Resource Summary Report

Generated by SPARC SAWG on Jul 28, 2026

FishingCNV

RRID:SCR_013038
Type: Tool

Proper Citation

FishingCNV (RRID:SCR_013038)

Resource Information

URL: http://sourceforge.net/projects/fishingcnv/

Proper Citation: FishingCNV (RRID:SCR_013038)

Description: A software tool developed at McGill University, is a tool for comprehensive analysis of rare copy number variations in high-throughput exome sequencing data.

Abbreviations: FishingCNV

Synonyms: FishingCNV - Copy number variation detection in exome sequencing data, FishingCNV - CNV detection in exome sequencing data, FishingCNV - Copy number variation (CNV) detection in exome sequencing data

Resource Type: software resource

Defining Citation: PMID:23539306

Availability: Commercial license

Resource Name: FishingCNV

Resource ID: SCR_013038

Alternate IDs: OMICS_00334

Record Creation Time: 20220129T080313+0000

Record Last Update: 20260725T190744+0000

Ratings and Alerts

No rating or validation information has been found for FishingCNV.

No alerts have been found for FishingCNV.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 11 mentions in open access literature.

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

Kim YJ, et al. (2021) Identification of a Homozygous PEX26 Mutation in a Heimler Syndrome Patient. Genes, 12(5).

Aamir A, et al. (2021) Discordant phenotypes in twins with infantile nystagmus. Scientific reports, 11(1), 2826.

Gordeeva V, et al. (2021) Benchmarking germline CNV calling tools from exome sequencing data. Scientific reports, 11(1), 14416.

De Vilder EYG, et al. (2021) Rare Modifier Variants Alter the Severity of Cardiovascular Disease in Pseudoxanthoma Elasticum: Identification of Novel Candidate Modifier Genes and Disease Pathways Through Mixture of Effects Analysis. Frontiers in cell and developmental biology, 9, 612581.

Sadler B, et al. (2020) Rare and de novo duplications containing SHOX in clubfoot. Journal of medical genetics, 57(12), 851.

Salloum R, et al. (2017) Characterizing temporal genomic heterogeneity in pediatric high-grade gliomas. Acta neuropathologica communications, 5(1), 78.

Thomas MG, et al. (2017) Development and clinical utility of a novel diagnostic nystagmus gene panel using targeted next-generation sequencing. European journal of human genetics : EJHG, 25(6), 725.

Watson CM, et al. (2016) Enhanced diagnostic yield in Meckel-Gruber and Joubert syndrome through exome sequencing supplemented with split-read mapping. BMC medical genetics, 17, 1.

Nikbakht H, et al. (2016) Spatial and temporal homogeneity of driver mutations in diffuse intrinsic pontine glioma. Nature communications, 7, 11185.

Barclay SF, et al. (2015) Rapid-Onset Obesity with Hypothalamic Dysfunction, Hypoventilation, and Autonomic Dysregulation (ROHHAD): exome sequencing of trios, monozygotic twins and tumours. Orphanet journal of rare diseases, 10, 103.

Poulter JA, et al. (2015) A distinctive oral phenotype points to FAM20A mutations not identified by Sanger sequencing. Molecular genetics & genomic medicine, 3(6), 543.