Resource Summary Report

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SpliceAid-F

RRID:SCR_002082
Type: Tool

Proper Citation

SpliceAid-F (RRID:SCR_002082)

Resource Information

URL: http://srv00.ibbe.cnr.it/SpliceAidF/

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Description: A database of human splicing factors and their RNA - binding sites. For each splicing factor (SF) the database reports its functional domains and its protein and chemical interactors. Furthermore, experimentally validated RNA-SF interactions are collected, including relevant information on the RNA binding sites such as the genes where these sites lie, their genomic coordinates, the splicing effects, experimental procedures, as well as the corresponding bibliographic references. Information from experiments showing no RNA-SF binding is also collected, at least in the assayed conditions. SpliceAid-F contains 4227 interactions, 2622 RNA binding sites and 1170 no-binding sites, including information on binding and no-binding specificity in different cellular contexts. SpliceAid-F can provide significant information to explain an observed splicing pattern as well as the effect of mutations in functional regulatory elements.

Abbreviations: SpliceAid-F

Synonyms: SpliceAid-F: a database of human splicing factors and their binding sites

Resource Type: database, data or information resource

Defining Citation: PMID:23118479

Keywords: splicing, protein, rna, splicing factor, interaction, binding site, no-binding site, splicing pattern, mutation, regulatory element, splicing factor

Funding:

Availability: Acknowledgement requested

Resource Name: SpliceAid-F

Resource ID: SCR_002082

Alternate IDs: OMICS_01893

Record Creation Time: 20220129T080211+0000

Record Last Update: 20250519T204626+0000

Ratings and Alerts

No rating or validation information has been found for SpliceAid-F.

No alerts have been found for SpliceAid-F.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 10 mentions in open access literature.

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

Fuchs S, et al. (2023) Defining the landscape of circular RNAs in neuroblastoma unveils a global suppressive function of MYCN. Nature communications, 14(1), 3936.

Busso-Lopes AF, et al. (2022) Connecting multiple microenvironment proteomes uncovers the biology in head and neck cancer. Nature communications, 13(1), 6725.

Pinto EM, et al. (2022) Clinical and Functional Significance of TP53 Exon 4-Intron 4 Splice Junction Variants. Molecular cancer research : MCR, 20(2), 207.

Sánchez-Ceinos J, et al. (2021) Impaired mRNA splicing and proteostasis in preadipocytes in obesity-related metabolic disease. eLife, 10.

Zheng X, et al. (2021) Comprehensive analysis of aberrant alternative splicing related to carcinogenesis and prognosis of papillary thyroid cancer. Aging, 13(19), 23149.

Pan X, et al. (2021) Alternative Splicing Dynamics of the Hypothalamus-Pituitary-Ovary Axis During Pubertal Transition in Gilts. Frontiers in genetics, 12, 592669.

Cai Y, et al. (2020) Identification of prognostic alternative splicing signatures in hepatitis B or/and C viruses related hepatocellular carcinoma. Genomics, 112(5), 3396.

Raj T, et al. (2018) Integrative transcriptome analyses of the aging brain implicate altered splicing in Alzheimer's disease susceptibility. Nature genetics, 50(11), 1584.

Giudice G, et al. (2016) ATtRACT-a database of RNA-binding proteins and associated motifs. Database : the journal of biological databases and curation, 2016.

Macossay-Castillo M, et al. (2014) Synonymous constraint elements show a tendency to encode intrinsically disordered protein segments. PLoS computational biology, 10(5), e1003607.