

Resource Summary Report

Generated by [kravitz2](#) on Jul 31, 2026

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

Resource Name: SegSeq

Resource ID: SCR_010826

Alternate IDs: OMICS_00352

Record Creation Time: 20220129T080300+0000

Record Last Update: 20260725T190703+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 [kravitz2](#) .

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.

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.

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.

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.

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.

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.

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

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

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.