

Resource Summary Report

Generated by ASWG on Aug 23, 2026

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

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: 20260815T182318+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 [ASWG](#) .

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.

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

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.

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

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.