

Resource Summary Report

Generated by [NIF](#) on Aug 9, 2026

ComBat

RRID:SCR_010974

Type: Tool

Proper Citation

ComBat (RRID:SCR_010974)

Resource Information

URL: <http://www.bu.edu/jlab/wp-assets/ComBat/Abstract.html>

Proper Citation: ComBat (RRID:SCR_010974)

Description: Adjusting batch effects in microarray expression data using Empirical Bayes methods.

Abbreviations: ComBat

Resource Type: software resource

Resource Name: ComBat

Resource ID: SCR_010974

Alternate IDs: OMICS_00857

Record Creation Time: 20220129T080301+0000

Record Last Update: 20260808T185940+0000

Ratings and Alerts

No rating or validation information has been found for ComBat.

No alerts have been found for ComBat.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 3983 mentions in open access literature.

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

Simmons SK, et al. (2026) Experimental and computational methods for allelic imbalance analysis from single-nucleus RNA-seq data. *Genome biology*, 27(1).

Ding C, et al. (2026) Glioblastoma-Secreted C1QL1 Orchestrates Tumor Microtube Expansion and Neural Synaptic Pruning to Drive Malignant Synapse Formation and Recurrence. *Cancer discovery*, 16(6), 1176.

Zhao W, et al. (2026) A Prognostic Signature for Lung Adenocarcinoma in Patients Who Have Never Smoked. *Cancer discovery*, 16(3), 460.

Huang KK, et al. (2026) Mutational Signatures and Clonal Hematopoiesis in Intestinal Metaplasia across Countries with Varying Stomach Cancer Incidence. *Cancer discovery*, 16(3), 497.

Suresh V, et al. (2026) Modelling EWS::FLI1 protein fluctuations reveal determinants of tumor plasticity in Ewing sarcoma. *EMBO molecular medicine*, 18(2), 646.

Deconinck T, et al. (2026) Comparative evaluation of oncolytic viruses reveals opposing preferences for glioblastoma subtypes. *Molecular therapy. Oncology*, 34(3), 201263.

Ferrier K, et al. (2026) Epigenome-wide association study meta-analysis of BMI in African Americans. *HGG advances*, 7(1), 100552.

Rhoads CA, et al. (2026) A Meta-Analysis of the Effects of Acute Sleep Deprivation on the Cortical Transcriptome in Rodent Models. *Journal of sleep research*, 35(3), e70205.

Tripathi U, et al. (2026) Senolytic-Resistant Senescent Cells Have a Distinct SASP Profile and Functional Impact: The Path to Developing Senosensitizers. *Aging cell*, 25(1), e70358.

Yang R, et al. (2026) Exploring and Validating the Molecular Mechanisms Linking Fatty Acid Metabolism and Sarcopenia. *IET systems biology*, 20(1), e70052.

Guo J, et al. (2026) Multi-omics analysis of key lipid metabolism-related genes involved in the anti-hepatocellular carcinoma effect of dihydroartemisinin. *Discover oncology*, 17(1), 237.

Xie H, et al. (2026) B2M regulates ELANE in pyroptosis to affect pancreatic cancer progression. *Translational oncology*, 63, 102613.

Zhu Z, et al. (2026) Identification of A p300-SP1-BRD4 Transcriptional Axis as a Key Driver of AR Hyperactivation in Polycystic Ovarian Syndrome. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 13(23), e18185.

Wang W, et al. (2026) Integrative transcriptomic and machine learning framework reveals candidate genes and potential mechanisms of aflatoxin B1 exposure in breast cancer. *Scientific reports*, 16(1).

Camp SY, et al. (2026) Single-cell epigenetic profiling reveals a tumor-intrinsic interferon response program in ccRCC tied to poor prognosis and BAP1 loss. *Science advances*, 12(8), eadv5457.

Qin H, et al. (2026) Cuproptosis-associated PDHA1 promotes sarcoma progression and immunotherapy responsiveness via the E2F1-PD-L1 axis: a multi-omics and clinical validation study. *NPJ precision oncology*, 10(1).

Chen Y, et al. (2026) Identification of metabolism and inflammation-related biomarkers and potential drugs for schizophrenia based on comprehensive bioinformatics and machine learning. *BMC psychiatry*, 26(1).

Liao X, et al. (2026) Transcriptomic analysis reveals synaptic dysregulation and mitochondrial dysfunction in autism spectrum disorder. *Brain, behavior, & immunity - health*, 53, 101197.

Luo Z, et al. (2026) Identifying neurophenotypes of major depressive disorder through normative model of regional homogeneity. *Translational psychiatry*, 16(1).

Tang S, et al. (2026) Single-cell RNA sequencing analysis reveals the evolution and regulatory features of specialized endothelial cell subsets in non-traumatic osteonecrosis of the femoral head. *Biology direct*, 21(1).