

Resource Summary Report

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Clust

RRID:SCR_025283

Type: Tool

Proper Citation

Clust (RRID:SCR_025283)

Resource Information

URL: <https://github.com/BaselAbujamous/clust>

Proper Citation: Clust (RRID:SCR_025283)

Description: Software package for automatic extraction of optimal co-expressed gene clusters from gene expression data. Automatic and optimised consensus clustering of one or more heterogeneous datasets.

Resource Type: software toolkit, software resource, source code

Defining Citation: [PMID:30359297](#)

Keywords: automatic extraction, optimal co-expressed gene clusters, gene expression data,

Funding: Bill and Melinda Gates Foundation ;
Royal Society ;
European Union Horizon 2020

Availability: Free, Available for download, Freely available

Resource Name: Clust

Resource ID: SCR_025283

License: GNU LGPL v3.0

Record Creation Time: 20240426T053251+0000

Record Last Update: 20260813T055322+0000

Ratings and Alerts

No rating or validation information has been found for Clust.

No alerts have been found for Clust.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 24 mentions in open access literature.

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

López-González C, et al. (2025) Species-specific phylloplane responses to changes in external pH. *Journal of experimental botany*, 76(17), 5102.

Rasoul A, et al. (2025) Propelling sustainable energy: Multi-omics analysis of pennycress FATTY ACID ELONGATION1 knockout for biofuel production. *Plant physiology*, 197(2).

Lauterbach M, et al. (2024) Leaf transcriptomes from C3, C3-C4 intermediate, and C4Neurachne species give insights into C4 photosynthesis evolution. *Plant physiology*, 197(1).

de Assis MA, et al. (2024) A Multiomics Perspective on Plant Cell Wall-Degrading Enzyme Production: Insights from the Unexploited Fungus *Trichoderma erinaceum*. *Journal of fungi (Basel, Switzerland)*, 10(6).

Kongari R, et al. (2024) The Transcriptional Program of *Staphylococcus aureus* Phage K Is Affected by a Host *rpoC* Mutation That Confers Phage K Resistance. *Viruses*, 16(11).

Rabaglino MB, et al. (2023) Maternal blood transcriptome as a sensor of fetal organ maturation at the end of organogenesis in cattle†. *Biology of reproduction*, 109(5), 749.

Li Z, et al. (2023) Genome-wide analysis of long noncoding RNAs in response to salt stress in *Nicotiana tabacum*. *BMC plant biology*, 23(1), 646.

Zhou X, et al. (2023) Time-Course Transcriptome Profiling Reveals Differential Resistance Responses of Tomato to a Phytotoxic Effector of the Pathogenic Oomycete *Phytophthora cactorum*. *Plants (Basel, Switzerland)*, 12(4).

Moolhuijzen P, et al. (2023) Spatiotemporal patterns of wheat response to *Pyrenophora tritici-repentis* in asymptomatic regions revealed by transcriptomic and X-ray fluorescence microscopy analyses. *Journal of experimental botany*, 74(15), 4707.

Rocks D, et al. (2023) Early-life stress and ovarian hormones alter transcriptional regulation in the nucleus accumbens resulting in sex-specific responses to cocaine. *Cell reports*, 42(10), 113187.

Burghardt E, et al. (2023) Transcriptome analysis reveals temporally regulated genetic networks during *Drosophila* border cell collective migration. *BMC genomics*, 24(1), 728.

Fernandes I, et al. (2022) Salt Stress Tolerance in *Casuarina glauca*: Insights from the Branchlets Transcriptome. *Plants (Basel, Switzerland)*, 11(21).

Dudka W, et al. (2022) Targeting integrated stress response with ISRIB combined with imatinib treatment attenuates RAS/RAF/MAPK and STAT5 signaling and eradicates chronic myeloid leukemia cells. *BMC cancer*, 22(1), 1254.

Colgan TJ, et al. (2021) Evolution and Expression of the Immune System of a Facultatively Anadromous Salmonid. *Frontiers in immunology*, 12, 568729.

Li Q, et al. (2021) Transcriptome and Resequencing Analyses Provide Insight into Differences in Organic Acid Accumulation in Two Pear Varieties. *International journal of molecular sciences*, 22(17).

Siadjeu C, et al. (2021) Insights into Regulation of C2 and C4 Photosynthesis in *Amaranthaceae/Chenopodiaceae* Using RNA-Seq. *International journal of molecular sciences*, 22(22).

Zhu Y, et al. (2020) Conserved and Opposite Transcriptome Patterns during Germination in *Hordeum vulgare* and *Arabidopsis thaliana*. *International journal of molecular sciences*, 21(19).

Perrin E, et al. (2020) Diauxie and co-utilization of carbon sources can coexist during bacterial growth in nutritionally complex environments. *Nature communications*, 11(1), 3135.

Sun S, et al. (2020) Analysis of Spatio-Temporal Transcriptome Profiles of Soybean (*Glycine max*) Tissues during Early Seed Development. *International journal of molecular sciences*, 21(20).

Sielemann K, et al. (2020) Distinct Myocardial Transcriptomic Profiles of Cardiomyopathies Stratified by the Mutant Genes. *Genes*, 11(12).