Resource Summary Report

Generated by NIF on Apr 19, 2025

SPLITREAD

RRID:SCR_005264
Type: Tool

Proper Citation

SPLITREAD (RRID:SCR_005264)

Resource Information

URL: http://splitread.sourceforge.net/

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Description: Software for detecting INDELs (small insertions and deletion with size less than 50bp) as well as large deletions that are within the coding regions from the exome sequencing data. It also can be applied to the whole genome sequencing data.

Abbreviations: SPLITREAD

Synonyms: SPLITREAD - Split read based INDEL/SV Caller

Resource Type: software resource

Keywords: deletion, insertion, indel, genome, exome

Funding:

Resource Name: SPLITREAD

Resource ID: SCR_005264

Alternate IDs: OMICS_00323

Record Creation Time: 20220129T080229+0000

Record Last Update: 20250410T065240+0000

Ratings and Alerts

No rating or validation information has been found for SPLITREAD.

No alerts have been found for SPLITREAD.

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.

Hintzsche JD, et al. (2016) A Survey of Computational Tools to Analyze and Interpret Whole Exome Sequencing Data. International journal of genomics, 2016, 7983236.

Lin YL, et al. (2015) The evolution and functional impact of human deletion variants shared with archaic hominin genomes. Molecular biology and evolution, 32(4), 1008.

Keane TM, et al. (2014) Identification of structural variation in mouse genomes. Frontiers in genetics, 5, 192.