# **Resource Summary Report**

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# PANTHER

RRID:SCR\_004869 Type: Tool

**Proper Citation** 

PANTHER (RRID:SCR\_004869)

#### **Resource Information**

URL: http://www.pantherdb.org/

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**Description:** System that classifies genes by their functions, using published scientific experimental evidence and evolutionary relationships to predict function even in absence of direct experimental evidence. Orthologs view is curated orthology relationships between genes for human, mouse, rat, fish, worm, and fly.

Abbreviations: PANTHER

**Synonyms:** PANTHER Classification System, Protein ANalysis THrough Evolutionary Relationships Classification System, Protein ANalysis THrough Evolutionary Relationships, PANTHER (Protein ANalysis THrough Evolutionary Relationships) Classification System

**Resource Type:** production service resource, database, analysis service resource, data analysis service, service resource, ontology, controlled vocabulary, data or information resource

Defining Citation: PMID:23193289, PMID:20015972, PMID:12952881

**Keywords:** hidden markov model, human, mouse, genome, protein, gene, function, pathway, ortholog, phylogenetic tree, gene ortholog, protein family, gene function, evolution, data set, molecular function, biological process, cellular component, transcript, FASEB list

Funding: NIGMS GM081084

Availability: Free, Freely available

**Resource Name: PANTHER** 

Resource ID: SCR\_004869

Alternate IDs: SCR\_015893, nlx\_84521

**Record Creation Time:** 20220129T080227+0000

Record Last Update: 20250503T055710+0000

## **Ratings and Alerts**

No rating or validation information has been found for PANTHER.

No alerts have been found for PANTHER.

## Data and Source Information

Source: <u>SciCrunch Registry</u>

#### **Usage and Citation Metrics**

We found 7805 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>ASWG</u>.

Abuzahra M, et al. (2025) A novel p.127Val>lle single nucleotide polymorphism in the MTNR1A gene and its relation to litter size in Thin-tailed Indonesian ewes. Animal bioscience, 38(2), 209.

Utley D, et al. (2025) Camelina circRNA landscape: Implications for gene regulation and fatty acid metabolism. The plant genome, 18(1), e20537.

Neuman K, et al. (2025) Static Magnetic Stimulation and Magnetic Microwires Synergistically Enhance and Guide Neurite Outgrowth. Advanced healthcare materials, 14(3), e2403956.

Shen X, et al. (2025) The tomato gene Ty-6, encoding DNA polymerase delta subunit 1, confers broad resistance to Geminiviruses. TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik, 138(1), 22.

Carvalho CA, et al. (2025) SUMO-mediated regulation of H3K4me3 reader SET-26 controls germline development in C. elegans. PLoS biology, 23(1), e3002980.

Zhang X, et al. (2025) Identification of SLC35A1 as an essential host factor for the transduction of multi-serotype recombinant adeno-associated virus (AAV) vectors. mBio, 16(1), e0326824.

Pleguezuelos-Manzano C, et al. (2025) Dual RNA sequencing of a co-culture model of Pseudomonas aeruginosa and human 2D upper airway organoids. Scientific reports, 15(1), 2222.

Liu S, et al. (2025) Multi-Omics Analysis for Identifying Cell-Type-Specific Druggable Targets in Alzheimer's Disease. medRxiv : the preprint server for health sciences.

James M, et al. (2025) Multi-scale phenotyping of senescence-related changes in roots of rapeseed in response to nitrate limitation. Journal of experimental botany, 76(2), 312.

Thanasukarn V, et al. (2025) Discovery of novel serum peptide biomarkers for cholangiocarcinoma recurrence through MALDI-TOF MS and LC-MS/MS peptidome analysis. Scientific reports, 15(1), 2582.

Ehn E, et al. (2025) A de novo, mosaic and complex chromosome 21 rearrangement causes APP triplication and familial autosomal dominant early onset Alzheimer disease. Scientific reports, 15(1), 2912.

Shumanska M, et al. (2025) Mitochondrial calcium uniporter complex controls T-cellmediated immune responses. EMBO reports, 26(2), 407.

Ye L, et al. (2025) Multi?omics identification of a novel signature for serous ovarian carcinoma in the context of 3P medicine and based on twelve programmed cell death patterns: a multi-cohort machine learning study. Molecular medicine (Cambridge, Mass.), 31(1), 5.

Shang L, et al. (2025) Statistical identification of cell type-specific spatially variable genes in spatial transcriptomics. Nature communications, 16(1), 1059.

Li W, et al. (2025) Integrating proteomics and metabolomics to elucidate the regulatory mechanisms of pimpled egg production in chickens: Multi-omics analysis of the mechanism of pimpled egg formation. Poultry science, 104(2), 104818.

Guo Q, et al. (2025) Systemic factors associated with antler growth promote complete wound healing. NPJ Regenerative medicine, 10(1), 4.

Li J, et al. (2025) A noncanonical role of roX RNAs in autosomal epigenetic repression. Nature communications, 16(1), 155.

Zhou N, et al. (2025) Proteomic patterns associated with ketamine response in major depressive disorders. Cell biology and toxicology, 41(1), 26.

Ries F, et al. (2025) A truncated variant of the ribosome-associated trigger factor specifically contributes to plant chloroplast ribosome biogenesis. Nature communications, 16(1), 629.

Abdelazim AA, et al. (2025) In-silico screening and analysis of missense SNPs in human CYP3A4/5 affecting drug-enzyme interactions of FDA-approved COVID-19 antiviral drugs. Scientific reports, 15(1), 2153.