

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 processing software, software resource, software application, web application, data visualization software, database, data or information resource

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 ;
NIGMS R01 GM098316;
NHLBI U54 HL127624;
NCI U54 CA189201

Availability: Freely available, Free, Available for download

Resource Name: Harmonizome

Resource ID: SCR_016176

Record Creation Time: 20220129T080329+0000

Record Last Update: 20260805T044350+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 127 mentions in open access literature.

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

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.

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

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.

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.

Zeng C, et al. (2025) Integrated bulk and single-cell transcriptomic analysis unveiled a novel cuproptosis-related lipid metabolism gene molecular pattern and a risk index for predicting prognosis and antitumor drug sensitivity in breast cancer. *Discover oncology*, 16(1), 318.

Viesi E, et al. (2025) APBIO: bioactive profiling of air pollutants through inferred bioactivity signatures and prediction of novel target interactions. *Journal of cheminformatics*, 17(1), 13.

Oshaghi S, et al. (2025) The 3D nuclear position and compartmentalization of genes prime their response to mechano-confinement. *bioRxiv : the preprint server for biology*.

Zhou X, et al. (2025) Identification of a novel anoikis-related gene signature to predict prognosis and tumor microenvironment in intrahepatic cholangiocarcinoma carcinoma. *Discover oncology*, 16(1), 1051.

Panjabud P, et al. (2025) Prenatal exposure to bisphenol A disrupts RNA splicing in the prefrontal cortex and promotes behaviors related to autism in offspring. *Scientific reports*, 15(1), 25996.

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.

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).

Chow JT, et al. (2025) A microRNA CRISPR screen reveals microRNA-483-3p as an apoptotic regulator in prostate cancer cells. *Cell death & disease*, 16(1), 752.

Lin L, et al. (2025) Single-cell profiling reveals a reduced epithelial defense system, decreased immune responses and the immune regulatory roles of different fibroblast subpopulations in chronic atrophic gastritis. *Journal of translational medicine*, 23(1), 159.

Diamant I, et al. (2025) Harmonizome 3.0: integrated knowledge about genes and proteins from diverse multi-omics resources. *Nucleic acids research*, 53(D1), D1016.

Mogire RM, et al. (2025) OSBPL11 is an African-specific locus associated with 25-hydroxyvitamin D concentrations and cardiometabolic health. *medRxiv : the preprint server for health sciences*.

Liu X, et al. (2025) Construction of a prognostic model for lung adenocarcinoma based on necroptosis genes and its exploration of the potential for tumor immunotherapy. *Translational cancer research*, 14(5), 2563.

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

Metzner E, et al. (2025) Multiome Perturb-seq unlocks scalable discovery of integrated perturbation effects on the transcriptome and epigenome. *Cell systems*, 16(1), 101161.