Resource Summary Report

Generated by dkNET on May 20, 2025

VariationHunter

RRID:SCR_004865
Type: Tool

Proper Citation

VariationHunter (RRID:SCR_004865)

Resource Information

URL: http://compbio.cs.sfu.ca/software-variation-hunter

Proper Citation: VariationHunter (RRID:SCR_004865)

Description: A software tool for discovery of structural variation in one or more individuals simultaneously using high throughput technologies.

Abbreviations: VariationHunter

Synonyms: VariationHunter-CommonLaw

Resource Type: software resource

Defining Citation: PMID:22048523, PMID:20529927

Keywords: structural variation, genome, next-generation sequencing

Funding:

Resource Name: VariationHunter

Resource ID: SCR_004865

Alternate IDs: OMICS_00328

Record Creation Time: 20220129T080227+0000

Record Last Update: 20250519T203338+0000

Ratings and Alerts

No rating or validation information has been found for VariationHunter.

No alerts have been found for VariationHunter.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 12 mentions in open access literature.

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

Kathuria K, et al. (2020) SVXplorer: Three-tier approach to identification of structural variants via sequential recombination of discordant cluster signatures. PLoS computational biology, 16(3), e1007737.

Sun L, et al. (2019) TDNAscan: A Software to Identify Complete and Truncated T-DNA Insertions. Frontiers in genetics, 10, 685.

Kosugi S, et al. (2019) Comprehensive evaluation of structural variation detection algorithms for whole genome sequencing. Genome biology, 20(1), 117.

Russell CW, et al. (2019) Comprehensive Identification of Fim-Mediated Inversions in Uropathogenic Escherichia coli with Structural Variation Detection Using Relative Entropy. mSphere, 4(2).

Eslami Rasekh M, et al. (2017) Discovery of large genomic inversions using long range information. BMC genomics, 18(1), 65.

Haraksingh RR, et al. (2017) Comprehensive performance comparison of high-resolution array platforms for genome-wide Copy Number Variation (CNV) analysis in humans. BMC genomics, 18(1), 321.

Soylev A, et al. (2017) Toolkit for automated and rapid discovery of structural variants. Methods (San Diego, Calif.), 129, 3.

Xia LC, et al. (2016) A genome-wide approach for detecting novel insertion-deletion variants of mid-range size. Nucleic acids research, 44(15), e126.

Hénaff E, et al. (2015) Jitterbug: somatic and germline transposon insertion detection at single-nucleotide resolution. BMC genomics, 16, 768.

Ewing AD, et al. (2015) Transposable element detection from whole genome sequence data. Mobile DNA, 6, 24.

Han BW, et al. (2015) piPipes: a set of pipelines for piRNA and transposon analysis via small RNA-seq, RNA-seq, degradome- and CAGE-seq, ChIP-seq and genomic DNA sequencing. Bioinformatics (Oxford, England), 31(4), 593.

Wong LP, et al. (2013) Deep whole-genome sequencing of 100 southeast Asian Malays. American journal of human genetics, 92(1), 52.