

Resource Summary Report

Generated by [NIF](#) on Sep 1, 2026

BEDOPS

RRID:SCR_012865

Type: Tool

Proper Citation

BEDOPS (RRID:SCR_012865)

Resource Information

URL: <https://github.com/bedops/bedops>

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Description: A suite of tools to address common questions raised in genomic studies - mostly with regard to overlap and proximity relationships between data sets.

Abbreviations: BEDOPS

Synonyms: BEDOPS: high-performance genomic feature operations

Resource Type: software resource

Defining Citation: [PMID:22576172](#), [DOI:10.1093/bioinformatics/bts277](#)

Availability: GNU General Public License, v3

Resource Name: BEDOPS

Resource ID: SCR_012865

Alternate IDs: OMICS_00949

Alternate URLs: <https://sources.debian.org/src/bedops/>

Record Creation Time: 20220129T080312+0000

Record Last Update: 20260829T182434+0000

Ratings and Alerts

No rating or validation information has been found for BEDOPS.

No alerts have been found for BEDOPS.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 237 mentions in open access literature.

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

Farhan M, et al. (2026) Genome-wide association analysis reveals natural genetic variations controlling canopy architecture traits in bread wheat. *Scientific reports*, 16(1), 6433.

Kim SK, et al. (2026) Integrative analysis of in silico predictions and clinical evidence to delineate the capability of HiFi long-read sequencing in paralogous genes. *NPJ genomic medicine*, 11(1).

Okino ML, et al. (2026) Functional genomics reveals mediators of beta cell survival in ER stress and type 2 diabetes risk. *bioRxiv : the preprint server for biology*.

Kishino K, et al. (2026) Cessation of Gene Flow Associated With the Reduction of a Sexually Selected Phenotype in the Island Stag Beetle. *Molecular ecology*, 35(12), e70435.

Luo Y, et al. (2026) A trans-piRNA network and transcriptional antagonism shape piRNA cluster function. *bioRxiv : the preprint server for biology*.

Carey JL, et al. (2026) RNA G-quadruplexes function as a tunable switch of FUS phase separation. *Nucleic acids research*, 54(12).

Ringeval A, et al. (2026) Multi-omics characterization of toxin expression and producing organs in the predatory gastropods *Monoplex corrugatus* and *Stramonita haemastoma*. *BMC genomics*, 27(1).

Moulds TP, et al. (2026) Graded Calorie Restriction Causes Graded Slowing of Epigenetic Ageing in Mice. *Aging cell*, 25(1), e70342.

Herrmann M, et al. (2026) TSniffer: unbiased de novo identification of RNA editing sites and quantification of editing activity in RNA-seq data. *Genome biology*, 27(1), 5.

Denisko D, et al. (2026) Inverted Alu repeats in loop-out exon skipping across hominoid evolution. *Nucleic acids research*, 54(6).

Wright SN, et al. (2026) Common and rare genetic variants show network convergence for a majority of human traits. *EMBO reports*, 27(8), 1918.

Li H, et al. (2026) CASER: A semi-supervised model with multi-omics data integration prioritizes cancer-associated epigenetic regulator genes. *PLoS computational biology*, 22(4), e1014253.

So J, et al. (2026) Serum Response Factor (SRF) promotes actin cytoskeletal organization in adipocytes to support adaptive hypertrophic expansion and tissue remodeling during obesity in mice. *Metabolism: clinical and experimental*, 178, 156548.

Schrettenbrunner L, et al. (2026) Comprehensive mapping of the 5' and 3' untranslated regions of *Aspergillus fumigatus* reveals diverse mechanisms of mRNA processing including premature transcription termination. *RNA (New York, N.Y.)*, 32(2), 250.

Knudson LA, et al. (2026) Muscleblind-like proteins dimerize by forming disulfide bonds to regulate alternative splicing and pathogenic RNA foci formation. *Nucleic acids research*, 54(10).

Li X, et al. (2026) Characterizing breed-shared and breed-specific genetic regulatory effects of gene expression across three pig breeds. *Journal of animal science and biotechnology*, 17(1).

Luo Y, et al. (2026) piRNA direct the chromatin reader to its genomic targets. *bioRxiv : the preprint server for biology*.

Tollenaere A, et al. (2026) Mechanisms of gene regulation by SRCAP and H2A.Z. *Nature communications*, 17(1).

Placzek S, et al. (2025) Orchestration of pluripotent stem cell genome reactivation during mitotic exit. *Cell reports*, 44(4), 115486.

Wright SN, et al. (2025) State of the interactomes: an evaluation of molecular networks for generating biological insights. *Molecular systems biology*, 21(1), 1.