CITATION REPORT
List of articles citing

GENCODE 2021

#	Paper	IF	Citations
319	The Evolution of G-quadruplex Structure in mRNA Untranslated Region. **2021**, 17, 11769343211035140		1
318	Understanding Human Body Maintenance, Protection, and Modification: Antibodies, Genetics, Stem Cells and Connected Artificial Intelligence Applications Where Are We?. **2021**, 13, 766-776		
317	Identification of long noncoding RNAs with machine learning methods: a review. **2021**, 20, 174-180		1
316	Cost-effective mapping of genetic interactions in mammalian cells.		
315	A community-driven roadmap to advance research on translated open reading frames detected by Ribo-seq.		4
314	Newly synthesized RNA Sequencing Characterizes Transcription Dynamics in Three Pluripotent States.		0
313	Extending the Horizon of Homology Detection with Coevolution-based Structure Prediction. **2021**, 433, 167106		1
312	Identification of the cell-type-specific ER membrane protein Tanmp expressed in hypothalamic tanycytes and subsets of neurons.		
311	PCaDB - a comprehensive and interactive database for transcriptomes from prostate cancer population cohorts.		4
310	Promotes Tumor Progression and Indicates Poor Prognosis of Liver Cancer. **2021**, 22,		2
309	From Junk to Function: LncRNAs in CNS Health and Disease. **2021**, 14, 714768		3
308	The value of primary transcripts to the clinical and non-clinical genomics community: Survey results and roadmap for improvements. **2021**, e1786		2
307	Cost-Effective Mapping of Genetic Interactions in Mammalian Cells. **2021**, 12, 703738		
306	Role of Virus-Induced Host Cell Epigenetic Changes in Cancer. **2021**, 22,		7
305	Altered DNA Methylation Profiles in Mutated CLL Patients. **2021**, 22,		0
304	Performance Evaluation of SpliceAI for the Prediction of Splicing of Variants. **2021**, 12,		1
303	Translational Applications of Linear and Circular Long Noncoding RNAs in Endometriosis. **2021**, 22,		1

302   Automatic Prediction and Annotation: There Are Strong Biases for Multigenic Families. **2021**, 12, 697477

301   Micro-dissection and integration of long and short reads to create a robust catalog of kidney compartment-specific isoforms.

300   COVID19db: a comprehensive database platform to discover potential drugs and targets of COVID-19 at whole transcriptomic scale. *Nucleic Acids Research*, **2021**,   20.1   1

299   Comprehensive Genomic Characterization Analysis Identifies an Oncogenic Pseudogene RP11-3543B.1 in Human Gastric Cancer. **2021**, 9, 743652   0

298   Non-coding Natural Antisense Transcripts: Analysis and Application. **2021**, 340, 75-101   4

297   Genome-wide analysis of primary microRNA expression using H3K36me3 ChIP-seq data. **2021**, 19, 1944-1955   0

296   The Functions and Unique Features of LncRNAs in Cancer Development and Tumorigenesis. **2021**, 22,   37

295   Detection of complex structural variation from paired-end sequencing data.   5

294   ReMap 2022: a database of Human, Mouse, Drosophila and Arabidopsis regulatory regions from an integrative analysis of DNA-binding sequencing experiments. *Nucleic Acids Research*, **2021**,   20.1   9

293   Ensembl 2022. *Nucleic Acids Research*, **2021**,   20.1   72

292   Mouse Genome Informatics (MGI): latest news from MGD and GXD. **2021**, 1   3

291   Functional Roles of Non-coding RNAs in the Interaction Between Host and Influenza A Virus. **2021**, 12, 742984   1

290   Impact of human gene annotations on RNA-seq differential expression analysis. **2021**, 22, 730   3

289   Gene losses in the common vampire bat illuminate molecular adaptations to blood feeding.   0

288   Rapid nuclear deadenylation of mammalian messenger RNA.   1

287   Origins and Function of VL30 lncRNA Packaging in Small Extracellular Vesicles: Implications for Cellular Physiology and Pathology. **2021**, 9,   1

286   What is beyond LncRNAs in breast cancer: A special focus on colon cancer-associated Transcript-1 (CCAT-1).. **2021**, 6, 174-186   1

285   Characterizing the Copy Number Variation of Non-Coding RNAs Reveals Potential Therapeutic Targets and Prognostic Markers of LUSC.. **2021**, 12, 779155   0

284   GENCODE Annotation for the Human and Mouse Genome: A User Perspective. **2021**, 1-25   o

283   ImReLnc: Identifying Immune-Related LncRNA Characteristics in Human Cancers Based on Heuristic Correlation Optimization.. **2021**, 12, 792541   o

282   Sequencing of individual barcoded cDNAs on Pacific Biosciences and Oxford Nanopore reveals platform-specific error patterns.

281   MGcount: a total RNA-seq quantification tool to address multi-mapping and multi-overlapping alignments ambiguity in non-coding transcripts.. **2022**, 23, 39   o

280   Will Cannabigerol Trigger Neuroregeneration after a Spinal Cord Injury? An In Vitro Answer from NSC-34 Scratch-Injured Cells Transcriptome.. **2022**, 15,   o

279   Reciprocal modulation of long noncoding RNA EMS and p53 regulates tumorigenesis.. **2022**, 119,   1

278   Delineation of biliary epithelial cell dynamics in maternal liver during pregnancy.. **2021**,

277   Distinct transcription kinetics of pluripotent cell states.. **2022**, 18, e10407   o

276   The Structure-Selective Endonucleases GEN1 and MUS81 are Functionally Complementary in Safeguarding the Genome of Proliferating B Lymphocytes.

275   Understanding the Critical Role of Glycolysis-Related lncRNAs in Lung Adenocarcinoma Based on Three Molecular Subtypes.. **2022**, 2022, 7587398   o

274   Mouse genomic and cellular annotations.. **2022**, 33, 19

273   The potential of long noncoding RNA therapies.. **2022**,   3

272   RefSeq Functional Elements as experimentally assayed nongenic reference standards and functional interactions in human and mouse. **2021**,   o

271   CriSNPr: a single interface for the curated and de-novo design of gRNAs for CRISPR diagnostics using diverse Cas systems.

270   xcore: an R package for inference of gene expression regulators.

269   Deciphering of Somatic Mutational Signatures of Cancer.

268   RNA transcription and degradation of Alu retrotransposons depends on sequence features and evolutionary history.. **2022**,

267   Single molecule, long-read Apoer2 sequencing identifies conserved and species-specific splicing patterns.. **2022**, 110318   o

248 Interferon inducible pseudouridine modification in human mRNA by quantitative nanopore profiling. **2021**, 22, 330

6

247 Annotating and prioritizing genomic variants using the Ensembl Variant Effect Predictor-A tutorial. **2021**,

0

246 Missing (RNAs) in Alzheimer's Disease?. **2021**, 13,

0

245 TMC-SNPdb 2.0: an ethnic-specific database of Indian germline variants.. **2022**, 2022,

244 "Pseudo-pseudogenes" in bacterial genomes: Proteogenomics reveals a wide but low protein expression of pseudogenes in Salmonella enterica.. *Nucleic Acids Research*, **2022**,

20.1   0

243 Stratification of radiosensitive brain metastases based on an actionable S100A9/RAGE resistance mechanism.. **2022**,

0

242 Inferring functions of coding and non-coding genes using epigenomic patterns and deciphering the effect of combinatorics of transcription factors binding at promoters.

241 m5CRegpred: Epitranscriptome Target Prediction of 5-Methylcytosine (m5C) Regulators Based on Sequencing Features.. **2022**, 13,

1

240 Micro-dissection and integration of long and short reads to create a robust catalog of kidney compartment-specific isoforms.. **2022**, 18, e1010040

239 OUP accepted manuscript.

0

238 Comprehensive Analysis of Long Noncoding RNA Modified by mA Methylation in Oxidative and Glycolytic Skeletal Muscles.. **2022**, 23,

0

237 Comprehensive Analysis of Subtypes and Identification of Key lncRNAs Based on Glutamine Metabolism-Related Long Noncoding RNAs.. **2022**, 2022, 2807354

236 Skin-Expressing lncRNAs in Inflammatory Responses.. **2022**, 13, 835740

0

235 Comprehensive Analysis of lncRNA Expression Profile and the Potential Role of ENST00000604491 in Graves' Disease.. **2022**, 2022, 8067464

234 HiCognition: a visual exploration and hypothesis testing tool for 3D genomics.

233 Pediatric Pan-Central Nervous System Tumor Methylome Analyses Reveal Immune-Related LncRNAs. **2022**, 13,

0

232 Pervasive role of the long noncoding RNA DNM3OS in development and diseases.. **2022**, e1736

0

231 Advances in Data Repositories for ncRNA-Protein Interaction Predictions Based on Machine Learning: A Mini-Review. **2022**, 02,

230	The third international hackathon for applying insights into large-scale genomic composition to use cases in a wide range of organisms. 11, 530	
229	Identification of miRNA biomarkers for stomach adenocarcinoma.. **2022**, 23, 181	0
228	The product of BMP-directed differentiation protocols for human primed pluripotent stem cells is placental trophoblast and not amnion. **2022**,	2
227	Deciphering the Impact of Genetic Variation on Human Polyadenylation.	0
226	NanoSplicer: Accurate identification of splice junctions using Oxford Nanopore sequencing.	0
225	Uncovering Hidden Enhancers Through Unbiased In Vivo Testing.	0
224	P-TEFb controls cell fate upon p53 activation by modulating intrinsic apoptosis pathway.	
223	The evolution of two transmissible cancers in Tasmanian devils.	0
222	Proteogenomic characterization of age and sex interactions in cardiac gene expression.	
221	Association between Triplex-Forming Sites of Cardiac Long Noncoding RNA GATA6-AS1 and Chromatin Organization. **2022**, 8, 41	1
220	Polygenic Transcriptome Risk Scores Can Translate Genetic Results Between Species.	
219	CI-SpliceAI Improving machine learning predictions of disease causing splicing variants using curated alternative splice sites. **2022**, 17, e0269159	0
218	Long non-coding RNAs act as novel therapeutic targets by regulating molecular networks associated with ischemic stroke. **2022**, 34, 102119	
217	The Landscape of Noncoding RNA in Pulmonary Hypertension. **2022**, 12, 796	2
216	A network of DZF proteins controls alternative splicing regulation and fidelity.	
215	PRES: a webserver for decoding the functional perturbations of RNA editing sites.	
214	On the origin of Omicron's unique Spike gene insertion.	2
213	Slitrk2 deficiency causes hyperactivity with altered vestibular function and serotonergic dysregulation. **2022**, 25, 104604	

| 212 | The βTrCP-Mediated Pathway Cooperates with the Keap1-Mediated Pathway in Nrf2 Degradation In Vivo. | 2 |

| 211 | Coordinated transcriptional and catabolic programs support iron dependent adaptation to RAS-MAPK pathway inhibition in pancreatic cancer. | 3 |

| 210 | Metabolic and epigenetic dysfunctions underlie the arrest of in vitro fertilized human embryos in a senescent-like state. **2022**, 20, e3001682 | 0 |

| 209 | Core transcription programs controlling injury-induced neurodegeneration of retinal ganglion cells. **2022**, | 2 |

| 208 | rGREAT: an R/Bioconductor package for functional enrichment on genomic regions. | 0 |

| 207 | Whole-exome sequencing in 415,422 individuals identifies rare variants associated with mitochondrial DNA copy number. | |

| 206 | Tissue-specific regulation of gene expression via unproductive splicing. | |

| 205 | The effects of sequencing depth on the assembly of coding and noncoding transcripts in the human genome. **2022**, 23, | 0 |

| 204 | High Sox2 expression predicts taste lineage competency of lingual progenitors in vitro. | |

| 203 | A Draft Human Pangenome Reference. | 1 |

| 202 | Mutant KRAS regulates transposable element RNA and innate immunity via KRAB zinc-finger genes. **2022**, 40, 111104 | 0 |

| 201 | Revised eutherian gene collections. **2022**, 23, | |

| 200 | A standardised nomenclature for long non-coding RNAs. | 0 |

| 199 | Transcriptome profiling implicates a role for Wnt signaling during epileptogenesis in a mouse model of temporal lobe epilepsy. | |

| 198 | Functional interplay between long non-coding RNAs and Breast CSCs. **2022**, 22, | 0 |

| 197 | Current challenges and best practices for cell-free long RNA biomarker discovery. **2022**, 10, | 1 |

| 196 | Mouse B2 SINE elements function as IFN-inducible enhancers. | |

| 195 | Ferroptosis-related lncRNAs signature to predict the survival and immune evasion for lung squamous cell carcinoma. 13, | |

| 194 | GATK-gCNV: A Rare Copy Number Variant Discovery Algorithm and Its Application to Exome Sequencing in the UK Biobank. | 0 |

| 193 | Expansion of the RNAStructuromeDB to include secondary structural data spanning the human protein-coding transcriptome. **2022**, 12, | |

| 192 | Signature and Molecular Mechanism of Mitochondrial Energy Metabolism Pathway-Related Genes in Lung Adenocarcinoma. **2022**, 2022, 1-19 | |

| 191 | Single-cell RNA binding protein regulatory network analyses reveal oncogenic HNRNPK-MYC signalling pathway in cancer. | |

| 190 | Proteogenomics reveals sex biased aging genes and coordinated splicing in cardiac aging. | 1 |

| 189 | Readout of histone methylation by Trim24 locally restricts chromatin opening by p53. | |

| 188 | dbEmbryo multi-omics database for analyses of synergistic regulation in early mammalian embryo development. **2022**, 32, 1612-1625 | |

| 187 | Flnc: Machine Learning Improves the Identification of Novel Full-length Long Noncoding RNAs from RNA Sequencing Data Without Transcriptional Initiation Profiles. | |

| 186 | Alternative Splicing in Multiple Myeloma is Associated with the Non-Homologous End Joining Pathway. | |

| 185 | In silico discovery of repetitive elements as key sequence determinants of 3D genome folding. | |

| 184 | Long Non-Coding RNAs: The New Frontier into Understanding the Etiology of Alcohol Use Disorder. **2022**, 8, 59 | 1 |

| 183 | Detection of alternative isoforms of gene fusions from long-read RNA-seq with FLAIR-fusion. | |

| 182 | Construction of a predictive model for immunotherapy efficacy in lung squamous cell carcinoma based on the degree of tumor-infiltrating immune cells and molecular typing. **2022**, 20, | 0 |

| 181 | Genomic Analyses of Non-Coding RNAs Overlapping Transposable Elements and Its Implication to Human Diseases. **2022**, 23, 8950 | 1 |

| 180 | Characterization of Macrophage-Tropic HIV-1 Infection of Central Nervous System Cells and the Influence of Inflammation. | 0 |

| 179 | In vivo genome-wide CRISPR activation screening identifies functionally important long non-coding RNAs in hepatocellular carcinoma. **2022**, | 0 |

| 178 | Variability of cross-tissue X-chromosome inactivation characterizes timing of human embryonic lineage specification events. **2022**, 57, 1995-2008.e5 | 1 |

| 177 | Transcriptomics and Proteomics Analyses Reveal JAK Signaling and Inflammatory Phenotypes during Cellular Senescence in Blind Mole Rats: The Reflections of Superior Biology. **2022**, 11, 1253 | 1 |

176	Most protein domains exist as multiple variants with distinct structure and function.	
175	Discovery and characterization of LNCSOX17 as an essential regulator in human endoderm formation.	0
174	Redefining normal breast cell populations using long noncoding RNAs.	0
173	Techniques for Analyzing Genome-wide Expression of Non-coding RNA. **2023**, 163-184	0
172	A roadmap for the functional annotation of protein families: a community perspective. **2022**, 2022,	1
171	FGF/FGFR-related lncRNAs based classification predicts prognosis and guides therapy in gastric cancer. 13,	0
170	Computational prediction and CRISPR-Cas12a knockout and rescue assays identify many functionally conserved lncRNAs from zebrafish to human.	0
169	TAIGET: A small-molecule target identification and annotation web server. 13,	0
168	Small Molecule Quercetin Binds MALAT1 Triplex and Modulates its Cellular Function. **2022**,	0
167	Mapping the Constrained Coding Regions in the human genome to their corresponding proteins.	0
166	Emerging functions of mitochondria-encoded noncoding RNAs. **2022**,	1
165	APPRIS principal isoforms and MANE Select transcripts define reference splice variants. **2022**, 38, ii89-ii94	0
164	Systematic investigation of allelic regulatory activity of schizophrenia-associated common variants.	0
163	The emerging roles and potential applications of circular RNAs in ovarian cancer: a comprehensive review.	0
162	Immune Isoform Atlas: Landscape of alternative splicing in human immune cells.	0
161	Towards In-Silico CLIP-seq: Predicting Protein-RNA Interaction via Sequence-to-Signal Learning.	1
160	Genetic control of RNA editing in Neurodegenerative disease.	1
159	Whole-exome sequencing in 415,422 individuals identifies rare variants associated with mitochondrial DNA copy number. **2022**, 100147	0

140	Some roads ahead for noncoding RNAs.	0
139	SMAD2/3 mediate oncogenic effects of TGF-⬜ in the absence of SMAD4. **2022**, 5,	2
138	Integrative dissection of gene regulatory elements at base resolution.	0
137	Recent insights into crosstalk between genetic parasites and their host genome.	0
136	SurvivalML: an integrative platform for the discovery and exploration of prognostic models in multi-center cancer cohorts.	0
135	Identifying Genetic Regulatory Variants that Affect Transcription Factor Activity.	0
134	Mechanisms of epigenetic regulation of transcription by lncRNAs in plants.	0
133	CellTracer: a comprehensive database to dissect the causative multilevel interplay contributing to cell development trajectories.	1
132	Flnc: Machine Learning Improves the Identification of Novel Long Noncoding RNAs from Stand-Alone RNA-Seq Data. **2022**, 8, 70	0
131	Intercellular Communication Reveals Therapeutic Potential of Epithelial-Mesenchymal Transition in Triple-Negative Breast Cancer. **2022**, 12, 1478	1
130	RM2Target: a comprehensive database for targets of writers, erasers⬜ and readers of RNA modifications.	0
129	GAE-LGA: integration of multi-omics data with graph autoencoders to identify lncRNA⬜PCG associations.	0
128	Metformin Treatment Modulates Long Non-Coding RNA Isoforms Expression in Human Cells. **2022**, 8, 68	0
127	Predicting the potential human lncRNA⬜miRNA interactions based on graph convolution network with conditional random field.	1
126	Analysis of Y chromosome haplogroups in Parkinson⬜s disease.	0
125	Characterization of sialylation-related long noncoding RNAs to develop a novel signature for predicting prognosis, immune landscape, and chemotherapy response in colorectal cancer. 13,	0
124	Multivariate variance components analysis uncovers genetic architecture of brain isoform expression and novel psychiatric disease mechanisms.	0
123	CellMarker 2.0: an updated database of manually curated cell markers in human/mouse and web tools based on scRNA-seq data.	1

122	Development and Validation of Ferroptosis-Related lncRNAs as Prognosis and Diagnosis Biomarkers for Breast Cancer. **2022**, 2022, 1-14	0
121	Transcriptome Profiling of the Hippocampal Seizure Network Implicates a Role for Wnt Signaling during Epileptogenesis in a Mouse Model of Temporal Lobe Epilepsy. **2022**, 23, 12030	0
120	ASCancer Atlas: a comprehensive knowledgebase of alternative splicing in human cancers.	0
119	DeepASmRNA: Reference-free prediction of alternative splicing events with a scalable and interpretable deep learning model. **2022**, 25, 105345	0
118	Ensembl 2023.	1
117	A Systems Biology Approach on the Regulatory Footprint of Human Endogenous Retroviruses (HERVs). **2022**, 10, 98	1
116	Multiple-low-dose therapy: effective killing of high-grade serous ovarian cancer cells with ATR and CHK1 inhibitors. **2022**, 4,	0
115	Origins and evolution of human tandem duplicated exon substitution events.	0
114	Efficient multitool/multiplex gene engineering with TALE-BE. 10,	0
113	rGREAT: an R/Bioconductor package for functional enrichment on genomic regions.	0
112	lncRNASNP v3: an updated database for functional variants in long non-coding RNAs.	1
111	Deciphering the impact of genetic variation on human polyadenylation using APARENT2. **2022**, 23,	0
110	Probing the dynamic RNA structurome and its functions.	1
109	Silc1 long noncoding RNA is an immediate-early gene promoting efficient memory formation.	0
108	DirectRMDB: a database of post-transcriptional RNA modifications unveiled from direct RNA sequencing technology.	0
107	The alternative proteome in neurobiology. 16,	0
106	TPP1 promoter mutations cooperate with TERT promoter mutations to lengthen telomeres in melanoma. **2022**, 378, 664-668	0
105	Mapping the Constrained Coding Regions in the Human Genome to Their Corresponding Proteins. **2023**, 435, 167892	0

104	Methylmap: visualization of modified nucleotides for large cohort sizes.	0
103	The UCSC Genome Browser database: 2023 update.	0
102	Efficient integrated analytical method for incomplete omics data: novel training strategy (Preprint).	0
101	Adaptive nanopore sequencing for single cell characterization of cancer mutations and gene rearrangements.	0
100	Importance of adopting standardized MANE transcripts in clinical reporting. **2022**, 100331	0
99	GENCODE: reference annotation for the human and mouse genomes in 2023.	0
98	TDP-43 safeguards the embryo genome from L1 retrotransposition. **2022**, 8,	0
97	Exosomes Released by Influenza-Virus-Infected Cells Carry Factors Capable of Suppressing Immune Defense Genes in Naïve Cells. **2022**, 14, 2690	0
96	Long noncoding RNA study: Genome-wide approaches. **2022**,	0
95	A large-scale benchmark study of tools for the classification of protein-coding and non-coding RNAs. **2022**, 50, 12094-12111	0
94	Comparison of oocyte vitrification using a semi-automated or a manual closed system in human siblings: survival and transcriptomic analyses. **2022**, 15,	1
93	SAFB associates with nascent RNAs to promote gene expression in mouse embryonic stem cells.	0
92	A multiomics approach reveals RNA dynamics promote cellular sensitivity to DNA hypomethylation.	0
91	Gene expression associations with body mass index in the Multi-Ethnic Study of Atherosclerosis.	0
90	Analysis of Gene Expression Heterogeneity Reveals Therapeutic Targets and Novel Regulators of Metastasis.	0
89	Assessment of Spatial and Temporal Variation in the Skin Transcriptome of Atopic Dermatitis by Use of 1.5 mm Mini Punch Biopsies. **2022**,	0
88	Predicting potential interactions between lncRNAs and proteins via combined graph auto-encoder methods.	0
87	Integrating extrusion complex-associated pattern to predict cell type-specific long-range chromatin loops. **2022**, 25, 105687	0

86	Nanopore sequencing unveils the complexity of the cold-activated murine brown adipose tissue transcriptome.	0
85	Proximity-dependent recruitment of Polycomb Repressive Complexes by the lncRNAAirn.	0
84	NcPath: a novel platform for visualization and enrichment analysis of human non-coding RNA and KEGG signaling pathways.	0
83	RNA binding protein PRRC2B mediates translation of specific proteins and regulates cell cycle progression.	0
82	Long non-coding RNAs: definitions, functions, challenges and recommendations.	5
81	Schlafen 12 Slows TNBC Tumor Growth, Induces Luminal Markers, and Predicts Favorable Survival. **2023**, 15, 402	0
80	Adaptation to an acid microenvironment promotes pancreatic cancer organoid growth and drug resistance in a p53-dependent manner.	0
79	Accurate isoform discovery with IsoQuant using long reads.	0
78	Culture Protocol and Transcriptomic Analysis of Murine SVZ NPCs and OPCs.	0
77	Dynamic transcriptome analyses reveal m6A regulated immune non-coding RNAs during dengue disease progression. **2023**, 9, e12690	0
76	Metagenomic analysis of viral genes integrated in whole genome sequencing data of Thai patients with Brugada syndrome. **2022**, 20, e44	0
75	EVlncRNA-Dpred: improved prediction of experimentally validated lncRNAs by deep learning. **2023**, 24,	1
74	Impact of sequencing technologies on long non-coding RNA computational identification. **2022**,	0
73	Genome-wide compendium of super-long noncoding RNAs during mouse heart development. **2022**,	0
72	Deciphering gene contributions and etiologies of somatic mutational signatures of cancer.	0
71	Bromodomain-containing Protein 4 Regulates Innate Inflammation in Airway Epithelial Cells via Modulation of Alternative Splicing.	0
70	T-REX17 is a transiently expressed non-coding RNA essential for human endoderm formation. 12,	0
69	Identification of Hub Genes and Potential ceRNA Networks of Diabetic Cardiomyopathy.	0

| 68 | A proteomics analysis of 5xFAD mouse brain regions reveals the lysosome-associated protein Arl8b as a candidate biomarker for Alzheimer's disease. | 0 |

| 67 | Genetic association studies using disease liabilities from deep neural networks. | 0 |

| 66 | Delineating genotypes and phenotypes of individual cells from long-read single cell transcriptomes. | 0 |

| 65 | Single-cell RNA binding protein regulatory network analyses reveal oncogenic HNRNPK-MYC signalling pathway in cancer. **2023**, 6, | 0 |

| 64 | SCN1A: bioinformatically-informed revised boundaries for promoter and enhancer regions. | 0 |

| 63 | lncHUB2: aggregated and inferred knowledge about human and mouse lncRNAs. **2023**, 2023, | 0 |

| 62 | Integrated transcriptional analysis reveals gene expression-based AML subtypes with distinct outcomes and drug responses. | 0 |

| 61 | Cellular energy regulates mRNA translation and degradation in a codon-specific manner. | 0 |

| 60 | GTPase splice variants RAC1 and RAC1B display isoform-specific differences in localization, prenylation, and interaction with the chaperone protein SmgGDS. **2023**, 104698 | 0 |

| 59 | Hunter-gatherer admixture facilitated natural selection in Neolithic European farmers. **2023**, 33, 1365-1371.e3 | 0 |

| 58 | Characterization of genome-wide STR variation in 6487 human genomes. **2023**, 14, | 0 |

| 57 | The landscape of cryptic antisense transcription in human cancers reveals an oncogenic noncoding RNA in lung cancer. **2023**, 9, | 0 |

| 56 | Multi-view graph neural network with cascaded attention for lncRNA-miRNA interaction prediction. **2023**, 268, 110492 | 0 |

| 55 | Polycyclic aromatic hydrocarbons exposure and plasma lncRNA signature: A profile and functional analysis. **2023**, 877, 162932 | 0 |

| 54 | Tissue-specific regulation of gene expression via unproductive splicing. | 0 |

| 53 | Differentially expressed transcript isoforms associate with resistance to tuberculin skin test and interferon gamma release assay conversion. **2023**, 18, e0284498 | 0 |

| 52 | NeRNA: A negative data generation framework for machine learning applications of noncoding RNAs. **2023**, 159, 106861 | 0 |

| 51 | Computational approach to evaluate scRNA-seq data quality and gene body coverage with SkewC. **2023**, 4, 102038 | 0 |

50	Molecular quantitative trait loci. **2023**, 3,	0
49	P-TEFb promotes cell survival upon p53 activation by suppressing intrinsic apoptosis pathway. **2023**, 51, 1687-1706	0
48	Lens Epithelial Explants Treated with Vitreous Humor Undergo Alterations in Chromatin Landscape with Concurrent Activation of Genes Associated with Fiber Cell Differentiation and Innate Immune Response. **2023**, 12, 501	1
47	CriSNPr, a single interface for the curated and de novo design of gRNAs for CRISPR diagnostics using diverse Cas systems. 12,	0
46	Human Satellite 1A analysis provides evidence of pericentromeric transcription. **2023**, 21,	2
45	Mousepost 2.0, a major expansion of the resource. **2023**, 51, 1652-1661	0
44	ExomiRHub: a comprehensive database platform to integrate and analyze human extracellular miRNA transcriptome for discovering non-invasive biomarkers.	0
43	Multivariate adaptive shrinkage improves cross-population transcriptome prediction for transcriptome-wide association studies in underrepresented populations.	0
42	NPAS4 in the medial prefrontal cortex mediates chronic social defeat stress-induced anhedonia-like behavior and reductions in excitatory synapses. 12,	0
41	CVD-associated SNPs with regulatory potential drive pathologic non-coding RNA expression.	0
40	Analysis of Genetic Ancestry from NGS Data Using EthSEQ. **2023**, 3,	0
39	Investigating the suitability of in vitro cell lines as models for the major subtypes of epithelial ovarian cancer. 11,	0
38	A Systematic Benchmark of Machine Learning Methods for Protein-RNA Interaction Prediction.	0
37	AMLs harboring DNMT3A-destabilizing variants show increased intratumor DNA methylation heterogeneity at bivalent chromatin domains.	0
36	High Sox2 expression predicts taste lineage competency of lingual progenitors in vitro. **2023**, 150,	1
35	Neuronal APOE4 removal protects against tau-mediated gliosis, neurodegeneration and myelin deficits. **2023**, 3, 275-296	0
34	A Comprehensive Genetic Analysis of Slovenian Families with Multiple Cases of Orofacial Clefts Reveals Novel Variants in the Genes IRF6, GRHL3, and TBX22. **2023**, 24, 4262	0
33	Treg-selective IL-2 starvation synergizes with CD40 activation to sustain durable responses in lymphoma models. **2023**, 11, e006263	0

32	Large-Scale Immunopeptidome Analysis Reveals Recurrent Posttranslational Splicing of Cancer- and Immune-Associated Genes. **2023**, 22, 100519	0
31	Using Nanocompore to Identify RNA Modifications from Direct RNA Nanopore Sequencing Data. **2023**, 3,	0
30	A genome-wide CRISPR activation screen identifies SCREEM a novel SNAI1 super-enhancer demarcated by eRNAs. 10,	0
29	Functional Genetics to Understand the Etiology of Autoimmunity. **2023**, 14, 572	0
28	Nicotinamide riboside supplementation is not associated with altered methylation homeostasis in Parkinson's disease. **2023**, 26, 106278	0
27	CVD-associated SNPs with regulatory potential drive pathologic non-coding RNA expression.	0
26	genomepy: genes and genomes at your fingertips. **2023**, 39,	0
25	Transcriptome analysis reveals tumor microenvironment changes in glioblastoma. **2023**, 41, 678-692.e7	0
24	Leveraging Base Pair Mammalian Constraint to Understand Genetic Variation and Human Disease.	0
23	Transcriptomic changes predict metabolic alterations in LC3 associated phagocytosis in aged mice.	0
22	An in silico approach to the identification of diagnostic and prognostic markers in low-grade gliomas. 11, e15096	0
21	Evolution and implications of de novo genes in humans.	0
20	Role of Histone Variant H2A.J in Fine-Tuning Chromatin Organization for the Establishment of Ionizing Radiation-Induced Senescence. **2023**, 12, 916	0
19	Identification and validation of ferroptosis-related genes and immune cell infiltration in thyroid associated ophthalmopathy. 14,	0
18	Global detection of human variants and isoforms by deep proteome sequencing.	0
17	Normal and cancer tissues are accurately characterised by intergenic transcription at RNA polymerase 2 binding sites.	0
16	Hidden Genetic Regulation of Human Complex Traits via Brain Isoforms.	0
15	Toward a comprehensive catalog of regulatory elements.	0

14	Single-cell long-read mRNA isoform regulation is pervasive across mammalian brain regions, cell types, and development.	0
13	Cross-species regulatory landscapes and elements revealed by novel joint systematic integration of human and mouse blood cell epigenomes.	0
12	Transcriptomic Changes Predict Metabolic Alterations in LC3 Associated Phagocytosis in Aged Mice. **2023**, 24, 6716	0
11	Ribosomal protein RPL39L is an efficiency factor in the cotranslational folding of proteins with alpha helical domains.	0
10	Predicting response to enzalutamide and abiraterone in metastatic prostate cancer using whole-omics machine learning. **2023**, 14,	0
9	The Chromatin Landscape of Pathogenic Transcriptional Cell States in Rheumatoid Arthritis.	0
8	Transfer learning in a biomaterial fibrosis model identifies in vivo senescence heterogeneity and contributions to vascularization and matrix production across species and diverse pathologies.	0
7	The evolution of two transmissible cancers in Tasmanian devils. **2023**, 380, 283-293	0
6	Molecular cytogenomics of human genetic disorders. **2023**, 721-741	0
5	The emerging roles of long non-coding RNA in host immune response and intracellular bacterial infections. 13,	0
4	Transcription factor binding site orientation and order are major drivers of gene regulatory activity. **2023**, 14,	0
3	Evolutionary constraint and innovation across hundreds of placental mammals. **2023**, 380,	0
2	AstroglialHmgb1regulates postnatal astrocyte morphogenesis and cerebrovascular maturation.	0
1	Mouse B2 SINE elements function as IFN-inducible enhancers. 12,	0