

Resource Summary Report

Generated by [kravitz2](#) on Sep 18, 2026

FRCbam

RRID:SCR_005189

Type: Tool

Proper Citation

FRCbam (RRID:SCR_005189)

Resource Information

URL: https://github.com/vezzi/FRC_align

Proper Citation: FRCbam (RRID:SCR_005189)

Description: Software package containing tools to process bam files in order to evaluate and analyze de novo assembly / assemblers and identify Structural Variations suspicious genomics regions. The tools have been already successfully applied in several de novo and resequencing projects. This package contains two tools: # FRCbam: tool to compute Feature Response Curves in order to validate and rank assemblies and assemblers # FindTranslocations: tool to identify chromosomal rearrangements using Mate Pairs

Resource Type: software resource

Defining Citation: [PMID:23284938](#)

Keywords: standalone software, sam, bam

Availability: GNU General Public License, v3

Resource Name: FRCbam

Resource ID: SCR_005189

Alternate IDs: OMICS_04070

Record Creation Time: 20220129T080228+0000

Record Last Update: 20260912T195622+0000

Ratings and Alerts

No rating or validation information has been found for FRCbam.

No alerts have been found for FRCbam.

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 [kravitz2](#) .

Papa Y, et al. (2023) Genome assembly and isoform analysis of a highly heterozygous New Zealand fisheries species, the tarakihi (*Nemadactylus macropterus*). *G3* (Bethesda, Md.), 13(2).

Fuller T, et al. (2023) A reference assembly for the legume cover crop hairy vetch (*Vicia villosa*). *GigaByte* (Hong Kong, China), 2023, gigabyte98.

Harris RA, et al. (2022) Construction of a new chromosome-scale, long-read reference genome assembly for the Syrian hamster, *Mesocricetus auratus*. *GigaScience*, 11.

Lai S, et al. (2022) metaMIC: reference-free misassembly identification and correction of de novo metagenomic assemblies. *Genome biology*, 23(1), 242.

Urban JM, et al. (2021) High contiguity de novo genome assembly and DNA modification analyses for the fungus fly, *Sciara coprophila*, using single-molecule sequencing. *BMC genomics*, 22(1), 643.

Grillová L, et al. (2021) Genetic diversity of *Leptospira* isolates in Lao PDR and genome analysis of an outbreak strain. *PLoS neglected tropical diseases*, 15(12), e0010076.

Li R, et al. (2021) A near complete genome for goat genetic and genomic research. *Genetics, selection, evolution : GSE*, 53(1), 74.

Wang W, et al. (2020) The draft nuclear genome assembly of *Eucalyptus pauciflora*: a pipeline for comparing de novo assemblies. *GigaScience*, 9(1).

Í Kongsstovu S, et al. (2019) Using long and linked reads to improve an Atlantic herring (*Clupea harengus*) genome assembly. *Scientific reports*, 9(1), 17716.

Morales-Hojas R, et al. (2018) The genome of the biting midge *Culicoides sonorensis* and gene expression analyses of vector competence for bluetongue virus. *BMC genomics*, 19(1), 624.

Schneider VA, et al. (2017) Evaluation of GRCh38 and de novo haploid genome assemblies demonstrates the enduring quality of the reference assembly. *Genome research*, 27(5), 849.