Resource Summary Report

Generated by ASWG on Apr 30, 2025

APPRIS

RRID:SCR_012019
Type: Tool

Proper Citation

APPRIS (RRID:SCR_012019)

Resource Information

URL: http://appris.bioinfo.cnio.es/

Proper Citation: APPRIS (RRID:SCR_012019)

Description: A database that houses annotations of human splice isoforms. It adds reliable protein structural and functional data and information from cross-species conservation. A visual representation of the annotations for each gene allows users to easily identify functional changes brought about by splicing events. In addition to collecting, integrating and analyzing reliable predictions of the effect of splicing events, it also selects a single reference sequence for each gene, termed the principal isoform, based on the annotations of structure, function and conservation for each transcript.

Abbreviations: APPRIS

Synonyms: APPRIS - A system for annotating alternative splice isoforms

Resource Type: database, data or information resource

Defining Citation: PMID:23161672

Keywords: isoform, function, annotation, splice, reference sequence, structure, conservation, transcript, FASEB list

Funding:

Availability: Free

Resource Name: APPRIS

Resource ID: SCR_012019

Alternate IDs: OMICS_01881

Record Creation Time: 20220129T080308+0000

Record Last Update: 20250430T055801+0000

Ratings and Alerts

No rating or validation information has been found for APPRIS.

No alerts have been found for APPRIS.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 75 mentions in open access literature.

Listed below are recent publications. The full list is available at ASWG.

Fradkin P, et al. (2024) Orthrus: Towards Evolutionary and Functional RNA Foundation Models. bioRxiv : the preprint server for biology.

Boumelha J, et al. (2024) CRISPR-Cas9 Screening Identifies KRAS-Induced COX2 as a Driver of Immunotherapy Resistance in Lung Cancer. Cancer research, 84(14), 2231.

Rappol T, et al. (2024) tRNA expression and modification landscapes, and their dynamics during zebrafish embryo development. Nucleic acids research, 52(17), 10575.

Insana G, et al. (2024) Improved selection of canonical proteins for reference proteomes. NAR genomics and bioinformatics, 6(2), lqae066.

Rodriguez-Flores JL, et al. (2024) NOTCH3 p.Arg1231Cys is markedly enriched in South Asians and associated with stroke. Nature communications, 15(1), 8029.

Crowl S, et al. (2024) A systematic analysis of the effects of splicing on the diversity of post-translational modifications in protein isoforms. bioRxiv : the preprint server for biology.

Rodriguez JM, et al. (2024) Evidence for widespread translation of 5' untranslated regions. Nucleic acids research, 52(14), 8112.

Zheng D, et al. (2024) Predicting the translation efficiency of messenger RNA in mammalian

cells. bioRxiv : the preprint server for biology.

Maquedano M, et al. (2024) More than 2,500 coding genes in the human reference gene set still have unsettled status. bioRxiv : the preprint server for biology.

Gaynor SM, et al. (2024) Yield of genetic association signals from genomes, exomes and imputation in the UK Biobank. Nature genetics, 56(11), 2345.

Hsu DJ, et al. (2023) Arginine limitation drives a directed codon-dependent DNA sequence evolution response in colorectal cancer cells. Science advances, 9(1), eade9120.

Ren Y, et al. (2023) Spatial transcriptomics reveals niche-specific enrichment and vulnerabilities of radial glial stem-like cells in malignant gliomas. Nature communications, 14(1), 1028.

Sun KY, et al. (2023) A deep catalog of protein-coding variation in 985,830 individuals. bioRxiv : the preprint server for biology.

Campagne S, et al. (2023) Molecular basis of RNA-binding and autoregulation by the cancer-associated splicing factor RBM39. Nature communications, 14(1), 5366.

Pagni S, et al. (2023) SCN1A: bioinformatically informed revised boundaries for promoter and enhancer regions. Human molecular genetics, 32(10), 1753.

Ziyatdinov A, et al. (2023) Genotyping, sequencing and analysis of 140,000 adults from Mexico City. Nature, 622(7984), 784.

Hsu DJ, et al. (2023) Arginine limitation causes a directed DNA sequence evolution response in colorectal cancer cells. bioRxiv : the preprint server for biology.

Tung KF, et al. (2022) TEx-MST: tissue expression profiles of MANE select transcripts. Database : the journal of biological databases and curation, 2022.

Abrusán G, et al. (2022) Known allosteric proteins have central roles in genetic disease. PLoS computational biology, 18(2), e1009806.

Miao YR, et al. (2022) Developing high-affinity decoy receptors to treat multiple myeloma and diffuse large B cell lymphoma. The Journal of experimental medicine, 219(9).