Resource Summary Report

Generated by T1D on Jul 31, 2026

APPRIS

RRID:SCR_012019
Type: Tool

Proper Citation

APPRIS (RRID:SCR_012019)

Resource Information

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

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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: data or information resource, database

Defining Citation: PMID:23161672

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

Availability: Free

Resource Name: APPRIS

Resource ID: SCR_012019

Alternate IDs: OMICS_01881

Record Creation Time: 20220129T080308+0000

Record Last Update: 20260729T044259+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 85 mentions in open access literature.

Listed below are recent publications. The full list is available at T1D .

Ferraresso M, et al. (2025) Replenishing co-downregulated miR-100-5p and miR-125b-5p in malignant germ cell tumors causes growth inhibition through cell cycle disruption. Molecular oncology, 19(4), 1203.

Stanek TJ, et al. (2025) Recombination Suppression Drives Expansion of the Drosophila Dot Chromosome. Molecular biology and evolution, 42(12).

Foord C, et al. (2025) A spatial long-read approach at near-single-cell resolution reveals developmental regulation of splicing and polyadenylation sites in distinct cortical layers and cell types. bioRxiv : the preprint server for biology.

Rodschinka G, et al. (2025) Comparative CRISPRi screens reveal a human stem cell dependence on mRNA translation-coupled quality control. Nature structural & molecular biology, 32(10), 1932.

Kodama H, et al. (2025) Systematic identification of exercise-induced anti-aging processes involving intron retention. The journals of gerontology. Series A, Biological sciences and medical sciences, 80(8).

Maquedano M, et al. (2025) The state of the human coding gene catalogues. Database : the journal of biological databases and curation, 2025.

Foord C, et al. (2025) A spatial long-read approach at near-single-cell resolution reveals developmental regulation of splicing and polyadenylation sites in distinct cortical layers and cell types. Nature communications, 16(1), 8093.

van Deventer BS, et al. (2025) Next generation sequencing: a possible answer to sudden unexplained deaths in a young South African cohort? Forensic science, medicine, and pathology, 21(3), 1081.

Voutsinos V, et al. (2025) A complete map of human cytosolic degrons and their relevance for disease. bioRxiv : the preprint server for biology.

Martinez-Jañez N, et al. (2025) Co-clinical trial targeting ER, FGFR and CDK4/6 in resistant hormone-positive breast cancer with FGFR alterations. NPJ precision oncology, 9(1), 343.

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.

Fradkin P, et al. (2024) Orthrus: Towards Evolutionary and Functional RNA Foundation Models. 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.

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

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

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

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.