

Resource Summary Report

Generated by [PRECISE-TBI](#) on Aug 1, 2026

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: 20260801T190447+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 37 mentions in open access literature.

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

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.

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.

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.

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.

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

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.

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).

Garcia A, et al. (2021) miR-204-5p and Platelet Function Regulation: Insight into a Mechanism Mediated by CDC42 and GPIIb/IIIa. *Thrombosis and haemostasis*, 121(9), 1206.