

Resource Summary Report

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ConsensusClusterPlus

RRID:SCR_016954

Type: Tool

Proper Citation

ConsensusClusterPlus (RRID:SCR_016954)

Resource Information

URL: <http://bioconductor.org/packages/release/bioc/html/ConsensusClusterPlus.html>

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Description: Software written in R for determining cluster count and membership by stability evidence in unsupervised analysis. Provides quantitative and visual stability evidence for estimating the number of unsupervised classes in a dataset with item tracking, item consensus and cluster consensus plots.

Resource Type: data analysis software, data processing software, software application, software resource

Defining Citation: [PMID:20427518](#)

Keywords: cluster, count, stability, evidence, unsupervised, analysis, , bio.tools

Funding: NCI F32CA142039;
NCI U24 CA126554;
Thomas G. Labrecque Foundation

Availability: Free, Available for download, Freely available

Resource Name: ConsensusClusterPlus

Resource ID: SCR_016954

Alternate IDs: biotools:consensusclusterplus

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

License: GPL 2

Record Creation Time: 20220129T080332+0000

Record Last Update: 20260912T195846+0000

Ratings and Alerts

No rating or validation information has been found for ConsensusClusterPlus.

No alerts have been found for ConsensusClusterPlus.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 196 mentions in open access literature.

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

Gámez-Pozo A, et al. (2026) Immune classification of advanced melanoma identifies non-responders to anti-PD1 therapy. *Cancer immunology, immunotherapy* : CII, 75(5).

Chong AS, et al. (2026) Tracing the molecular route to progression in miRNA-biogenesis-defective thyroid lesions. *JCI insight*, 11(3).

Chen Y, et al. (2026) Exploring the role of disulfidptosis?related signatures in immune microenvironment, prognosis and therapeutic strategies of cholangiocarcinoma. *Oncology reports*, 55(2).

Namba S, et al. (2026) A cross-population compendium of gene-environment interactions. *Nature*, 651(8106), 688.

Yan Y, et al. (2026) Ecotypes of triple-negative breast cancer in response to chemotherapy. *Nature*, 654(8120), 1088.

Altendorf L, et al. (2026) Molecular changes during AT/RT progression associated with epithelial-mesenchymal transition and extracellular matrix changes. *Acta neuropathologica*, 152(1).

Duan X, et al. (2026) Machine Learning Reveals the Association Between Gene Expression and Immune Infiltration in Colorectal Cancer: A Comprehensive Study From Single-Cell to Survival Analysis. *Journal of cellular and molecular medicine*, 30(5), e71049.

Du J, et al. (2026) Novel fatty acid metabolism-related molecular subtyping and prognostic signature for breast cancer. *Translational cancer research*, 15(1), 29.

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.

Li JZ, et al. (2026) DNA Methylation-Based Risk Stratification and Classification of Pediatric Thyroid Carcinoma. *Clinical cancer research : an official journal of the American*

Association for Cancer Research, 32(9), 1898.

Rosenbaum E, et al. (2026) Association of Circulating T Cell and Tumor Microenvironment Profiles with Immune Checkpoint Blockade Outcomes in Sarcoma. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 32(9), 1777.

Shulman ED, et al. (2026) AI-predicted spatial transcriptomics unlocks breast cancer biomarkers from pathology. *Cell*, 189(14), 4225.

Ding C, et al. (2026) MYO1G Facilitates Caveolin 1-Mediated Endocytosis of the N-Terminal Fragments of Gasdermin E to Restrain Pyroptosis and Chemotherapy Efficacy. *Cancer research*, 86(15), 3741.

Ding C, et al. (2025) The signature based on interleukin family and receptors identified IL19 and IL20RA in promoting nephroblastoma progression through STAT3 pathway. *Scientific reports*, 15(1), 11639.

Li Q, et al. (2025) Investigating the Prognostic Role of Telomerase-Related Cellular Senescence Gene Signatures in Breast Cancer Using Machine Learning. *Biomedicines*, 13(4).

Zheng L, et al. (2025) A gene signature related to programmed cell death to predict immunotherapy response and prognosis in colon adenocarcinoma. *PeerJ*, 13, e18895.

Liu Y, et al. (2025) Identification of HES4 as a novel prognostic marker and therapeutic target in hepatocellular carcinoma. *Discover oncology*, 16(1), 156.

Wu H, et al. (2025) Determination of high-grade serous ovarian cancer stem cell-based subtypes and prognostic model and identification of highly expressed VSIG4 and STAB1 in macrophages. *Journal of ovarian research*, 18(1), 159.

Pei C, et al. (2025) Identification of immunometabolism-associated genes and immune infiltration in sepsis-induced cardiomyopathy using integrated bioinformatics and machine learning approaches. *The Journal of international medical research*, 53(11), 3000605251395584.

Haller A, et al. (2025) Interaction of lncRNA LENT with DHX36 regulates translation and suppresses autophagy in melanoma. *Cell death & disease*, 17(1), 121.