

Resource Summary Report

Generated by [NIF](#) on Aug 10, 2026

Open Targets

RRID:SCR_014622

Type: Tool

Proper Citation

Open Targets (RRID:SCR_014622)

Resource Information

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

Proper Citation: Open Targets (RRID:SCR_014622)

Description: A public–private initiative that supports research that provides evidence on the biological validity of therapeutic targets and that gain insight into the effectiveness of pharmacological intervention. It aims to provide a research and development framework that applies human disease. It shares its information openly.

Synonyms: Centre for Therapeutic Target Validation, Center for Therapeutic Target Validation

Keywords: initiative, therapeutic, pharmacology, intervention, research and development, framework, man disease

Availability: Open, Can interact with companies

Resource Name: Open Targets

Resource ID: SCR_014622

Alternate URLs: <http://www.ebi.ac.uk/about/news/press-releases/open-targets-new-name-new-data#annotations:B-esfHqUEeaXCGe7nJasQw>

License URLs: <http://www.ebi.ac.uk/about/terms-of-use>
<http://www.ebi.ac.uk/about/privacy>

Record Creation Time: 20220129T080321+0000

Record Last Update: 20260808T190028+0000

Ratings and Alerts

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

No alerts have been found for Open Targets.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 143 mentions in open access literature.

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

Deutsch EW, et al. (2026) The ProteomeXchange consortium in 2026: making proteomics data FAIR. *Nucleic acids research*, 54(D1), D459.

Mitsumori R, et al. (2026) Genome and transcriptome-wide association studies identify multiple novel loci for dementia with grain in Japanese. *Journal of human genetics*, 71(5), 301.

Chen Z, et al. (2026) Mixed-model and transcriptome-wide association analyses identify transcription factors and genes associated with colorectal cancer susceptibility. *Nature communications*, 17(1), 1377.

Li Z, et al. (2026) Research on the molecular mechanism of celastrol targeting CTNNB1/STAT3 to inhibit uveal melanoma based on network pharmacology and multi-omics analysis. *Scientific reports*, 16(1), 6140.

Duggan MR, et al. (2026) CMV titer associations with cognition and the plasma proteome implicate FLT1 and neurovascular mechanisms as potential moderators. *Journal of neuroinflammation*, 23(1).

Kalidass B, et al. (2026) In Silico Profiling of Phytochemicals for Modulating Amyloid Beta-Mediated Immune Regulation and Neuroinflammation in Alzheimer's Disease. *ACS omega*, 11(9), 14947.

Alayash Z, et al. (2026) Proteome-Guided Drug Target Discovery for Periodontitis. *Journal of clinical periodontology*, 53(1), 127.

Lindbohm JV, et al. (2026) Population and single-cell analyses reveal immune cell-specific expression profiles associated with Alzheimer's disease risk. *Alzheimer's & dementia : the journal of the Alzheimer's Association*, 22(3), e71282.

Ravichandran P, et al. (2025) Spatiomolecular mapping reveals anatomical organization of heterogeneous cell types in the human nucleus accumbens. *bioRxiv : the preprint server for biology*.

Ma W, et al. (2025) Prognostic and immunotherapeutic significance of NCAPD2 in pan-cancer and its role in hepatocellular carcinoma progression via the AKT/GSK-3 β signaling

pathway. Scientific reports, 15(1), 21675.

Yuan Y, et al. (2025) Profiling of immune cell subsets and functional characteristics of cervical cancer based on single cell RNA sequencing. Frontiers in immunology, 16, 1658705.

Lerga-Jaso J, et al. (2025) Tracing human genetic histories and natural selection with precise local ancestry inference. Nature communications, 16(1), 4576.

Greenwood E, et al. (2025) Haplotype rather than single causal variants effects contribute to regulatory gene expression associations in human myeloid cells. bioRxiv : the preprint server for biology.

Cruz-Castillo C, et al. (2025) Associations on the Fly, a new feature aiming to facilitate exploration of the Open Targets Platform evidence. Bioinformatics (Oxford, England), 41(4).

Buniello A, et al. (2025) Open Targets Platform: facilitating therapeutic hypotheses building in drug discovery. Nucleic acids research, 53(D1), D1467.

Enzan N, et al. (2025) Genome-wide analysis of heart failure yields insights into disease heterogeneity and enables prognostic prediction in the Japanese population. Nature communications, 16(1), 9680.

Avocegamou R, et al. (2025) Proteome-wide mendelian randomization reveals circulating proteins causally associated with childhood body mass index. Scientific reports, 16(1), 2093.

Lorenz A, et al. (2025) The effect of Alzheimer's disease genetic factors on limbic white matter microstructure. Alzheimer's & dementia : the journal of the Alzheimer's Association, 21(4), e70130.

Güler M, et al. (2025) Clustering of lymphoid neoplasms by cell of origin, somatic mutation and drug usage profiles: a multi-trait genome-wide association study. Blood cancer journal, 15(1), 147.

Hu S, et al. (2025) Fine-scale population structure and widespread conservation of genetic effect sizes between human groups across traits. Nature genetics, 57(2), 379.