

Resource Summary Report

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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: 20260919T195701+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 [nidm-terms](#).

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 LOXL2¹³. *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.