

Resource Summary Report

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Broad Institute

RRID:SCR_007073

Type: Tool

Proper Citation

Broad Institute (RRID:SCR_007073)

Resource Information

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

Proper Citation: Broad Institute (RRID:SCR_007073)

Description: Biomedical and genomic research center located in Cambridge, Massachusetts, United States. Nonprofit research organization under the name Broad Institute Inc., and is partners with Massachusetts Institute of Technology, Harvard University, and the five Harvard teaching hospitals. Dedicated to advance understanding of biology and treatment of human disease to improve human health.

Abbreviations: Broad

Synonyms: Broad Institute of MIT and Harvard, Broad Institute Inc.

Resource Type: institution

Keywords: biomedical, genomic, research, center, nonprofit, organization, human, biology, disease

Funding: Eli and Edythe Broad ; individual donors

Resource Name: Broad Institute

Resource ID: SCR_007073

Alternate IDs: nif-0000-31438, grid.66859.34, Wikidata: Q4971893

Alternate URLs: <https://ror.org/05a0ya142>

Record Creation Time: 20220129T080239+0000

Record Last Update: 20260801T190327+0000

Ratings and Alerts

No rating or validation information has been found for Broad Institute.

No alerts have been found for Broad Institute.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1897 mentions in open access literature.

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

Williams EC, et al. (2026) Expression of endogenous retroviral elements is associated with extracellular matrix remodeling in prostate cancer. *Mobile DNA*, 17(1), 1.

Huang X, et al. (2025) CDK4/6 Inhibition Reverses MEIS2 Suppression of CRL4 CRBN to Enhance Immunomodulatory Drug Therapy in Multiple Myeloma. *bioRxiv : the preprint server for biology*.

Chengalroyen MD, et al. (2025) Disruption of riboflavin biosynthesis in mycobacteria establishes riboflavin pathway intermediates as key precursors of MAIT cell agonists. *PLoS pathogens*, 21(7), e1012632.

Zhang Y, et al. (2025) Machine learning-based prediction model for lung ischemia-reperfusion injury: insights from disulfidptosis-related genes. *Frontiers in pharmacology*, 16, 1545111.

Wang Z, et al. (2025) Mechanism of NUMBL enhancing axitinib resistance in clear cell renal cell carcinoma by UCHL1-mediated deubiquitination of MMP9. *The Journal of biological chemistry*, 301(12), 110873.

Yao X, et al. (2025) Exploring the Mechanisms Linking Depression and Glaucoma: A Cohort Study of UK Biobank. *Translational vision science & technology*, 14(7), 5.

Kaushal K, et al. (2025) Ubiquitin specific protease 7 deubiquitinates and regulates Aurora B-mediated cytokinesis. *BMB reports*, 58(8), 350.

Zhang X, et al. (2025) LPIN3 promotes colorectal cancer growth by dampening intratumoral CD8+ T cell effector function. *Cancer immunology, immunotherapy : CII*, 74(4), 135.

Mohamed Ismail N, et al. (2025) A new ANMerge-based blood transcriptomic resource to support Alzheimer's disease research. *medRxiv : the preprint server for health sciences*.

Peng T, et al. (2025) Multi-omics integration analysis identifies INPP4B as a T-cell-specific activation suppressor. *Clinical and translational medicine*, 15(8), e70430.

Li G, et al. (2025) Discovery and validation of proliferative exhausted T cells as a favorable prognostic biomarker in esophageal squamous cell carcinoma. *Scientific reports*, 15(1), 41619.

Mohmed MM, et al. (2025) Genomic profiling of AKT1 and NRAS mutations using NGS in Egyptian hepatocellular carcinoma. *Discover oncology*, 16(1), 2191.

Del Burgo FG, et al. (2025) The chromatin reader Dido3 is a regulator of the gene network that controls B cell differentiation. *Cell & bioscience*, 15(1), 56.

Temme N, et al. (2025) Host-induced gene silencing of the amino acid biosynthesis gene acetolactate synthase of *Phytophthora infestans* caused strong enhanced late blight resistance of potato in the field. *Plant biotechnology journal*, 23(8), 3054.

Bi J, et al. (2025) Systematic decoding of functional enhancer connectomes and risk variants in human glioma. *Nature cell biology*, 27(10), 1838.

Katayama M, et al. (2025) Exercise-induced methylation of the *Serhl2* promoter and implication for lipid metabolism in rat skeletal muscle. *Molecular metabolism*, 92, 102081.

Forissier V, et al. (2025) The LRP4/YAP axis drives the radiation-tolerant persister (RTP) cell state in breast cancer. *Theranostics*, 15(15), 7528.

Tao J, et al. (2025) Prognostic and immunological implications of cathepsin Z overexpression in prostate cancer. *Frontiers in immunology*, 16, 1618487.

Starrett GJ, et al. (2024) Multiomics Profiling Distinguishes Sebaceous Carcinoma from Benign Sebaceous Neoplasms and Provides Insight into the Genetic Evolution of Sebaceous Carcinogenesis. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 30(21), 4887.

Plitt G, et al. (2024) The Genomic Landscape of Benign and Malignant Thyroid Tumors from Individuals Carrying Germline PTEN Variants Is Distinct from Sporadic Thyroid Cancers. *Cancer research*, 84(21), 3657.