and affects the tumor immune cell microenvironment in colorectal cancer by regulating SATB2. <i>Molecular Cancer</i> , 2019, 18, 135.	7.9	205
43	Whole Genome Analyses of Chinese Population and De Novo Assembly of A Northern Han Genome. <i>Genomics, Proteomics and Bioinformatics</i> , 2019, 17, 229-247.	3.0	42
44	Simultaneous profiling of 3D genome structure and DNA methylation in single human cells. <i>Nature Methods</i> , 2019, 16, 999-1006.	9.0	200
45	H3K4me3, H3K9ac, H3K27ac, H3K27me3 and H3K9me3 Histone Tags Suggest Distinct Regulatory Evolution of Open and Condensed Chromatin Landmarks. <i>Cells</i> , 2019, 8, 1034.	1.8	64
46	Orphan Nuclear Receptor NR2F6 Suppresses T Follicular Helper Cell Accumulation through Regulation of IL-21. <i>Cell Reports</i> , 2019, 28, 2878-2891.e5.	2.9	20
47	The Atherosclerosis Risk Variant rs2107595 Mediates Allele-Specific Transcriptional Regulation of <i>HDAC9</i> via E2F3 and Rb1. <i>Stroke</i> , 2019, 50, 2651-2660.	1.0	38
48	DNA methylation loss promotes immune evasion of tumours with high mutation and copy number load. <i>Nature Communications</i> , 2019, 10, 4278.	5.8	263
49	Nascent transcript analysis of glucocorticoid crosstalk with TNF defines primary and cooperative inflammatory repression. <i>Genome Research</i> , 2019, 29, 1753-1765.	2.4	36
50	Epstein-Barr virus subverts mevalonate and fatty acid pathways to promote infected B-cell proliferation and survival. <i>PLoS Pathogens</i> , 2019, 15, e1008030.	2.1	57
51	Visualising three-dimensional genome organisation in two dimensions. <i>Development (Cambridge)</i> , 2019, 146, .	1.2	10
52	CGGBP1 regulates CTCF occupancy at repeats. <i>Epigenetics and Chromatin</i> , 2019, 12, 57.	1.8	14
53	CDK4/6 inhibitors target SMARCA4-determined cyclin D1 deficiency in hypercalcemic small cell carcinoma of the ovary. <i>Nature Communications</i> , 2019, 10, 558.	5.8	76
54	EpiAlignment: alignment with both DNA sequence and epigenomic data. <i>Nucleic Acids Research</i> , 2019, 47, W11-W19.	6.5	3

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56	Can Epigenetics of Endothelial Dysfunction Represent the Key to Precision Medicine in Type 2 Diabetes Mellitus?. <i>International Journal of Molecular Sciences</i> , 2019, 20, 2949.	1.8	27
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59	Best practice for CRISPR design using current tools and resources. <i>Methods</i> , 2019, 164-165, 3-17.	1.9	9
60	An in-silico approach for discovery of microRNA-TF regulation of DISC1 interactome mediating neuronal migration. <i>Npj Systems Biology and Applications</i> , 2019, 5, 17.	1.4	7
61	Growth disrupting mutations in epigenetic regulatory molecules are associated with abnormalities of epigenetic aging. <i>Genome Research</i> , 2019, 29, 1057-1066.	2.4	38
62	Spatial Chromosome Folding and Active Transcription Drive DNA Fragility and Formation of Oncogenic MLL Translocations. <i>Molecular Cell</i> , 2019, 75, 267-283.e12.	4.5	104
63	Retrotransposon elements among initial sites of hepatitis B virus integration into human genome in the HepG2-NTCP cell infection model. <i>Cancer Genetics</i> , 2019, 235-236, 39-56.	0.2	12
64	ETV6-RUNX1 interacts with a region in SPIB intron 1 to regulate gene expression in pre-B-cell acute lymphoblastic leukemia. <i>Experimental Hematology</i> , 2019, 73, 50-63.e2.	0.2	6
65	METTL1 Promotes let-7 MicroRNA Processing via m7G Methylation. <i>Molecular Cell</i> , 2019, 74, 1278-1290.e9.	4.5	288
66	Atlas of RNA sequencing profiles for normal human tissues. <i>Scientific Data</i> , 2019, 6, 36.	2.4	75
67	The long non-coding road to endogenous cardiac regeneration. <i>Heart Failure Reviews</i> , 2019, 24, 587-600.	1.7	5
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69	Multi-dimensional Transcriptional Remodeling by Physiological Insulin In Vivo. <i>Cell Reports</i> , 2019, 26, 3429-3443.e3.	2.9	62
70	Making Sense of the Epigenome Using Data Integration Approaches. <i>Frontiers in Pharmacology</i> , 2019, 10, 126.	1.6	58
71	Genome-wide association study of blood lipids in Indians confirms universality of established variants. <i>Journal of Human Genetics</i> , 2019, 64, 573-587.	1.1	22
72	Computational analysis of the evolutionarily conserved Missing In Metastasis/Metastasis Suppressor 1 gene predicts novel interactions, regulatory regions and transcriptional control. <i>Scientific Reports</i> , 2019, 9, 4155.	1.6	4

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73	The Promoter Regions of Intellectual Disability-Associated Genes Are Uniquely Enriched in LTR Sequences of the MER41 Primate-Specific Endogenous Retrovirus: An Evolutionary Connection Between Immunity and Cognition. <i>Frontiers in Genetics</i> , 2019, 10, 321.	1.1	10
74	Proteomics and Precision Medicine. <i>Small Methods</i> , 2019, 3, 1900075.	4.6	5
75	Clinical application of next-generation sequencing to the practice of neurology. <i>Lancet Neurology</i> , The, 2019, 18, 492-503.	4.9	76
76	Evolution of Immune Systems From Viruses and Transposable Elements. <i>Frontiers in Microbiology</i> , 2019, 10, 51.	1.5	53
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78	GenoSurf: metadata driven semantic search system for integrated genomic datasets. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	1.4	35
79	Deleterious Impact of Mutational Processes on Transcription Factor Binding Sites in Human Cancer. , 2019, , .		0
80	Multifaced regulator: RNA binding proteins and their roles in hematopoiesis. <i>Blood Science</i> , 2019, 1, 69-72.	0.4	0
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82	The landscape of multiscale transcriptomic networks and key regulators in Parkinsonâ€™s disease. <i>Nature Communications</i> , 2019, 10, 5234.	5.8	82
83	Ketamine and Active Ketamine Metabolites Regulate STAT3 and the Type I Interferon Pathway in Human Microglia: Molecular Mechanisms Linked to the Antidepressant Effects of Ketamine. <i>Frontiers in Pharmacology</i> , 2019, 10, 1302.	1.6	32
84	DIANA-LncBase v3: indexing experimentally supported miRNA targets on non-coding transcripts. <i>Nucleic Acids Research</i> , 2020, 48, D101-D110.	6.5	137
85	Promoter-specific dynamics of TATA-binding protein association with the human genome. <i>Genome Research</i> , 2019, 29, 1939-1950.	2.4	23
86	EnhancerAtlas 2.0: an updated resource with enhancer annotation in 586 tissue/cell types across nine species. <i>Nucleic Acids Research</i> , 2020, 48, D58-D64.	6.5	142
87	A systems biology approach reveals neuronal and muscle developmental defects after chronic exposure to ionising radiation in zebrafish. <i>Scientific Reports</i> , 2019, 9, 20241.	1.6	10
88	SyntDB:Â‘defining orthologues of human long noncoding RNAs across primates. <i>Nucleic Acids Research</i> , 2019, 48, D238-D245.	6.5	16
89	Whole-exome sequencing in multiplex preeclampsia families identifies novel candidate susceptibility genes. <i>Journal of Hypertension</i> , 2019, 37, 997-1011.	0.3	19
90	The ENCODE Portal as an Epigenomics Resource. <i>Current Protocols in Bioinformatics</i> , 2019, 68, e89.	25.8	23

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92	POSTAR2: deciphering the post-transcriptional regulatory logics. <i>Nucleic Acids Research</i> , 2019, 47, D203-D211.	6.5	145
93	Hi-C analysis: from data generation to integration. <i>Biophysical Reviews</i> , 2019, 11, 67-78.	1.5	68
94	Rare copy number variation in extremely impulsively violent males. <i>Genes, Brain and Behavior</i> , 2019, 18, e12536.	1.1	9
95	Cistrome Data Browser: expanded datasets and new tools for gene regulatory analysis. <i>Nucleic Acids Research</i> , 2019, 47, D729-D735.	6.5	527
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98	RNA-Binding Protein <i>ZFP36L1</i> Suppresses Hypoxia and Cell-Cycle Signaling. <i>Cancer Research</i> , 2020, 80, 219-233.	0.4	40
99	Methods for comparative ChIA-PET and Hi-C data analysis. <i>Methods</i> , 2020, 170, 69-74.	1.9	11
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105	Atypical chromatin structure of immune-related genes expressed in chicken erythrocytes. <i>Biochemistry and Cell Biology</i> , 2020, 98, 171-177.	0.9	10
106	The how and why of lncRNA function: An innate immune perspective. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2020, 1863, 194419.	0.9	196
107	Influenza Vaccine Effectiveness in the Inpatient Setting: Evaluation of Potential Bias in the Test-Negative Design by Use of Alternate Control Groups. <i>American Journal of Epidemiology</i> , 2020, 189, 250-260.	1.6	7
108	Individual Responsibilities in Partial Compliance: Skilled Health Worker Emigration from Under-Served Regions. <i>Public Health Ethics</i> , 2020, 13, 89-98.	0.4	0

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109	Gene regulatory network inference resources: A practical overview. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2020, 1863, 194430.	0.9	93
110	New developments on the Encyclopedia of DNA Elements (ENCODE) data portal. <i>Nucleic Acids Research</i> , 2020, 48, D882-D889.	6.5	381
111	CD44 Promotes PD-L1 Expression and Its Tumor-Intrinsic Function in Breast and Lung Cancers. <i>Cancer Research</i> , 2020, 80, 444-457.	0.4	88
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115	Omics in Neurodegenerative Disease: Hope or Hype?. <i>Trends in Genetics</i> , 2020, 36, 152-159.	2.9	38
116	Chromatin interactome mapping at 139 independent breast cancer risk signals. <i>Genome Biology</i> , 2020, 21, 8.	3.8	27
117	From parts lists to functional significance of RNA-protein interactions in gene regulation. <i>Wiley Interdisciplinary Reviews RNA</i> , 2020, 11, e1582.	3.2	21
118	Defining Functionally Relevant Spatial Chromatin Domains: It is a TAD Complicated. <i>Journal of Molecular Biology</i> , 2020, 432, 653-664.	2.0	45
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124	Linking genetic variation with epigenetic profiles in Sjögren's syndrome. <i>Clinical Immunology</i> , 2020, 210, 108314.	1.4	10
125	Long Non-coding RNAs Involved in Resistance to Chemotherapy in Ovarian Cancer. <i>Frontiers in Oncology</i> , 2019, 9, 1549.	1.3	37
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127	Heterozygous de novo variants in <i>CSNK1G1</i> are associated with syndromic developmental delay and autism spectrum disorder. <i>Clinical Genetics</i> , 2020, 98, 571-576.	1.0	10
128	Epstein-Barr Virus Episome Physically Interacts with Active Regions of the Host Genome in Lymphoblastoid Cells. <i>Journal of Virology</i> , 2020, 94, .	1.5	26
129	HMST-Seq-Analyzer: A new python tool for differential methylation and hydroxymethylation analysis in various DNA methylation sequencing data. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 2877-2889.	1.9	4
130	Ultrafast and scalable variant annotation and prioritization with big functional genomics data. <i>Genome Research</i> , 2020, 30, 1789-1801.	2.4	14
131	Tissue-specific usage of transposable element-derived promoters in mouse development. <i>Genome Biology</i> , 2020, 21, 255.	3.8	55
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133	The mutational signature profile of known and suspected human carcinogens in mice. <i>Nature Genetics</i> , 2020, 52, 1189-1197.	9.4	84
134	Genome-wide study of the effect of blood collection tubes on the cell-free DNA methylome. <i>Epigenetics</i> , 2021, 16, 797-807.	1.3	21
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136	Harmonization of L1CAM expression facilitates axon outgrowth and guidance of a motor neuron. <i>Development (Cambridge)</i> , 2020, 147, .	1.2	6
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140	Theoretical characterisation of strand cross-correlation in ChIP-seq. <i>BMC Bioinformatics</i> , 2020, 21, 417.	1.2	4
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142	A Bisulfite-free Approach for Base-Resolution Analysis of Genomic 5-Carboxylcytosine. <i>Cell Reports</i> , 2020, 32, 108155.	2.9	13
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148	Co-option of the lineage-specific <i>LAVA</i> retrotransposon in the gibbon genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 19328-19338.	3.3	16
149	Cross-species regulatory sequence activity prediction. <i>PLoS Computational Biology</i> , 2020, 16, e1008050.	1.5	116
150	ABC-GWAS: Functional Annotation of Estrogen Receptor-Positive Breast Cancer Genetic Variants. <i>Frontiers in Genetics</i> , 2020, 11, 730.	1.1	3
151	Methods in epigenetics-based systems biology and their applications. , 2020, , 615-646.		0
152	GWAS SNPs Impact Shared Regulatory Pathways Amongst Multimorbid Psychiatric Disorders and Cognitive Functioning. <i>Frontiers in Psychiatry</i> , 2020, 11, 560751.	1.3	7
153	Multi-Omics Identifies Circulating miRNA and Protein Biomarkers for Facioscapulohumeral Dystrophy. <i>Journal of Personalized Medicine</i> , 2020, 10, 236.	1.1	15
154	Histone H3.3G34-Mutant Interneuron Progenitors Co-opt PDGFRA for Gliomagenesis. <i>Cell</i> , 2020, 183, 1617-1633.e22.	13.5	93
155	PDmethDB: A curated Parkinson's disease associated methylation information database. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 3745-3749.	1.9	6
156	SNP-SNP Interaction in Genes Encoding PD-1/PD-L1 Axis as a Potential Risk Factor for Clear Cell Renal Cell Carcinoma. <i>Cancers</i> , 2020, 12, 3521.	1.7	7
157	Computational gene expression profiling in the exploration of biomarkers, non-coding functional RNAs and drug perturbagens for COVID-19. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, 40, 3681-3696.	2.0	13
158	Robust inference of positive selection on regulatory sequences in the human brain. <i>Science Advances</i> , 2020, 6, .	4.7	20
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