Resource Summary Report

Generated by NIF on May 20, 2025

SKIPPY

RRID:SCR_005430
Type: Tool

Proper Citation

SKIPPY (RRID:SCR_005430)

Resource Information

URL: http://research.nhgri.nih.gov/skippy/index.shtml

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Description: A Web-based tool that allows users to input a set of exonic variants to score them for a number of features (such as changes in splicing regulatory elements) that have been shown to be predictive of known genome variations that cause exon skipping or activation of ectopic splice sites. In this way, variants can be either prioritized for further splicing-based functional analysis or the results can be used as further genomic evidence in cases in which the causative variant is already known.

Abbreviations: SKIPPY

Synonyms: SKIPPY - A Tool for the Detection of Exonic Variants that Modulate Splicing

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

Defining Citation: PMID:20158892

Keywords: exonic variant, splicing, genome variation, coding variant

Funding:

Resource Name: SKIPPY

Resource ID: SCR_005430

Alternate IDs: OMICS_02258

Record Creation Time: 20220129T080230+0000

Record Last Update: 20250519T204658+0000

Ratings and Alerts

No rating or validation information has been found for SKIPPY.

No alerts have been found for SKIPPY.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Umair M, et al. (2020) EMC10 homozygous variant identified in a family with global developmental delay, mild intellectual disability, and speech delay. Clinical genetics, 98(6), 555.

Shi F, et al. (2019) Computational identification of deleterious synonymous variants in human genomes using a feature-based approach. BMC medical genomics, 12(Suppl 1), 12.