

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.

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.

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

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.