

Resource Summary Report

Generated by [dkNET](#) on Sep 11, 2026

HCLUST

RRID:SCR_009154

Type: Tool

Proper Citation

HCLUST (RRID:SCR_009154)

Resource Information

URL: <http://wpicr.wpic.pitt.edu/WPICCompGen/hclust/hclust.htm>

Proper Citation: HCLUST (RRID:SCR_009154)

Description: Software application that is a simple clustering method that can be used to rapidly identify a set of tag SNP's based upon genotype data (entry from Genetic Analysis Software), THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: HCLUST

Synonyms: R/HCLUST

Resource Type: software application, software resource

Keywords: gene, genetic, genomic, r, bio.tools

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: HCLUST

Resource ID: SCR_009154

Alternate IDs: biotools:h-clust, SCR_009102, nlx_154195, nlx_154331

Alternate URLs: <https://bio.tools/h-clust>

Record Creation Time: 20220129T080251+0000

Record Last Update: 20260905T133045+0000

Ratings and Alerts

No rating or validation information has been found for HCLUST.

No alerts have been found for HCLUST.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1460 mentions in open access literature.

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

Zhou Z, et al. (2026) Using an Unbiased Coexpression Network to Reveal Cross-Talking Pathways of Phosphoinositide-3-Kinase Regulatory Subunit 1 in Skin Aging and Rejuvenation. *FASEB journal : official publication of the Federation of American Societies for Experimental Biology*, 40(2), e71466.

Bleve A, et al. (2025) ROR?? Bridges Cancer-Driven Lipid Dysmetabolism and Myeloid Immunosuppression. *Cancer discovery*, 15(7), 1505.

Ausems ANMA, et al. (2025) Sex-specific variation in breeding-ground departure decisions and detection rates during southbound migration in West Atlantic Flyway Whimbrels (*Numenius phaeopus*). *Scientific reports*, 15(1), 6735.

Ni C, et al. (2025) Single-cell transcriptomic analysis reveals prognosis-related stromal signatures that potentiate stratification of patients with extrahepatic cholangiocarcinoma. *BMC gastroenterology*, 25(1), 235.

Bao Q, et al. (2025) Identification of immune-related cervical cancer prognostic biomarkers and construction of prognostic model based on tumor microenvironment. *European journal of medical research*, 30(1), 261.

Hamazaki Y, et al. (2025) Generation and characterization of induced pluripotent stem cells of small apes. *Frontiers in cell and developmental biology*, 13, 1536947.

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

An Y, et al. (2025) Identification of a LncRNA based CeRNA network signature to establish a prognostic model and explore potential therapeutic targets in gastric cancer. *Scientific reports*, 15(1), 20891.

Wang K, et al. (2025) Circadian rhythm genes and immune cell infiltration in myasthenia gravis: A comprehensive analysis. *PloS one*, 20(7), e0327829.

Lerga-Jaso J, et al. (2025) Optimization of multi-ancestry polygenic risk score disease prediction models. *Scientific reports*, 15(1), 17495.

Sutharsan R, et al. (2025) Single-cell mitochondrial morphomics reveals cellular heterogeneity and predicts complex I, III, and ATP synthase Inhibition responses. *Scientific reports*, 15(1), 16715.

Wang Y, et al. (2025) Integrative bioinformatics analysis reveals STAT1, ORC2, and GTF2B as critical biomarkers in lupus nephritis with Monkeypox virus infection. *Scientific reports*, 15(1), 13589.

Sun M, et al. (2025) Exploring the potential mechanisms of sorafenib resistance in hepatocellular carcinoma cell lines based on RNA sequencing. *Cancer cell international*, 25(1), 91.

Geng D, et al. (2025) Identification of key genes associated with residual feed intake in small-sized meat ducks through integrated analysis of mRNA and miRNA transcriptomes. *Poultry science*, 104(5), 105058.

McCarthy OS, et al. (2025) Using Community Composition and Successional Theory to Guide Site-Specific Coral Reef Management. *Global change biology*, 31(1), e70050.

Zeng PYF, et al. (2025) Cellular blueprint of healthy and diseased human epiglottis and subglottis-a study of the Canadian Airways Research (CARE) group. *EBioMedicine*, 114, 105631.

Zhang N, et al. (2025) Integration of multi-omics data accelerates molecular analysis of common wheat traits. *Nature communications*, 16(1), 2200.

Liu Y, et al. (2025) Differential transcriptomic profiling of lipid metabolism and collagen remodeling in fast- and slow-twitch skeletal muscles in aging. *FASEB journal : official publication of the Federation of American Societies for Experimental Biology*, 39(2), e70335.

Miebach J, et al. (2025) Importance, structure, cultivability, and resilience of the bacterial microbiota during infection of laboratory-grown *Haematococcus* spp. by the blastocladialean pathogen *Paraphysoderma sedebokerense*: evidence for a domesticated microbiota and its potential for biocontrol. *FEMS microbiology ecology*, 101(2).

Torrado H, et al. (2025) Evolutionary Genomics of Two Co-occurring Congeneric Fore Reef Coral Species on Guam (Mariana Islands). *Genome biology and evolution*, 17(1).