

GENCODE reference annotation for the human and mouse genomes

Nucleic Acids Research

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Citation Report

#	ARTICLE	IF	CITATIONS
1	DNA co-methylation analysis of lincRNAs across nine cancer types reveals novel potential epigenetic biomarkers in cancer. <i>Epigenomics</i> , 2019, 11, 1177-1190.	1.0	3
2	Screening for genes that accelerate the epigenetic aging clock in humans reveals a role for the H3K36 methyltransferase NSD1. <i>Genome Biology</i> , 2019, 20, 146.	3.8	66
3	RNA sequencing: the teenage years. <i>Nature Reviews Genetics</i> , 2019, 20, 631-656.	7.7	1,192
4	Nonparametric expression analysis using inferential replicate counts. <i>Nucleic Acids Research</i> , 2019, 47, e105-e105.	6.5	54
5	Obesity-Associated Extracellular Matrix Remodeling Promotes a Macrophage Phenotype Similar to Tumor-Associated Macrophages. <i>American Journal of Pathology</i> , 2019, 189, 2019-2035.	1.9	62
6	Sleeping beauty genetic screen identifies miR-23b::BTBD7 gene interaction as crucial for colorectal cancer metastasis. <i>EBioMedicine</i> , 2019, 46, 79-93.	2.7	13
7	Spatial chromatin architecture alteration by structural variations in human genomes at the population scale. <i>Genome Biology</i> , 2019, 20, 148.	3.8	36
8	Identification of the m6Am Methyltransferase PCIF1 Reveals the Location and Functions of m6Am in the Transcriptome. <i>Molecular Cell</i> , 2019, 75, 631-643.e8.	4.5	183
9	Streamlined Low-Input Transcriptomics through EASY-RNAseq. <i>Journal of Molecular Biology</i> , 2019, 431, 5075-5085.	2.0	9
10	A systematic evaluation of single cell RNA-seq analysis pipelines. <i>Nature Communications</i> , 2019, 10, 4667.	5.8	190
11	The Protein-coding Human Genome: Annotating High-Hanging Fruits. <i>BioEssays</i> , 2019, 41, e1900066.	1.2	17
12	Local activity of comets: an indicator of non-uniform composition. <i>Monthly Notices of the Royal Astronomical Society</i> , 2019, 490, 2050-2055.	1.6	2
13	Characterization of MRSA in Canada from 2007 to 2016. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, iv55-iv63.	1.3	19
14	Active and Repressed Chromatin Domains Exhibit Distinct Nucleosome Segregation during DNA Replication. <i>Cell</i> , 2019, 179, 953-963.e11.	13.5	116
15	PyGMQL: scalable data extraction and analysis for heterogeneous genomic datasets. <i>BMC Bioinformatics</i> , 2019, 20, 560.	1.2	15
16	A Functional Link between Nuclear RNA Decay and Transcriptional Control Mediated by the Polycomb Repressive Complex 2. <i>Cell Reports</i> , 2019, 29, 1800-1811.e6.	2.9	32
17	The Many Faces of Emerging and Reemerging Infectious Disease. <i>Epidemiologic Reviews</i> , 2019, 41, 1-5.	1.3	5
18	EPD in 2020: enhanced data visualization and extension to ncRNA promoters. <i>Nucleic Acids Research</i> , 2020, 48, D65-D69.	6.5	26

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19	NPInter v4.0: an integrated database of ncRNA interactions. <i>Nucleic Acids Research</i> , 2020, 48, D160-D165.	6.5	106
20	Ensembl 2020. <i>Nucleic Acids Research</i> , 2020, 48, D682-D688.	6.5	1,076
21	ExonSkipDB: functional annotation of exon skipping event in human. <i>Nucleic Acids Research</i> , 2020, 48, D896-D907.	6.5	29
22	Comprehensive analysis of differentially expressed profiles and reconstruction of a competing endogenous RNA network in papillary renal cell carcinoma. <i>Molecular Medicine Reports</i> , 2019, 19, 4685-4696.	1.1	11
23	DeepCOP: deep learning-based approach to predict gene regulating effects of small molecules. <i>Bioinformatics</i> , 2020, 36, 813-818.	1.8	21
24	An expanded landscape of human long noncoding RNA. <i>Nucleic Acids Research</i> , 2019, 47, 7842-7856.	6.5	92
25	Interplay of LIS1 and MeCP2: Interactions and Implications With the Neurodevelopmental Disorders Lissencephaly and Rett Syndrome. <i>Frontiers in Cellular Neuroscience</i> , 2019, 13, 370.	1.8	12
26	Association rule mining to identify transcription factor interactions in genomic regions. <i>Bioinformatics</i> , 2020, 36, 1007-1013.	1.8	14
27	IRES-mediated cap-independent translation, a path leading to hidden proteome. <i>Journal of Molecular Cell Biology</i> , 2019, 11, 911-919.	1.5	136
28	Cell-type-specific analysis of alternative polyadenylation using single-cell transcriptomics data. <i>Nucleic Acids Research</i> , 2019, 47, 10027-10039.	6.5	71
29	Comprehensive Analysis of Human microRNA-mRNA Interactome. <i>Frontiers in Genetics</i> , 2019, 10, 933.	1.1	105
30	LTR retroelement expansion of the human cancer transcriptome and immunopeptidome revealed by de novo transcript assembly. <i>Genome Research</i> , 2019, 29, 1578-1590.	2.4	66
31	LPI-BLS: Predicting lncRNA-protein interactions with a broad learning system-based stacked ensemble classifier. <i>Neurocomputing</i> , 2019, 370, 88-93.	3.5	48
32	Diverse roles of noncoding RNAs in vascular calcification. <i>Archives of Pharmacal Research</i> , 2019, 42, 244-251.	2.7	21
33	Eutherian third-party data gene collections. <i>Gene Reports</i> , 2019, 16, 100414.	0.4	4
34	Comprehensive epigenetic analyses reveal master regulators driving lung metastasis of breast cancer. <i>Journal of Cellular and Molecular Medicine</i> , 2019, 23, 5415-5431.	1.6	17
35	p73 regulates epidermal wound healing and induced keratinocyte programming. <i>PLoS ONE</i> , 2019, 14, e0218458.	1.1	20
36	Identification of HIV transmitting CD11c+ human epidermal dendritic cells. <i>Nature Communications</i> , 2019, 10, 2759.	5.8	77

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37	LnCompare: gene set feature analysis for human long non-coding RNAs. <i>Nucleic Acids Research</i> , 2019, 47, W523-W529.	6.5	20
38	A comparison of two workflows for regulome and transcriptome-based prioritization of genetic variants associated with myocardial mass. <i>Genetic Epidemiology</i> , 2019, 43, 717-726.	0.6	1
39	Long noncoding RNA in cardiac aging and disease. <i>Journal of Molecular Cell Biology</i> , 2019, 11, 860-867.	1.5	32
40	Systematic analysis of dark and camouflaged genes reveals disease-relevant genes hiding in plain sight. <i>Genome Biology</i> , 2019, 20, 97.	3.8	122
41	ARMOR: An Automated Reproducible Modular Workflow for Preprocessing and Differential Analysis of RNA-seq Data. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2089-2096.	0.8	44
42	Predicting the change of exon splicing caused by genetic variant using support vector regression. <i>Human Mutation</i> , 2019, 40, 1235-1242.	1.1	6
43	Next-generation genome annotation: we still struggle to get it right. <i>Genome Biology</i> , 2019, 20, 92.	3.8	216
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49	The role of ABCA7 in Alzheimer's disease: evidence from genomics, transcriptomics and methylomics. <i>Acta Neuropathologica</i> , 2019, 138, 201-220.	3.9	132
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52	Genomic Characterization of the Zinc Transcriptional Regulatory Element Reveals Potential Functional Roles of ZNF658. <i>Biological Trace Element Research</i> , 2019, 192, 83-90.	1.9	3
53	Debutant iOS app and gene-disease complexities in clinical genomics and precision medicine. <i>Clinical and Translational Medicine</i> , 2019, 8, 26.	1.7	17
54	The global transcriptomic signature in sinonasal tissues reveals roles for tissue type and chronic rhinosinusitis disease phenotype. <i>Rhinology</i> , 2020, 58, 273-283.	0.7	8

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56	Multimodal Long Noncoding RNA Interaction Networks: Control Panels for Cell Fate Specification. Genetics, 2019, 213, 1093-1110.	1.2	24
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74	The European Bioinformatics Institute in 2018: tools, infrastructure and training. <i>Nucleic Acids Research</i> , 2019, 47, D15-D22.	6.5	33
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77	APAAtlas: decoding alternative polyadenylation across human tissues. <i>Nucleic Acids Research</i> , 2020, 48, D34-D39.	6.5	41
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88	The <i>Caenorhabditis elegans</i> RIG-I Homolog DRH-1 Mediates the Intracellular Pathogen Response upon Viral Infection. <i>Journal of Virology</i> , 2020, 94, .	1.5	50
89	Learning distributed representations of RNA and protein sequences and its application for predicting lncRNA-protein interactions. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 20-26.	1.9	31
90	The MathOmics Toolbox: General Analysis Utilities for Dynamic Omics Datasets. <i>Current Protocols in Bioinformatics</i> , 2020, 69, e91.	25.8	4
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99	A heterodimer of evolved designer-recombinases precisely excises a human genomic DNA locus. <i>Nucleic Acids Research</i> , 2020, 48, 472-485.	6.5	20
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124	LncRNA <i>Platr22</i> promotes super-enhancer activity and stem cell pluripotency. <i>Journal of Molecular Cell Biology</i> , 2021, 13, 295-313.	1.5	13
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135	XPC deficiency increases risk of hematologic malignancies through mutator phenotype and characteristic mutational signature. <i>Nature Communications</i> , 2020, 11, 5834.	5.8	17
136	Characterizing the function of EPB41L4A in the predisposition to papillary thyroid carcinoma. <i>Scientific Reports</i> , 2020, 10, 19984.	1.6	3
137	Prospects for Clinical Development of Stat5 Inhibitor IST5-002: High Transcriptomic Specificity in Prostate Cancer and Low Toxicity In Vivo. <i>Cancers</i> , 2020, 12, 3412.	1.7	3
138	Persistent or Transient Human $\beta$ Cell Dysfunction Induced by Metabolic Stress: Specific Signatures and Shared Gene Expression with Type 2 Diabetes. <i>Cell Reports</i> , 2020, 33, 108466.	2.9	65
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147	Comparative genomic analysis of eutherian fibroblast growth factor genes. <i>BMC Genomics</i> , 2020, 21, 542.	1.2	2
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153	Index and biological spectrum of human DNase I hypersensitive sites. <i>Nature</i> , 2020, 584, 244-251.	13.7	207
154	The role of CAPG in molecular communication between the embryo and the uterine endometrium: Is its function conserved in species with different implantation strategies?. <i>FASEB Journal</i> , 2020, 34, 11015-11029.	0.2	15
155	Defective heart chamber growth and myofibrillogenesis after knockout of adprhl1 gene function by targeted disruption of the ancestral catalytic active site. <i>PLoS ONE</i> , 2020, 15, e0235433.	1.1	8
156	Different effects of constitutive and induced microbiota modulation on microglia in a mouse model of Alzheimer's disease. <i>Acta Neuropathologica Communications</i> , 2020, 8, 119.	2.4	75
157	A lncRNA landscape in breast cancer reveals a potential role for AC009283.1 in proliferation and apoptosis in HER2-enriched subtype. <i>Scientific Reports</i> , 2020, 10, 13146.	1.6	24
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162	Mapping the Effects of Genetic Variation on Chromatin State and Gene Expression Reveals Loci That Control Ground State Pluripotency. <i>Cell Stem Cell</i> , 2020, 27, 459-469.e8.	5.2	31
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