

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 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 ;
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BINII ;
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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: 20260905T132541+0000

Ratings and Alerts

No rating or validation information has been found for ClueGO.

No alerts have been found for ClueGO.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2951 mentions in open access literature.

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

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

Rajkumar A, et al. (2026) SplitTurboID mapping of dimeric protein phosphatase complex interactomes. iScience, 29(4), 115195.

Podsiywa?ow-Bartnicka P, et al. (2026) Transcriptional readthrough precedes alternative splicing programs triggered in CML cells by imatinib. Science advances, 12(12), eaea2475.

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.

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

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

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

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

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

Fu J, et al. (2025) m1A regulator-mediated methylation modifications and gene signatures and their prognostic value in multiple myeloma. *Experimental and therapeutic medicine*, 29(1), 18.

Shi Y, et al. (2025) Acquired resistance to PD-L1 inhibition enhances a type I IFN-regulated secretory program in tumors. *EMBO reports*, 26(2), 521.

Lagache L, et al. (2025) Predicting Protein Pathways Associated to Tumor Heterogeneity by Correlating Spatial Lipidomics and Proteomics: The Dry Proteomic Concept. *Molecular & cellular proteomics : MCP*, 24(1), 100891.

Gouesbet G, et al. (2025) Strong resistance to γ -cyfluthrin in a strain of the beetle *Alphitobius diaperinus*: a de novo transcriptome analysis. *Insect science*, 32(1), 209.

Pareek CS, et al. (2025) Identification of trait-associated microRNA modules in liver transcriptome of pig fed with PUFAs-enriched supplementary diet. *Journal of applied genetics*, 66(2), 389.

Kukla-Bartoszek M, et al. (2025) Integrated Profiling Identifies Long-Term Molecular Consequences of Prenatal Dexamethasone Treatment in the Rat Brain-Potential Triggers of Depressive Phenotype and Cognitive Impairment. *Molecular neurobiology*, 62(4), 5183.

Gökçen Tosun N, et al. (2025) Dual targeting of HSP90 and BCL-2 in breast cancer cells using inhibitors BIIB021 and ABT-263. *Breast cancer research and treatment*, 210(2), 493.

Khan N, et al. (2025) β -Glucan reprograms neutrophils to promote disease tolerance against influenza A virus. *Nature immunology*, 26(2), 174.

Zhang M, et al. (2025) Increased SOAT2 expression in aged regulatory T cells is associated with altered cholesterol metabolism and reduced anti-tumor immunity. *Nature communications*, 16(1), 630.

Koff L, et al. (2025) Early Life Exposure to Deltamethrin Impairs Synaptic Function by Altering the Brain-Derived Extracellular Vesicle Proteome. *Molecular & cellular proteomics : MCP*, 24(2), 100902.

Salatta BM, et al. (2025) Skeletal muscle lncRNA profile associated with fatty acids in Nellore beef cattle. *Scientific reports*, 15(1), 26109.