Transcriptomic signatures across human tissues identif

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#	Article	IF	Citations
1	Reaching completion for GTEx. Nature Reviews Genetics, 2020, 21, 717-717.	7.7	18
2	Reframing Psychiatry for Precision Medicine. Journal of Personalized Medicine, 2020, 10, 144.	1.1	13
3	From FAANG to fork: application of highly annotated genomes to improve farmed animal production. Genome Biology, 2020, 21, 285.	3.8	74
4	The GTEx Consortium atlas of genetic regulatory effects across human tissues. Science, 2020, 369, 1318-1330.	6.0	2,385
5	Transcriptomic signatures across human tissues identify functional rare genetic variation. Science, 2020, 369, .	6.0	89
6	Searching for sex differences. Science, 2020, 369, 1298-1299.	6.0	4
7	Allele-specific alternative splicing and its functional genetic variants in human tissues. Genome Research, 2021, 31, 359-371.	2.4	17
8	Detection of aberrant splicing events in RNA-seq data using FRASER. Nature Communications, 2021, 12, 529.	5.8	78
9	Allele-specific expression: applications in cancer and technical considerations. Current Opinion in Genetics and Development, 2021, 66, 10-19.	1.5	11
11	Current knowledge on genetic variants shaping placental transcriptome and their link to gestational and postnatal health. Placenta, 2021, 116, 2-11.	0.7	6
12	Identification of rare and common regulatory variants in pluripotent cells using population-scale transcriptomics. Nature Genetics, 2021, 53, 313-321.	9.4	42
13	The genetics of mitochondrial disease: dissecting mitochondrial pathology using multiâ€omic pipelines. Journal of Pathology, 2021, 254, 430-442.	2.1	33
14	Genetic basis of mitochondrial diseases. FEBS Letters, 2021, 595, 1132-1158.	1.3	36
15	A Common 3â€²UTR Variant of the PHOX2B Gene Is Associated With Infant Life-Threatening and Sudden Death Events in the Italian Population. Frontiers in Neurology, 2021, 12, 642735.	1.1	10
17	Protein structureâ€“based gene expression signatures. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	5
18	Longitudinal proteomic analysis of severe COVID-19 reveals survival-associated signatures, tissue-specific cell death, and cell-cell interactions. Cell Reports Medicine, 2021, 2, 100287.	3.3	183
19	Population-scale tissue transcriptomics maps long non-coding RNAs to complex disease. Cell, 2021, 184, 2633-2648.e19.	13.5	94
20	ACTOR: a latent Dirichlet model to compare expressed isoform proportions to a reference panel. Biostatistics, 2023, 24, 388-405.	0.9	0

#	Article	IF	Citations
21	Rare variants regulate expression of nearby individual genes in multiple tissues. PLoS Genetics, 2021, 17, e1009596.	1.5	6
23	Multi-Omics Approaches in Immunological Research. Frontiers in Immunology, 2021, 12, 668045.	2.2	22
24	How Machine Learning and Statistical Models Advance Molecular Diagnostics of Rare Disorders Via Analysis of RNA Sequencing Data. Frontiers in Molecular Biosciences, 2021, 8, 647277.	1.6	12
25	Mutational sources of trans-regulatory variation affecting gene expression in Saccharomyces cerevisiae. ELife, 2021, 10, .	2.8	12
26	Non-cancer-related pathogenic germline variants and expression consequences in ten-thousand cancer genomes. Genome Medicine, 2021, 13, 147.	3.6	4
27	Technological Improvements in the Genetic Diagnosis of Rett Syndrome Spectrum Disorders. International Journal of Molecular Sciences, 2021, 22, 10375.	1.8	3
28	Computational Medicine: Past, Present and Future. Chinese Journal of Integrative Medicine, 2022, 28, 453-462.	0.7	2
29	utr.annotation: a tool for annotating genomic variants that could influence post-transcriptional regulation. Bioinformatics, 2021, 37, 3926-3928.	1.8	2
31	Progress and challenge for computational quantification of tissue immune cells. Briefings in Bioinformatics, 2021, 22, .	3.2	9
35	Harnessing big data to characterize immune-related adverse events. Nature Reviews Clinical Oncology, 2022, 19, 269-280.	12.5	41
36	scDALI: modeling allelic heterogeneity in single cells reveals context-specific genetic regulation. Genome Biology, 2022, 23, 8.	3.8	11
37	MRSD: A quantitative approach for assessing suitability of RNA-seq in the investigation of mis-splicing in Mendelian disease. American Journal of Human Genetics, 2022, 109, 210-222.	2.6	12
38	TOWARDS TRANSCRIPTOMICS AS A PRIMARY TOOL FOR RARE DISEASE INVESTIGATION. Journal of Physical Education and Sports Management, 2022, , mcs.a006198.	0.5	9
39	RNA sequencing role and application in clinical diagnostic. Pediatric Investigation, 2022, 6, 29-35.	0.6	12
40	Whole genome sequences discriminate hereditary hemorrhagic telangiectasia phenotypes by non-HHT deleterious DNA variation. Blood Advances, 2022, 6, 3956-3969.	2.5	9
43	Integrating whole-genome sequencing with multi-omic data reveals the impact of structural variants on gene regulation in the human brain. Nature Neuroscience, 2022, 25, 504-514.	7.1	27
44	Identifying genes with conserved splicing structure and orthologous isoforms in human, mouse and dog. BMC Genomics, 2022, 23, 216.	1.2	1
45	Clinical implementation of RNA sequencing for Mendelian disease diagnostics. Genome Medicine, 2022, 14, 38.	3.6	85

#	Article	IF	Citations
46	SRTdb: an omnibus for human tissue and cancer-specific RNA transcripts. Biomarker Research, 2022, 10, 27.	2.8	5
47	Comparative transcriptomics reveals circadian and pluripotency networks as two pillars of longevity regulation. Cell Metabolism, 2022, 34, 836-856.e5.	7.2	33
48	Molecular Quantitative Trait Locus Mapping in Human Complex Diseases. Current Protocols, 2022, 2, e426.	1.3	3
49	Integration of rare expression outlier-associated variants improves polygenic risk prediction. American Journal of Human Genetics, 2022, 109, 1055-1064.	2.6	8
51	Guidelines for clinical interpretation of variant pathogenicity using RNA phenotypes. Human Mutation, 2022, 43, 1056-1070.	1.1	8
53	Molecular Modelling Hurdle in the Next-Generation Sequencing Era. International Journal of Molecular Sciences, 2022, 23, 7176.	1.8	0
54	Transcriptome variation in human tissues revealed by long-read sequencing. Nature, 2022, 608, 353-359.	13.7	103
55	Bridging the splicing gap in human genetics with long-read RNA sequencing: finding the protein isoform drivers of disease. Human Molecular Genetics, 2022, 31, R123-R136.	1.4	10
57	Sources of Cancer Neoantigens beyond Single-Nucleotide Variants. International Journal of Molecular Sciences, 2022, 23, 10131.	1.8	16
60	Combining genetic constraint with predictions of alternative splicing to prioritize deleterious splicing in rare disease studies. BMC Bioinformatics, 2022, 23, .	1.2	7
61	QTLbase2: an enhanced catalog of human quantitative trait loci on extensive molecular phenotypes. Nucleic Acids Research, 2023, 51, D1122-D1128.	6.5	6
62	Systematic characterization of cancer transcriptome at transcript resolution. Nature Communications, 2022, 13, .	5.8	7
63	Accounting for cis-regulatory constraint prioritizes genes likely to affect species-specific traits. Genome Biology, 2023, 24, .	3.8	7
64	Molecular quantitative trait loci. Nature Reviews Methods Primers, 2023, 3, .	11.8	13
65	Rare diseases of epigenetic origin: Challenges and opportunities. Frontiers in Genetics, 0, 14, .	1.1	3
66	Genetics of mitochondrial diseases: Current approaches for the molecular diagnosis. Handbook of Clinical Neurology / Edited By P J Vinken and G W Bruyn, 2023, , 141-165.	1.0	7
67	RNA-seq data science: From raw data to effective interpretation. Frontiers in Genetics, 0, 14, .	1.1	16
68	Current sequence-based models capture gene expression determinants in promoters but mostly ignore distal enhancers. Genome Biology, 2023, 24, .	3.8	29

#	Article	IF	Citations
69	Computational approaches for detecting disease-associated alternative splicing events. Briefings in Bioinformatics, 2023, 24, .	3.2	1
71	Single-cell genomics meets human genetics. Nature Reviews Genetics, 2023, 24, 535-549.	7.7	18
77	Main Existing Datasets for Open Brain Research on Humans. Neuromethods, 2023, , 753-804.	0.2	0