Resource Summary Report

Generated by dkNET on Sep 9, 2026

HEXplorer score

RRID:SCR_022269
Type: Tool

Proper Citation

HEXplorer score (RRID:SCR_022269)

Resource Information

URL: https://www2.hhu.de/rna/html/hexplorer_score.php

Proper Citation: HEXplorer score (RRID:SCR_022269)

Description: Web tool for genomic HEXploring allows landscaping of novel potential splicing regulatory elements. Allows landscaping of splicing regulatory regions, provides quantitative measure of mutation effects on splice enhancing and silencing properties and permitts calculation of mutationally most effective nucleotide.

Resource Type: data access protocol, software resource, web service

Defining Citation: DOI:10.1093/nar/gku736

Keywords: Predicts splicing potential, splicing regulatory regions, mutation effects on splice enhancing and silencing properties

Funding: German Research Foundation

Availability: Free, Freely available

Resource Name: HEXplorer score

Resource ID: SCR_022269

Record Creation Time: 20220511T050132+0000

Record Last Update: 20260905T133012+0000

Ratings and Alerts

No rating or validation information has been found for HEXplorer score.

No alerts have been found for HEXplorer score.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 6 mentions in open access literature.

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

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.

Canson DM, et al. (2023) Splicing annotation of endometrial cancer GWAS risk loci reveals potentially causal variants and supports a role for NF1 and SKAP1 as susceptibility genes. HGG advances, 4(2), 100185.

Leman R, et al. (2022) SPiP: Splicing Prediction Pipeline, a machine learning tool for massive detection of exonic and intronic variant effects on mRNA splicing. Human mutation, 43(12), 2308.

Barbosa P, et al. (2022) Computational prediction of human deep intronic variation. GigaScience, 12.

Holcomb DD, et al. (2022) Protocol to identify host-viral protein interactions between coagulation-related proteins and their genetic variants with SARS-CoV-2 proteins. STAR protocols, 3(3), 101648.

Bueno-Mart??nez E, et al. (2021) RAD51D Aberrant Splicing in Breast Cancer: Identification of Splicing Regulatory Elements and Minigene-Based Evaluation of 53 DNA Variants. Cancers, 13(11).