

Resource Summary Report

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Harmonizome

RRID:SCR_016176

Type: Tool

Proper Citation

Harmonizome (RRID:SCR_016176)

Resource Information

URL: <http://amp.pharm.mssm.edu/Harmonizome/>

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Description: Web application that allows for searching, visualization, and prediction about genes and proteins. It contains a collection of processed datasets gathered to serve and mine knowledge about genes and proteins from major online resources.

Resource Type: data or information resource, data processing software, data visualization software, database, software application, software resource, web application

Defining Citation: [PMID:27374120](#)

Keywords: gene, protein, visualization, search, prediction, functional

Funding: BD2K-LINCS Data Coordination and Integration Center ;
Illuminating the Druggable Genome ;
Knowledge Management Center ;
NCI U54 CA189201;
NHLBI U54 HL127624;
NIGMS R01 GM098316

Availability: Freely available, Free, Available for download

Resource Name: Harmonizome

Resource ID: SCR_016176

Record Creation Time: 20220129T080329+0000

Record Last Update: 20260905T132804+0000

Ratings and Alerts

No rating or validation information has been found for Harmonizome.

No alerts have been found for Harmonizome.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 142 mentions in open access literature.

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

He J, et al. (2026) GPX7 marks fibroblast-associated stromal-innate immune crosstalk in ulcerative colitis. *Frontiers in immunology*, 17, 1856998.

Pruitt A, et al. (2026) Estradiol modulates neuronal network hyperexcitability in select NDD risk genes. *bioRxiv : the preprint server for biology*.

Su Y, et al. (2026) Systematic modeling predicts synergistic and safe drug combinations for parasitic diseases. *PLoS neglected tropical diseases*, 20(2), e0013991.

Strey K, et al. (2026) Computational identification of novel therapeutic candidates for *Streptococcus pyogenes* and influenza A coinfections through transcriptomic-based drug repositioning. *BMC microbiology*, 26(1).

Moberget T, et al. (2026) The genetic architecture of human cerebellar morphology supports a key role for the cerebellum in human evolution and psychopathology. *Communications biology*, 9(1).

Jackson-Strong M, et al. (2026) GATA2 controls alveolar macrophage inflammatory gene expression and metabolic function. *JCI insight*, 11(7).

Liu YW, et al. (2026) Integrative Analysis of Glycosylation-Related Genes Reveals Prognostic Subtypes, Immune Evasion, and Therapeutic Vulnerabilities in Lung Adenocarcinoma. *Oncology research*, 34(7), 18.

Srinivasan D, et al. (2026) DKK3 Initially Preserves Acinar Integrity Through MEK-Fos Signaling, but Later Switches to an Oncogenic Role in Pancreatic Cancer. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 13(3), e17606.

Okubo R, et al. (2026) Mixing features of transcription factors and genes enable accurate prediction of gene regulation relationships for unknown transcription factors. *NAR genomics and bioinformatics*, 8(1), lqag022.

Maher S, et al. (2026) MYCN inhibits TrkC-mediated differentiation in neuroblastoma cells via disruption of the PKA signalling pathway. *Cell death discovery*, 12(1).

Anjum SH, et al. (2026) Cerebral Venous Thrombosis in Previously Healthy Patients with Cryptococcal Meningitis. *The Journal of infectious diseases*, 233(2), e561.

Nakayama C, et al. (2026) NELF prevents transcriptional readthrough into DNA replication zones in cancer cells. *EMBO reports*, 27(7), 1720.

Zeller I, et al. (2025) Age-dependent gene expression trajectories during early childhood in children at increased risk for type 1 diabetes. *Genes and immunity*, 26(2), 173.

Yunes-Leites PS, et al. (2025) Phosphatase-independent activity of smooth-muscle calcineurin orchestrates a gene expression program leading to hypertension. *PLoS biology*, 23(5), e3003163.

Padam KSR, et al. (2025) Multifaceted regulation of the HOX cluster and its implications in oral cancer. *Clinical epigenetics*, 17(1), 126.

Qian Y, et al. (2025) Multi-omics analysis of the effects of pla2g4a on the prognosis of various cancers and its experimental validation in breast cancer cell lines. *Discover oncology*, 16(1), 1278.

Park IY, et al. (2025) A novel cardiomyopathy phenotype linked to a CHD7 missense variant. *Scientific reports*, 15(1), 19429.

Ott R, et al. (2025) Blood methylome signatures in children exposed to maternal type 1 diabetes are linked to protection against islet autoimmunity. *Nature metabolism*, 7(11), 2236.

Okano LM, et al. (2025) Identification of Epigenetic Regulatory Networks of Gene Methylation-miRNA-Transcription Factor Feed-Forward Loops in Basal-like Breast Cancer. *Cells*, 14(16).

Gao M, et al. (2025) Targeting the KLF5/PI3K/AKT axis as a therapeutic strategy to overcome neoadjuvant chemoresistance in colorectal cancer. *Frontiers in immunology*, 16, 1593639.