Resource Summary Report

Generated by dkNET on Apr 29, 2025

SPLINTER

RRID:SCR_005826
Type: Tool

Proper Citation

SPLINTER (RRID:SCR_005826)

Resource Information

URL: http://www.ibridgenetwork.org/wustl/splinter

Proper Citation: SPLINTER (RRID:SCR_005826)

Description: Software that detects and quantifies short IN/DELs as well as single nucleotide substitutions in pooled-DNA samples.

Abbreviations: SPLINTER

Synonyms: Short IN/DEL Prediction by Large deviation Inference and Non-linear True frequency Estimation by Recursion

Resource Type: software resource

Related Condition: Cancer

Funding:

Availability: Free for academic / non-profit use, Commercial use requires license

Resource Name: SPLINTER

Resource ID: SCR_005826

Alternate IDs: OMICS_00100

Record Creation Time: 20220129T080232+0000

Record Last Update: 20250420T014303+0000

Ratings and Alerts

No rating or validation information has been found for SPLINTER.

No alerts have been found for SPLINTER.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 13 mentions in open access literature.

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

Le Clercq LS, et al. (2023) PAReTT: A Python Package for the Automated Retrieval and Management of Divergence Time Data from the TimeTree Resource for Downstream Analyses. Journal of molecular evolution, 91(4), 502.

Ho JS, et al. (2021) HNRNPM controls circRNA biogenesis and splicing fidelity to sustain cancer cell fitness. eLife, 10.

Walter C, et al. (2019) Benchmarking of 4C-seq pipelines based on real and simulated data. Bioinformatics (Oxford, England), 35(23), 4938.

Ibanez L, et al. (2018) Pleiotropic Effects of Variants in Dementia Genes in Parkinson Disease. Frontiers in neuroscience, 12, 230.

Benitez BA, et al. (2016) Resequencing analysis of five Mendelian genes and the top genes from genome-wide association studies in Parkinson's Disease. Molecular neurodegeneration, 11, 29.

Torgerson DG, et al. (2015) Pooled Sequencing of Candidate Genes Implicates Rare Variants in the Development of Asthma Following Severe RSV Bronchiolitis in Infancy. PloS one, 10(11), e0142649.

Coghlan MA, et al. (2014) Sequencing of idiopathic pulmonary fibrosis-related genes reveals independent single gene associations. BMJ open respiratory research, 1(1), e000057.

Chun S, et al. (2013) Fine-mapping an association of FSHR with preterm birth in a Finnish population. PloS one, 8(10), e78032.

Benitez BA, et al. (2013) The PSEN1, p.E318G variant increases the risk of Alzheimer's disease in APOE-?4 carriers. PLoS genetics, 9(8), e1003685.

Jin SC, et al. (2012) Pooled-DNA sequencing identifies novel causative variants in PSEN1,

GRN and MAPT in a clinical early-onset and familial Alzheimer's disease Ibero-American cohort. Alzheimer's research & therapy, 4(4), 34.

Ramos E, et al. (2012) Population-based rare variant detection via pooled exome or custom hybridization capture with or without individual indexing. BMC genomics, 13, 683.

Li M, et al. (2012) A new approach for detecting low-level mutations in next-generation sequence data. Genome biology, 13(5), R34.

Vallania F, et al. (2012) Detection of rare genomic variants from pooled sequencing using SPLINTER. Journal of visualized experiments : JoVE(64).