

Resource Summary Report

Generated by [RRID](#) on Sep 10, 2026

PANTHER

RRID:SCR_004869

Type: Tool

Proper Citation

PANTHER (RRID:SCR_004869)

Resource Information

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

Proper Citation: PANTHER (RRID:SCR_004869)

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: analysis service resource, controlled vocabulary, data analysis service, data or information resource, database, ontology, production service resource, 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: 20260905T132525+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 8830 mentions in open access literature.

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

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

Trivedi R, et al. (2026) Annexin A2-dependent extracellular vesicle proteome modulates pre-metastatic stromal fibroblast behavior in triple-negative breast cancer. Cell communication and signaling : CCS, 24(1).

Kamimae-Lanning AN, et al. (2026) Metabolite-induced DNA damage drives stochastic stem cell loss and clonal hematopoiesis. Cell stem cell, 33(4), 642.

Wu X, et al. (2026) Locus-Specific Human Endogenous Retrovirus ERVK18 Expression Indicates an Inflamed Microenvironment and Favorable Immunotherapy Outcome in Small Cell Lung Cancer. Clinical cancer research : an official journal of the American Association for Cancer Research, 32(11), 2214.

Hung HF, et al. (2026) Centrosome linker protein CEP68 modulates cellular stress responses via nuclear condensate formation and HSP27 interaction. iScience, 29(7), 116491.

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

Chu CY, et al. (2026) Protein C-terminal variations impact proteostasis. Nature communications, 17(1).

Bot??a M, et al. (2026) Potential new biomarkers in pig saliva for differentiating between the effects of different conditions of mixing and density at pre-slaughter: A preliminary proteomic study. *Animal welfare* (South Mimms, England), 35, e4.

Garcia Romeu H, et al. (2026) Organelle Sorting and Proteomic Analysis to Identify Proteins Involved in the Uptake and Intracellular Trafficking of Nanoparticles. *Small methods*, 10(3), e02004.

Zhang Z, et al. (2026) Turbo-RIP: A Protocol for TurboID-based RNA Immunopurification to Map RNA Landscapes in Plant Biomolecular Condensates. *Bio-protocol*, 16(3), e5587.

Pershing NL, et al. (2026) A prophage-encoded sRNA limits phage infection of adherent-invasive *E. coli*. *PLoS pathogens*, 22(1), e1013836.

Mogielnicka-Brzozowska M, et al. (2026) Potential Proteins Associated with Canine Epididymal Sperm Motility. *Cells*, 15(1).

Chen Y, et al. (2026) Farnesyltransferase Deficiency in Cardiomyocytes Initiates Senescence and Contributes to Cardiac Fibrosis. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(26), e11530.

Kitoh R, et al. (2026) Inflammation and Oxidative-Stress Pathways Are Associated with Idiopathic Sudden Hearing Loss: A Genome-Wide Association Study in 15,494 Japanese Individuals. *International journal of molecular sciences*, 27(4).

Zhao J, et al. (2026) Screening and Preliminary Validation of Parthanatos-Related Key Genes in Asthma Using Transcriptomic and Machine Learning Approaches. *Journal of inflammation research*, 19, 557154.

Queme B, et al. (2026) From SNPs to Pathways: A genome-wide benchmark of annotation discrepancies and their impact on protein- and pathway-level inference. *bioRxiv : the preprint server for biology*.

Barreto AD, et al. (2026) Discovery of kidney disease targets using multimodal human podocyte injury models. *Stem cell reports*, 21(4), 102868.

Lorenz K, et al. (2026) Tonsillar expression quantitative trait loci verify and expand genetic contributors to childhood atopic diseases. *bioRxiv : the preprint server for biology*.

Akkour K, et al. (2026) Proteomic Profiling of Endometrial Cancer Tissues Reveals Differential Expression of Proteomes in Obese Versus Non-Obese Patients. *Cells*, 15(6).

Liu Y, et al. (2026) Gingiva-Derived Decellularised Extracellular Matrix Hydrogel Supports Osteogenic and Angiogenic Phenotypes of 3D STRO-1+ GMSC/HUVEC Spheroids In Vitro. *International dental journal*, 76(4), 109603.