Resource Summary Report

Generated by RRID on Aug 19, 2026

pDESTsplice

RRID:Addgene_32484
Type: Plasmid

Proper Citation

RRID:Addgene_32484

Plasmid Information

URL: http://www.addgene.org/32484

Proper Citation: RRID:Addgene_32484

Bacterial Resistance: Chloramphenicol and Ampicillin

Defining Citation: PMID:18930792

Vector Backbone Description: Backbone Marker:Mo Bi Tec; Vector Backbone:pET01; Vector Types:; Bacterial Resistance:Chloramphenicol and Ampicillin

Plasmid Name: pDESTsplice

Record Creation Time: 20220422T222141+0000

Record Last Update: 20260815T081346+0000

Ratings and Alerts

No rating or validation information has been found for pDESTsplice.

No alerts have been found for pDESTsplice.

Data and Source Information

Source: Addgene

Usage and Citation Metrics

We found 14 mentions in open access literature.

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

Korhorn S, et al. (2026) Functional Analyses in Patient-Derived Neurons Establish Pathogenicity for STXBP1 Splice Variant c.429+5G>A. Human mutation, 2026, 1448702.

Dicke AK, et al. (2025) NXT2 is a key component of the RNA nuclear export factor complex in the human testis and essential for spermatogenesis. Nature communications, 16(1), 6254.

Tang S, et al. (2025) Antisense oligonucleotides modulate aberrant inclusion of poison exons in SCN1A-related Dravet syndrome. JCI insight, 10(7).

Rotte N, et al. (2025) Genotype-specific differences in infertile men due to loss-of-function variants in M1AP or ZZS genes. EMBO molecular medicine, 17(6), 1417.

Stallmeyer B, et al. (2024) Inherited defects of piRNA biogenesis cause transposon de-repression, impaired spermatogenesis, and human male infertility. Nature communications, 15(1), 6637.

Happ HC, et al. (2023) Long-read sequencing and profiling of RNA-binding proteins reveals the pathogenic mechanism of aberrant splicing of an SCN1A poison exon in epilepsy. bioRxiv : the preprint server for biology.

Dicke AK, et al. (2023) DDX3Y is likely the key spermatogenic factor in the AZFa region that contributes to human non-obstructive azoospermia. Communications biology, 6(1), 350.

Hirschi OR, et al. (2023) Combined Bioinformatic and Splicing Analysis of Likely Benign Intronic and Synonymous Variants Reveals Evidence for Pathogenicity. medRxiv : the preprint server for health sciences.

Alfen F, et al. (2022) Abnormal Pre-mRNA Splicing in Exonic Fabry Disease-Causing GLA Mutations. International journal of molecular sciences, 23(23).

Putscher E, et al. (2022) Genetic risk variants for multiple sclerosis are linked to differences in alternative pre-mRNA splicing. Frontiers in immunology, 13, 931831.

Putscher E, et al. (2021) Principles and Practical Considerations for the Analysis of Disease-Associated Alternative Splicing Events Using the Gateway Cloning-Based Minigene Vectors pDESTsplice and pSpliceExpress. International journal of molecular sciences, 22(10).

Chau KK, et al. (2021) Full-length isoform transcriptome of the developing human brain provides further insights into autism. Cell reports, 36(9), 109631.

Tang M, et al. (2020) Synonymous variants associated with Alzheimer disease in multiplex families. Neurology. Genetics, 6(4), e450.

Bartosovic M, et al. (2017) N6-methyladenosine demethylase FTO targets pre-mRNAs and regulates alternative splicing and 3'-end processing. Nucleic acids research, 45(19), 11356.