

# Resource Summary Report

Generated by [PRECISE-TBI](#) on Aug 1, 2026

## ClueGO

RRID:SCR\_005748

Type: Tool

### Proper Citation

ClueGO (RRID:SCR\_005748)

### Resource Information

**URL:** <http://www.ici.upmc.fr/cluego/>

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**Description:** A Cytoscape plug-in that visualizes the non-redundant biological terms for large clusters of genes in a functionally grouped network. It can be used in combination with GOLORIZE. The identifiers can be uploaded from a text file or interactively from a network of Cytoscape. The type of identifiers supported can be easily extended by the user. ClueGO performs single cluster analysis and comparison of clusters. From the ontology sources used, the terms are selected by different filter criteria. The related terms which share similar associated genes can be combined to reduce redundancy. The ClueGO network is created with kappa statistics and reflects the relationships between the terms based on the similarity of their associated genes. On the network, the node colour can be switched between functional groups and clusters distribution. ClueGO charts are underlying the specificity and the common aspects of the biological role. The significance of the terms and groups is automatically calculated. ClueGO is easy updatable with the newest files from Gene Ontology and KEGG. Platform: Windows compatible, Mac OS X compatible, Linux compatible, Unix compatible, THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16, 2025.

**Abbreviations:** ClueGO

**Resource Type:** software resource

**Defining Citation:** [PMID:19237447](#)

**Keywords:** statistical analysis, function, gene ontology, pathway, annotation, network, plugin, gene

**Funding:** National Institute of Health and Medical Research; Rennes; France ;  
Ville de Paris ;  
INCa ;  
Austrian Ministry for Science and Research ;

BINII ;  
European Union 7FP 202230

**Availability:** THIS RESOURCE IS NO LONGER IN SERVICE

**Resource Name:** ClueGO

**Resource ID:** SCR\_005748

**Alternate IDs:** nlx\_149209

**Record Creation Time:** 20220129T080232+0000

**Record Last Update:** 20260725T190611+0000

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## Ratings and Alerts

No rating or validation information has been found for ClueGO.

No alerts have been found for ClueGO.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 2943 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [PRECISE-TBI](#) .

Ferreira JV, et al. (2026) LAMP2A regulates endosomal protein composition and membrane identity in exosome biogenesis. iScience, 29(1), 114305.

Correia PD, et al. (2026) Injury-induced KIF4A neural expression and its role in Schwann cell proliferation suggest a dual function for this kinesin in neural regeneration. Neural regeneration research, 21(4), 1607.

Goshayeshi L, et al. (2025) Germline variants in patients from the Iranian hereditary colorectal cancer registry. Cancer cell international, 25(1), 140.

Kim LA, et al. (2025) Circulating RNA Markers Associated with Adenoma-Carcinoma Sequence in Colorectal Cancer. International journal of molecular sciences, 26(4).

Podszywa?ow-Bartnicka P, et al. (2025) Transcriptional readthrough precedes alternative splicing programs triggered in CML cells by imatinib. bioRxiv : the preprint server for biology.

Burge KY, et al. (2025) Spatial transcriptomics delineates potential differences in intestinal phenotypes of cardiac and classical necrotizing enterocolitis. iScience, 28(4), 112166.

Cao X, et al. (2025) Maturation and detoxification of synphilin-1 inclusion bodies regulated by sphingolipids. *eLife*, 12.

Tombácz D, et al. (2025) Temporal transcriptional profiling of host cells infected by a veterinary alphaherpesvirus using nanopore sequencing. *Scientific reports*, 15(1), 3247.

Khayer N, et al. (2025) A dynamic co-expression approach reveals Gins2 as a potential upstream modulator of HNSCC metastasis. *Scientific reports*, 15(1), 3322.

Farrokhi Yekta R, et al. (2025) Biomarker Panels Associated with Diagnosis and Overall Survival in Hepatocellular Carcinoma Revealed from Protein-Protein and mRNA-miRNA Interaction Networks. *Asian Pacific journal of cancer prevention : APJCP*, 26(1), 249.

Timme K, et al. (2025) Diet-induced obesity alters the ovarian chemical biotransformation and oxidative stress response proteins both basally and in response to 7,12-dimethylbenz[a]anthracene exposure. *Toxicological sciences : an official journal of the Society of Toxicology*, 204(1), 9.

Zhou W, et al. (2025) Deleting adipose FXR exacerbates metabolic defects and induces endocannabinoid lipid, 2-oleoyl glycerol, in obesity. *Journal of lipid research*, 66(3), 100754.

Errico A, et al. (2025) In vitro effect of hCG on cryptorchid patients' gubernacular cells: a predictive model for adjuvant personalized therapy. *Cell communication and signaling : CCS*, 23(1), 19.

Yao TX, et al. (2025) Integrated single-cell transcriptomic map of pig kidney cells across various periods and anatomical sites. *Zoological research*, 46(2), 469.

Daghino S, et al. (2025) Comparative genomics reveals substantial divergence in metal sensitive and metal tolerant isolates of the ericoid mycorrhizal fungus *Oidiodendron maius*. *Mycorrhiza*, 35(2), 24.

Lee Y, et al. (2025) MFGE-8, a Corona Protein on Extracellular Vesicles, Mediates Self-Renewal and Survival of Human Pluripotent Stem Cells. *Journal of extracellular vesicles*, 14(4), e70056.

Wei X, et al. (2025) Temporal Profiling of Male Cortical Astrocyte Transcription Predicts Molecular Shifts From Early Development to Aging. *Glia*, 73(7), 1349.

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.

Boehme JD, et al. (2025) Epigenetic changes and serotype-specific responses of alveolar type II epithelial cells to *Streptococcus pneumoniae* in resolving influenza A virus infection. *Cell communication and signaling : CCS*, 23(1), 278.

Lenoel I, et al. (2025) ALS/FTD-linked TBK1 deficiency in microglia induces an aged-like microglial signature and drives social recognition deficits in mice. *Nature communications*, 16(1), 7951.