

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: 20260905T132816+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 [Kravitz](#) .

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

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

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

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.

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

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

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.

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

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.

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.

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.

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

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.

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.

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).

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

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.