

Resource Summary Report

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BEDOPS

RRID:SCR_012865

Type: Tool

Proper Citation

BEDOPS (RRID:SCR_012865)

Resource Information

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

Proper Citation: BEDOPS (RRID:SCR_012865)

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: 20260725T190742+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 220 mentions in open access literature.

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

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

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.

Melino M, et al. (2025) Depleting the action of EZH2 through PI3K-mTOR inhibition to overcome metastasis and immunotherapy resistance in triple-negative breast cancer. *Molecular cancer therapeutics*.

Zhang H, et al. (2025) Reidentification of hybridization events with transcriptomic data and phylogenomic study in Seabuckthorn. *Scientific reports*, 15(1), 24121.

Suda K, et al. (2025) Mutation profile and chromosomal abnormality in adenomyosis. *Reproduction (Cambridge, England)*, 170(2).

Auxillos J, et al. (2025) True length of diverse capped RNA sequencing (TLDR-seq): 5'-3'-end sequencing of capped RNAs regardless of 3'-end status. *Nucleic acids research*, 53(6).

Pastore B, et al. (2025) The ribonuclease DISL-2 mediates piRNA degradation in *C. elegans*. *Cell reports*, 44(10), 116430.

Lee HK, et al. (2025) Rare germline JAK/STAT variants in a Korean cohort amplify innate immune responses to vaccination. *iScience*, 28(12), 114110.

Kesälahti R, et al. (2025) Optimising Exome Captures in Species With Large Genomes Using Species-Specific Repetitive DNA Blocker. *Molecular ecology resources*, 25(3), e14053.

Quaid K, et al. (2025) iPSCs and iPSC-derived cells as a model of human genetic and epigenetic variation. *Nature communications*, 16(1), 1750.

Sabarís G, et al. (2025) A mechanistic basis for genetic assimilation in natural fly populations. *Proceedings of the National Academy of Sciences of the United States of America*, 122(11), e2415982122.

Psatha N, et al. (2025) Large-scale discovery of potent, compact and erythroid specific enhancers for gene therapy vectors. *Nature communications*, 16(1), 4325.

Martinez-Hernandez JE, et al. (2025) Comparative and systems analyses of *Leishmania* spp. non-coding RNAs through developmental stages. *PLoS neglected tropical diseases*, 19(5), e0013108.

Hennighausen L, et al. (2025) Investigation of the transcriptional impact of rare germline JAK/STAT variants found in a Tyrolean alpine community. *BMC genomics*, 27(1), 8.

Buyan A, et al. (2025) Statistical framework for calling allelic imbalance in high-throughput sequencing data. *Nature communications*, 16(1), 1739.

Shirole NH, et al. (2025) Requirement for Cyclin D1 Underlies Cell-Autonomous HIF2 Dependence in Kidney Cancer. *Cancer discovery*, 15(7), 1484.

Schwarz EM, et al. (2025) Genomes of the entomopathogenic nematode *Steinernema hermaphroditum* and its associated bacteria. *Genetics*, 231(3).

Georgiou K, et al. (2025) MyoD1 localization at the nuclear periphery is mediated by association of WFS1 with active enhancers. *Nature communications*, 16(1), 2614.

Schwarz EM, et al. (2025) Hookworm genes encoding intestinal excreted-secreted proteins are transcriptionally upregulated in response to the host's immune system. *bioRxiv* : the preprint server for biology.