Resource Summary Report

Generated by dkNET on May 8, 2025

BRASS

RRID:SCR_017091
Type: Tool

Proper Citation

BRASS (RRID:SCR_017091)

Resource Information

URL: https://github.com/cancerit/BRASS

Proper Citation: BRASS (RRID:SCR_017091)

Description: Software tool for analysis of one or more related BAM files of paired end sequencing to determine potential rearrangement breakpoints. Identifies breaks and attempts to assemble rearrangements.

Resource Type: data analysis software, software application, data processing software, software resource

Keywords: analysis, BAM, file, paired, end, sequencing, determine, rearrangement, breakpoint, assemble

Funding:

Availability: Free, Available for download, Freely available

Resource Name: BRASS

Resource ID: SCR_017091

License: GNU AGPL v3

Record Creation Time: 20220129T080333+0000

Record Last Update: 20250508T065745+0000

Ratings and Alerts

No rating or validation information has been found for BRASS.

No alerts have been found for BRASS.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 34 mentions in open access literature.

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

Rekhtman N, et al. (2025) Chromothripsis-Mediated Small Cell Lung Carcinoma. Cancer discovery, 15(1), 83.

Anselmino N, et al. (2024) Integrative Molecular Analyses of the MD Anderson Prostate Cancer Patient-derived Xenograft (MDA PCa PDX) Series. Clinical cancer research : an official journal of the American Association for Cancer Research, 30(10), 2272.

Vergara X, et al. (2024) Widespread chromatin context-dependencies of DNA double-strand break repair proteins. Nature communications, 15(1), 5334.

Wu CC, et al. (2024) Whole genome and reverse protein phase array landscapes of patient derived osteosarcoma xenograft models. Scientific reports, 14(1), 19891.

Ijaz J, et al. (2024) Haplotype-specific assembly of shattered chromosomes in esophageal adenocarcinomas. Cell genomics, 4(2), 100484.

Koh GCC, et al. (2024) The chemotherapeutic drug CX-5461 is a potent mutagen in cultured human cells. Nature genetics, 56(1), 23.

Hu X, et al. (2024) The evolution of lung adenocarcinoma precursors is associated with chromosomal instability and transition from innate to adaptive immune response/evasion. Research square.

Keahi DL, et al. (2024) G-quadruplexes are a source of vulnerability in BRCA2 deficient granule cell progenitors and medulloblastoma. bioRxiv : the preprint server for biology.

Nunes L, et al. (2024) Prognostic genome and transcriptome signatures in colorectal cancers. Nature, 633(8028), 137.

Andersen LVB, et al. (2023) Non-BRCA1/BRCA2 high-risk familial breast cancers are not associated with a high prevalence of BRCAness. Breast cancer research : BCR, 25(1), 69.

Gadd S, et al. (2022) Genetic changes associated with relapse in favorable histology Wilms

tumor: A Children's Oncology Group AREN03B2 study. Cell reports. Medicine, 3(6), 100644.

Mitchell E, et al. (2022) Clonal dynamics of haematopoiesis across the human lifespan. Nature, 606(7913), 343.

Fabre MA, et al. (2022) The longitudinal dynamics and natural history of clonal haematopoiesis. Nature, 606(7913), 335.

Petljak M, et al. (2022) Mechanisms of APOBEC3 mutagenesis in human cancer cells. Nature, 607(7920), 799.

Buhigas C, et al. (2022) The architecture of clonal expansions in morphologically normal tissue from cancerous and non-cancerous prostates. Molecular cancer, 21(1), 183.

Szymansky A, et al. (2021) Neuroblastoma Risk Assessment and Treatment Stratification with Hybrid Capture-Based Panel Sequencing. Journal of personalized medicine, 11(8).

Zou X, et al. (2021) A systematic CRISPR screen defines mutational mechanisms underpinning signatures caused by replication errors and endogenous DNA damage. Nature cancer, 2(6), 643.

Diossy M, et al. (2021) A subset of lung cancer cases shows robust signs of homologous recombination deficiency associated genomic mutational signatures. NPJ precision oncology, 5(1), 55.

Lee S, et al. (2020) Molecular Analysis of Clinically Defined Subsets of High-Grade Serous Ovarian Cancer. Cell reports, 31(2), 107502.

Olafsson S, et al. (2020) Somatic Evolution in Non-neoplastic IBD-Affected Colon. Cell, 182(3), 672.