

Resource Summary Report

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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: 20260815T182507+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](#) .

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.

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.

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.

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

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.

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*.

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).

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*.

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.

Evans LD, et al. (2025) Tau uptake by human neurons depends on receptor LRP1 and kinase LRRK2. *The EMBO journal*, 44(18), 5149.

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.