

Resource Summary Report

Generated by [kravitz2](#) on Jul 30, 2026

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., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

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: service resource, data analysis service, ontology, controlled vocabulary, data or information resource, database, production service resource, analysis service 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: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: PANTHER

Resource ID: SCR_004869

Alternate IDs: SCR_015893, nlx_84521

Record Creation Time: 20220129T080227+0000

Record Last Update: 20260731T042704+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: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 8331 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Kohsar A, et al. (2026) Comprehensive analysis of spinal cord inflammatory factors in HIV Tat-induced neuropathy in mice. Neuroscience, 595, 205.

Li X, et al. (2026) Dynamic transcriptomic landscape of myogenesis in Muscovy ducks (Cairina moschata): integrative analysis of hub genes post-hatching. Animal bioscience, 39(1), 250159.

Durmaz E, et al. (2026) R-28 cell-derived extracellular vesicles protect retinal ganglion cells in glaucoma. Neural regeneration research, 21(5), 2073.

Huttunen M, et al. (2026) Canine parvovirus infection affects host cell nucleolar organization and ribosome biogenesis. Communications biology, 9(1), 10.

Li JG, et al. (2026) Auranofin potentiates linezolid activity against MRSA by disrupting redox homeostasis and inhibiting SarA-mediated virulence and biofilm. Virulence, 17(1), 2605759.

Respekta-D?ugosz N, et al. (2025) Integrated Transcriptomic and Proteomic Analysis of Omentin-1 Effects on Primary Anterior Pituitary Cells From Different Pig Breeds: An In Vitro Study. FASEB journal : official publication of the Federation of American Societies for Experimental Biology, 39(19), e71081.

Magalhães J, et al. (2025) Rac1 inhibition prevents axonal cytoskeleton dysfunction in transthyretin amyloid polyneuropathy. Cell reports, 44(10), 116411.

Munyoki SK, et al. (2025) The microbiota extends the reproductive lifespan of mice by safeguarding the ovarian reserve. *Cell host & microbe*.

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

Castro-Arnau J, et al. (2025) Post-testicular spermatozoa of a marine teleost can conduct de novo cytoplasmic and mitochondrial translation. *iScience*, 28(1), 111537.

van Hooff JJE, et al. (2025) Repeated duplications and losses shaped SMC complex evolution from archaeal ancestors to modern eukaryotes. *Cell reports*, 44(7), 115855.

Zhang F, et al. (2025) The ESCRT protein CHMP5 restricts bone formation by controlling endolysosome-mitochondrion-mediated cell senescence. *eLife*, 13.

Lee H, et al. (2025) Hi-GDT: A Hi-C-based 3D gene domain analysis tool for analyzing local chromatin contacts in plants. *GigaScience*, 14.

Mu W, et al. (2025) The haplotype-resolved T2T genome for *Bauhinia × blakeana* sheds light on the genetic basis of flower heterosis. *GigaScience*, 14.

Noor H, et al. (2025) Response to Antiangiogenic Therapy Is Associated with AIMP Protein Family Expression in Glioblastoma and Lower-Grade Gliomas. *Cancer research communications*, 5(9), 1651.

Seo S, et al. (2025) Allelic bias contributes to heterogeneous phenotypes of NK cell deficiency. *Cell reports*, 44(8), 116102.

Zhao YJ, et al. (2025) An endogenous aryl hydrocarbon receptor ligand dysregulates endothelial functions, transcriptome, and phosphoproteome. *American journal of physiology. Cell physiology*, 328(3), C954.

Miller AK, et al. (2025) Formalin-fixed paraffin-embedded (FFPE) samples help to investigate transcriptomic responses in wildlife disease. *Molecular ecology resources*, 25(5), e13805.

Cummins MJ, et al. (2025) Aging disrupts blood-brain and blood-spinal cord barrier homeostasis, but does not increase paracellular permeability. *GeroScience*, 47(1), 263.

Monteiro JPC, et al. (2025) Expression patterns of melanin-related genes are linked to crypsis and conspicuousness in a pumpkin toadlet. *Molecular ecology*, 34(15), e17458.