

Resource Summary Report

Generated by [dkNET](#) on Aug 26, 2026

PEMer

RRID:SCR_005263

Type: Tool

Proper Citation

PEMer (RRID:SCR_005263)

Resource Information

URL: <http://sv.gersteinlab.org/pemer/>

Proper Citation: PEMer (RRID:SCR_005263)

Description: Software package as computational framework with simulation-based error models for inferring genomic structural variants from massive paired-end sequencing data. Package is composed of three modules, PEMer workflow, SV-Simulation and BreakDB. PEMer workflow is a sensitive software for detecting SVs from paired-end sequence reads. SV-Simulation randomly introduces SVs into a given genome and generates simulated paired-end reads from novel genome.

Synonyms: Paired-End Mapper

Resource Type: software resource

Defining Citation: [PMID:19236709](#)

Keywords: structural variation, genome, next-generation sequencing, bio.tools, bio.tools

Resource Name: PEMer

Resource ID: SCR_005263

Alternate IDs: biotools:pemer, OMICS_00320

Alternate URLs: <https://bio.tools/pemer>, <https://bio.tools/pemer>

Record Creation Time: 20220129T080229+0000

Record Last Update: 20260821T193742+0000

Ratings and Alerts

No rating or validation information has been found for PEMer.

No alerts have been found for PEMer.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 7 mentions in open access literature.

Listed below are recent publications. The full list is available at [dkNET](#) .

Louw N, et al. (2023) Incorporating CNV analysis improves the yield of exome sequencing for rare monogenic disorders-an important consideration for resource-constrained settings. *Frontiers in genetics*, 14, 1277784.

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

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

Keane TM, et al. (2014) Identification of structural variation in mouse genomes. *Frontiers in genetics*, 5, 192.

Shyr D, et al. (2013) Next generation sequencing in cancer research and clinical application. *Biological procedures online*, 15(1), 4.

Zhao M, et al. (2013) Computational tools for copy number variation (CNV) detection using next-generation sequencing data: features and perspectives. *BMC bioinformatics*, 14 Suppl 11(Suppl 11), S1.

Magi A, et al. (2010) Bioinformatics for next generation sequencing data. *Genes*, 1(2), 294.