Resource Summary Report

Generated by NIF on May 20, 2025

HEXEvent

RRID:SCR_002106
Type: Tool

Proper Citation

HEXEvent (RRID:SCR_002106)

Resource Information

URL: http://hertellab.mmg.uci.edu/cgi-bin/HEXEvent/HEXEventWEB.cgi

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Description: A free database that provides a list of human internal exons and reports all their known splice events based on EST information from the UCSC Genome Browser. This list can be restricted by the user to either only a specific region in the genome (by specifying the chromosome, the strand and the start and end position), to a whole chromosome or to a group of genes. Furthermore, exons can be filtered according to their splicing type (constitutive exons, cassette exons and exons with one or more alternative 3' and/or 5' splice sites). In order to extract a customized set of exons, the user-specific definitions of exon types can be fixed. The user needs to specify in what fraction of ESTs an exon is allowed to be alternatively spliced in order to still be called constitutive. Furthermore, the user can restrict the set of requested cassette exons by a certain upper inclusion level, which, for instance, is useful when only looking for low-inclusion exons.

Abbreviations: HEXEvent

Synonyms: HEXEvent - a database of Human EXon splicing Events

Resource Type: database, data or information resource

Defining Citation: PMID:23118488

Keywords: exon, splicing, est, splice event, gene, chromosome, genome, splice

Funding:

Availability: Free

Resource Name: HEXEvent

Resource ID: SCR_002106

Alternate IDs: OMICS_01888

Record Creation Time: 20220129T080211+0000

Record Last Update: 20250519T204627+0000

Ratings and Alerts

No rating or validation information has been found for HEXEvent.

No alerts have been found for HEXEvent.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Cormier MJ, et al. (2022) Combining genetic constraint with predictions of alternative splicing to prioritize deleterious splicing in rare disease studies. BMC bioinformatics, 23(1), 482.

Hurst LD, et al. (2017) Depletion of somatic mutations in splicing-associated sequences in cancer genomes. Genome biology, 18(1), 213.

Marina RJ, et al. (2016) TET-catalyzed oxidation of intragenic 5-methylcytosine regulates CTCF-dependent alternative splicing. The EMBO journal, 35(3), 335.