

Resource Summary Report

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BEADS

RRID:SCR_013229

Type: Tool

Proper Citation

BEADS (RRID:SCR_013229)

Resource Information

URL: <http://beads.sourceforge.net/>

Proper Citation: BEADS (RRID:SCR_013229)

Description: Software for a normalization scheme that corrects nucleotide composition bias, mappability variations and differential local DNA structural effects in deep sequencing data.

Abbreviations: BEADS

Synonyms: BEADS: Bias Elimination Algorithm for Deep Sequencing, Bias Elimination Algorithm for Deep Sequencing

Resource Type: software resource

Defining Citation: [PMID:21646344](#)

Keywords: bio.tools

Resource Name: BEADS

Resource ID: SCR_013229

Alternate IDs: OMICS_00466, biotools:beads

Alternate URLs: <https://bio.tools/beads>

Record Creation Time: 20220129T080315+0000

Record Last Update: 20260919T195240+0000

Ratings and Alerts

No rating or validation information has been found for BEADS.

No alerts have been found for BEADS.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 38 mentions in open access literature.

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

Chahal G, et al. (2025) Epigenomics and transcriptomics profiles of developing zebrafish heart cells. *Scientific data*, 12(1), 1620.

Gonyea CR, et al. (2025) BEADS: An Interactive Semi-Automated Workflow for 3D Fibrin Angiogenesis Assays Enabling Co-Culture and Directionality Analysis. *bioRxiv : the preprint server for biology*.

Garcia-Cabau C, et al. (2025) Mis-splicing of a neuronal microexon promotes CPEB4 aggregation in ASD. *Nature*, 637(8045), 496.

Davies AR, et al. (2025) Advanced immunophenotyping of lymphocyte and monocyte subsets in healthy Australian adults using a novel spectral flow cytometry panel. *Frontiers in immunology*, 16, 1577206.

Mandal S, et al. (2025) Role of LEAFLESS, an AP2/ERF family transcription factor, in the regulation of trichome specialized metabolism. *The New phytologist*, 247(2), 774.

Feke A, et al. (2025) High resolution diel transcriptomes of autotetraploid potato reveal expression and sequence conservation among rhythmic genes. *BMC genomics*, 26(1), 925.

Dance A, et al. (2024) Exploring the role of purinergic receptor P2RY1 in type 2 diabetes risk and pathophysiology: Insights from human functional genomics. *Molecular metabolism*, 79, 101867.

Decsi K, et al. (2024) Transcriptome datasets of maize plant cultures treated with humic- and amino acids. *Data in brief*, 57, 110900.

Kim S, et al. (2024) Liquid Biopsy-Based Detection and Response Prediction for Depression. *ACS nano*, 18(47), 32498.

Alradi M, et al. (2024) A long-term high-fat diet induces differential gene expression changes in spatially distinct adipose tissue of male mice. *Physiological genomics*, 56(12), 819.

Tang C, et al. (2024) Electrocatalytic hydrogenation of acetonitrile to ethylamine in acid. *Nature communications*, 15(1), 3233.

Wang X, et al. (2023) Robust Spontaneous Raman Flow Cytometry for Single-Cell Metabolic Phenome Profiling via pDEP-DLD-RFC. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 10(16), e2207497.

Wang H, et al. (2023) Characterization of Stromatolite Organic Sedimentary Structure Based on Spectral Image Fusion. *Sensors* (Basel, Switzerland), 23(13).

Turkalj S, et al. (2023) A protocol for simultaneous high-sensitivity genotyping and chromatin accessibility profiling in single cells. *STAR protocols*, 4(4), 102641.

Theofilatos D, et al. (2022) Protocol to isolate mature thymic T cell subsets using fluorescence-activated cell sorting for assessing gene expression by RNA-seq and transcription factor binding across the genome by CUT&RUN. *STAR protocols*, 3(4), 101839.

Iannetta M, et al. (2021) Baseline T-lymphocyte subset absolute counts can predict both outcome and severity in SARS-CoV-2 infected patients: a single center study. *Scientific reports*, 11(1), 12762.

Avramia I, et al. (2021) Spent Brewer's Yeast as a Source of Insoluble β -Glucans. *International journal of molecular sciences*, 22(2).

Choi W, et al. (2021) Functional Characterization of the mazEF Toxin-Antitoxin System in the Pathogenic Bacterium *Agrobacterium tumefaciens*. *Microorganisms*, 9(5).

Miller BF, et al. (2021) Assessing ZNF154 methylation in patient plasma as a multicancer marker in liquid biopsies from colon, liver, ovarian and pancreatic cancer patients. *Scientific reports*, 11(1), 221.

Slyusarenko M, et al. (2021) Formation and Evaluation of a Two-Phase Polymer System in Human Plasma as a Method for Extracellular Nanovesicle Isolation. *Polymers*, 13(3).