

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 7, 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: 20260905T133202+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 97 mentions in open access literature.

Listed below are recent publications. The full list is available at [PRECISE-TBI](#) .

Voutsinos V, et al. (2026) A near-complete map of human cytosolic degrons and their relevance for disease. *Science advances*, 12(6), eadz3483.

Favier A, et al. (2026) COBT: a gene-based rare variant burden test for case-only study designs using aggregated genotypes from public reference cohorts. *Genome medicine*, 18(1).

Hu X, et al. (2026) The functional landscape of alternative splicing in hematopoietic lineage commitment. *Nature communications*, 17(1).

Mouren JC, et al. (2026) Exonic enhancers are a widespread class of dual-function regulatory elements. *Nature communications*, 17(1).

Choi JH, et al. (2026) Universal conditional knockout approach to multiple species, from fish to human induced pluripotent stem cells. *Nucleic acids research*, 54(9).

Litman A, et al. (2026) Variant-resolved prediction of context-specific isoform variation with a graph-based attention model. *Cell genomics*, 6(4), 101126.

Muscolino E, et al. (2026) Coronaviruses reprogram the tRNA epitranscriptome to favor viral protein expression. *Nature communications*, 17(1).

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.

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.

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*.

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

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).

Sethi S, et al. (2025) PSQAN: a pipeline to prioritize novel and biologically relevant transcripts from long-read RNA sequencing. *Bioinformatics advances*, 5(1), vbaf293.

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.

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

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.

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.