Resource Summary Report

Generated by T1D on Sep 9, 2026

ESEfinder 3.0

RRID:SCR_007088
Type: Tool

Proper Citation

ESEfinder 3.0 (RRID:SCR_007088)

Resource Information

URL: http://rulai.cshl.edu/cgi-bin/tools/ESE3/esefinder.cgi?process=home

Proper Citation: ESEfinder 3.0 (RRID:SCR_007088)

Description: A web-based resource that facilitates rapid analysis of exon sequences to identify putative exonic splicing enhancers (ESEs) responsive to the human SR proteins SF2/ASF, SC35, SRp40 and SRp55, and to predict whether exonic mutations disrupt such elements.

Abbreviations: ESEfinder

Resource Type: analysis service resource, data analysis service, production service resource, service resource

Defining Citation: PMID:12824367

Keywords: exonic splicing enhancer, sr protein, bio.tools

Funding: NIGMS GM42699;
NCI CA88351;
NHGRI HG01696

Availability: Free for non-profit use, Non-commercial, Acknowledgement requested, Commercial use with license

Resource Name: ESEfinder 3.0

Resource ID: SCR_007088

Alternate IDs: biotools:esefinder, nif-0000-30496

Alternate URLs: http://rulai.cshl.edu/tools/ESE2/, https://bio.tools/esefinder

Old URLs: http://exon.cshl.edu/ESE/

Record Creation Time: 20220129T080239+0000

Record Last Update: 20260905T133138+0000

Ratings and Alerts

No rating or validation information has been found for ESEfinder 3.0.

No alerts have been found for ESEfinder 3.0.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 213 mentions in open access literature.

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

Yang B, et al. (2026) A novel non-sense variant in GSDME causing exon skipping associated with DFNA5 in a large Chinese family. Frontiers in neurology, 17, 1752843.

Bychkov I, et al. (2025) Functional Analysis of Complex Structural and Splice-Altering Variants in the ARSB Gene Towards the Personalized Antisense-Based Therapy for Mucopolysaccharidosis Type VI Patients. Human mutation, 2025, 2250030.

Legebeke J, et al. (2025) Uplift of genetic diagnosis of rare respiratory disease using airway epithelium transcriptome analysis. Human molecular genetics, 34(2), 148.

Giuranna J, et al. (2025) Genetic and functional analyses of CTBP2 in anorexia nervosa and body weight regulation. Molecular psychiatry, 30(5), 1836.

Boulling A, et al. (2025) A bovine model of rhizomelic chondrodysplasia punctata caused by a deep intronic splicing variant in the GNPAT gene. Genetics, selection, evolution : GSE, 57(1), 23.

Khokhar ES, et al. (2025) CRYPTID-exon: streamlined detection of cryptic exons from RNA-seq data. bioRxiv : the preprint server for biology.

Jacinto J, et al. (2025) Exploring skeletal disorders in cattle and sheep: a WGS-based framework for diagnosis and classification. Genetics, selection, evolution : GSE, 57(1), 51.

Zhang Q, et al. (2025) Silent but significant: Functional elucidation of a synonymous ATP7B mutation in Wilson's disease pedigrees. Frontiers in genetics, 16, 1604683.

Munteanu CV, et al. (2024) In silico splicing analysis of the PMS2 gene: exploring alternative molecular mechanisms in PMS2-associated Lynch syndrome. BMC genomic data, 25(1), 100.

Pironon N, et al. (2024) Splice modulation strategy applied to deep intronic variants in COL7A1 causing recessive dystrophic epidermolysis bullosa. Proceedings of the National Academy of Sciences of the United States of America, 121(35), e2401781121.

Santos-Rebouças CB, et al. (2024) Immune response stability to the SARS-CoV-2 mRNA vaccine booster is influenced by differential splicing of HLA genes. Scientific reports, 14(1), 8982.

Pan D, et al. (2024) Splicing factor hnRNPA1 regulates alternative splicing of LOXL2 to enhance the production of LOXL2?13. The Journal of biological chemistry, 300(7), 107414.

Zhang Y, et al. (2024) Novel Germline KIT Variants in Families With Severe Piebaldism: Case Series and Literature Review. Journal of clinical laboratory analysis, 38(11-12), e25073.

Spangsberg Petersen US, et al. (2024) Regulating PCCA gene expression by modulation of pseudoexon splicing patterns to rescue enzyme activity in propionic acidemia. Molecular therapy. Nucleic acids, 35(1), 102101.

Koparir A, et al. (2024) Zebrafish as a model to investigate a biallelic gain-of-function variant in MSGN1, associated with a novel skeletal dysplasia syndrome. Human genomics, 18(1), 23.

Donelson CJH, et al. (2024) Functional evaluation of rare variants in complement factor I using a minigene assay. Frontiers in immunology, 15, 1446081.

García-Bohórquez B, et al. (2024) Exploring non-coding variants and evaluation of antisense oligonucleotides for splicing redirection in Usher syndrome. Molecular therapy. Nucleic acids, 35(4), 102374.

Jin B, et al. (2023) MEN1 is a regulator of alternative splicing and prevents R-loop-induced genome instability through suppression of RNA polymerase II elongation. Nucleic acids research, 51(15), 7951.

Liu L, et al. (2023) HBV Enhances Sorafenib Resistance in Hepatocellular Carcinoma by Reducing Ferroptosis via SRSF2-Mediated Abnormal PCLAF Splicing. International journal of molecular sciences, 24(4).

Choi SY, et al. (2023) Prediction of medication-related osteonecrosis of the jaws using machine learning methods from estrogen receptor 1 polymorphisms and clinical information. Frontiers in medicine, 10, 1140620.