

# Resource Summary Report

Generated by [RRID](#) on Aug 12, 2026

## Open Targets Platform

RRID:SCR\_021702

Type: Tool

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### Proper Citation

Open Targets Platform (RRID:SCR\_021702)

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### Resource Information

**URL:** <https://platform.opentargets.org/>

**Proper Citation:** Open Targets Platform (RRID:SCR\_021702)

**Description:** Platform for supporting systematic drug–target identification and prioritisation. Provides users with queryable knowledgebase and user interface to aid systematic target identification and prioritisation for drug discovery based upon underlying evidence.

**Resource Type:** data or information resource, service resource

**Defining Citation:** [DOI:10.1093/nar/gkaa1027](https://doi.org/10.1093/nar/gkaa1027)

**Keywords:** Evidence based systematic prioritisation, targets for disease treatment, drug–target identification, drug discovery

**Availability:** Free, Freely available

**Resource Name:** Open Targets Platform

**Resource ID:** SCR\_021702

**Alternate URLs:** <https://www.targetvalidation.org/>

**Record Creation Time:** 20220129T080357+0000

**Record Last Update:** 20260808T190218+0000

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### Ratings and Alerts

No rating or validation information has been found for Open Targets Platform.

No alerts have been found for Open Targets Platform.

## Data and Source Information

**Source:** [SciCrunch Registry](#)

## Usage and Citation Metrics

We found 173 mentions in open access literature.

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

Li H, et al. (2026) Identification of Treatment Targets in Allergic Conjunctivitis Through Proteome-Scale Mendelian Randomization Analysis. *Mediators of inflammation*, 2026, 6432686.

Preziosa P, et al. (2026) Spatial gene expression and functional network abnormalities in multiple sclerosis: exploring biological influence on brain functional reorganization. *Translational psychiatry*, 16(1).

Prakash O, et al. (2026) A network-driven computational framework for identifying FDA-approved drug repurposing across heterogeneous brain cancers. *Frontiers in molecular biosciences*, 13, 1768081.

Zhang H, et al. (2026) Single-cell transcriptome-wide Mendelian randomization during CD4+ T cell activation reveals immune-mediated mechanisms and drug targets for neuropsychiatric disorders. *Communications biology*, 9(1).

Zhang Q, et al. (2026) Genome-wide investigation highlights global and local pleiotropy linking neurodevelopmental disorders to acquired hearing problems. *Psychological medicine*, 56, e32.

Reales G, et al. (2026) Design and interpretation of eQTL-GWAS colocalisation studies: Lessons from a large-scale evaluation. *PLoS genetics*, 22(5), e1012141.

Wei S, et al. (2026) KG-bench: benchmarking graph neural network algorithms for drug repurposing. *Bioinformatics (Oxford, England)*, 42(5).

Fu S, et al. (2026) IRF7 is a novel prognostic biomarker in kidney renal clear cell carcinoma. *Scientific reports*, 16(1), 5523.

Scartozzi AC, et al. (2026) Genome-wide investigation of prosody perception: Shared genetic influences between speech rhythm, musical rhythm, and reading traits. *HGG advances*, 7(3), 100581.

Tsepilov YA, et al. (2026) The Human Pleiotropic Map of GWAS Associations and Therapeutic Implications. *bioRxiv : the preprint server for biology*.

Zhang X, et al. (2026) Single-Cell Transcriptome-Wide Mendelian Randomization and Colocalization Uncover Potential Immunocytes-Related Therapeutic Targets for Obesity. *Journal of cellular and molecular medicine*, 30(9), e71185.

Lin M, et al. (2026) Network pharmacology and molecular dynamics simulations reveal shared mechanisms and myopia-specific targets of atropine in myopia and dry eye disease. *Eye and vision (London, England)*, 13(1).

Al-Damook N, et al. (2026) Mapping metabolic reprogramming in lung and breast cancer through integrative bioinformatics. *PloS one*, 21(6), e0350628.

Mei H, et al. (2026) IL3RA identified as novel biomarker and therapeutic target for ER+ breast cancer through plasma proteome-wide mendelian randomization and TCGA database analysis. *Clinical proteomics*, 23(1).

Shaukat M, et al. (2026) Heritable pulmonary arterial hypertension: new genetic findings and environmental triggers. *Scientific reports*, 16(1), 4121.

Xu J, et al. (2026) Large-Scaled Proteomics Analysis for Glaucoma: Integrated Genetics, Multi-Omics, UK Biobank and Therapeutic Analysis. *Investigative ophthalmology & visual science*, 67(2), 4.

Kramarenko DR, et al. (2026) Leveraging the shared and opposing genetic mechanisms in the heritable cardiomyopathies. *Research square*.

Ma X, et al. (2026) Coptidis Rhizoma Alkaloids Alleviate Acetaminophen-Induced Liver Injury by Regulating GSH Metabolism and the TNF Signaling Pathway. *Antioxidants (Basel, Switzerland)*, 15(2).

Zeng D, et al. (2026) Cell type-stratified immunogenetic framework reveals immune drivers and therapeutic targets in kidney stone disease. *Molecular therapy. Nucleic acids*, 37(2), 102964.

Laman Trip DS, et al. (2026) A tissue-specific atlas of protein-protein associations enables prioritization of candidate disease genes. *Nature biotechnology*, 44(4), 654.