Resource Summary Report

Generated by dkNET on Apr 30, 2025

OncoSNP-SEQ

RRID:SCR_012742
Type: Tool

Proper Citation

OncoSNP-SEQ (RRID:SCR_012742)

Resource Information

URL: https://sites.google.com/site/oncosnpseq/

Proper Citation: OncoSNP-SEQ (RRID:SCR_012742)

Description: An analytical tool for characterizing copy number alterations and loss-of-heterozygosity (LOH) events in cancer samples from whole genome sequencing data.

Abbreviations: OncoSNP-SEQ

Resource Type: software resource

Funding:

Resource Name: OncoSNP-SEQ

Resource ID: SCR_012742

Alternate IDs: OMICS_00348

Record Creation Time: 20220129T080312+0000

Record Last Update: 20250420T014618+0000

Ratings and Alerts

No rating or validation information has been found for OncoSNP-SEQ.

No alerts have been found for OncoSNP-SEQ.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 6 mentions in open access literature.

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

Dharanipragada P, et al. (2018) iCopyDAV: Integrated platform for copy number variations-Detection, annotation and visualization. PloS one, 13(4), e0195334.

Riaz N, et al. (2017) Tumor and Microenvironment Evolution during Immunotherapy with Nivolumab. Cell, 171(4), 934.

Yu Z, et al. (2017) CLImAT-HET: detecting subclonal copy number alterations and loss of heterozygosity in heterogeneous tumor samples from whole-genome sequencing data. BMC medical genomics, 10(1), 15.

Giannoulatou E, et al. (2017) Whole-genome sequencing of spermatocytic tumors provides insights into the mutational processes operating in the male germline. PloS one, 12(5), e0178169.

Thangam M, et al. (2015) CRCDA--Comprehensive resources for cancer NGS data analysis. Database : the journal of biological databases and curation, 2015.

Liu B, et al. (2013) Computational methods for detecting copy number variations in cancer genome using next generation sequencing: principles and challenges. Oncotarget, 4(11), 1868.