Resource Summary Report

Generated by NIF on Apr 9, 2025

SegSeq

RRID:SCR_010826
Type: Tool

Proper Citation

SegSeq (RRID:SCR_010826)

Resource Information

URL: http://www.broadinstitute.org/software/cprg/?q=node/39

Proper Citation: SegSeq (RRID:SCR_010826)

Description: An algorithm to identify chromosomal breakpoints using massively parallel next generation sequence data.

Abbreviations: SegSeq

Resource Type: software resource

Funding:

Resource Name: SegSeq

Resource ID: SCR_010826

Alternate IDs: OMICS_00352

Record Creation Time: 20220129T080300+0000

Record Last Update: 20250214T183139+0000

Ratings and Alerts

No rating or validation information has been found for SegSeq.

No alerts have been found for SegSeq.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 20 mentions in open access literature.

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

Liu X, et al. (2022) The metabolic genomic atlas reveals potential drivers and clinically relevant insights into the etiology of esophageal squamous cell carcinoma. Theranostics, 12(14), 6160.

Zhou S, et al. (2021) Complex mosaic blastocysts after preimplantation genetic testing: prevalence and outcomes after re-biopsy and re-vitrification. Reproductive biomedicine online, 43(2), 215.

Ban Y, et al. (2020) Whole-Genome Sequencing and Target Validation Analysis of Müllerian Adenosarcoma: A Tumor With Complex but Specific Genetic Alterations. Frontiers in oncology, 10, 538.

Bi Y, et al. (2020) Decreased ZNF750 promotes angiogenesis in a paracrine manner via activating DANCR/miR-4707-3p/FOXC2 axis in esophageal squamous cell carcinoma. Cell death & disease, 11(4), 296.

Jian M, et al. (2020) A novel patient-derived organoids-based xenografts model for preclinical drug response testing in patients with colorectal liver metastases. Journal of translational medicine, 18(1), 234.

Wu S, et al. (2019) Whole-genome sequencing identifies ADGRG6 enhancer mutations and FRS2 duplications as angiogenesis-related drivers in bladder cancer. Nature communications, 10(1), 720.

Pan HX, et al. (2019) Detection of de novo genetic variants in Mayer-Rokitansky-Küster-Hauser syndrome by whole genome sequencing. European journal of obstetrics & gynecology and reproductive biology: X, 4, 100089.

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

Zhang W, et al. (2018) The chromosome 11q13.3 amplification associated lymph node metastasis is driven by miR-548k through modulating tumor microenvironment. Molecular cancer, 17(1), 125.

Zhou S, et al. (2018) Prevalence and authenticity of de-novo segmental aneuploidy (>16 Mb) in human blastocysts as detected by next-generation sequencing. Reproductive biomedicine online, 37(5), 511.

Du P, et al. (2017) Comprehensive genomic analysis of Oesophageal Squamous Cell Carcinoma reveals clinical relevance. Scientific reports, 7(1), 15324.

Hintzsche JD, et al. (2016) A Survey of Computational Tools to Analyze and Interpret Whole Exome Sequencing Data. International journal of genomics, 2016, 7983236.

Cheng C, et al. (2016) Genomic analyses reveal FAM84B and the NOTCH pathway are associated with the progression of esophageal squamous cell carcinoma. GigaScience, 5, 1.

Sun X, et al. (2016) Whole-genome re-sequencing for the identification of high contribution susceptibility gene variants in patients with type 2 diabetes. Molecular medicine reports, 13(5), 3735.

Wu K, et al. (2015) Frequent alterations in cytoskeleton remodelling genes in primary and metastatic lung adenocarcinomas. Nature communications, 6, 10131.

Pirooznia M, et al. (2015) Whole-genome CNV analysis: advances in computational approaches. Frontiers in genetics, 6, 138.

Elvers I, et al. (2015) Exome sequencing of lymphomas from three dog breeds reveals somatic mutation patterns reflecting genetic background. Genome research, 25(11), 1634.

Fernandez-Banet J, et al. (2014) Decoding complex patterns of genomic rearrangement in hepatocellular carcinoma. Genomics, 103(2-3), 189.

Yang L, et al. (2014) Targeted and genome-wide sequencing reveal single nucleotide variations impacting specificity of Cas9 in human stem cells. Nature communications, 5, 5507.

Kan Z, et al. (2013) Whole-genome sequencing identifies recurrent mutations in hepatocellular carcinoma. Genome research, 23(9), 1422.