Resource Summary Report

Generated by RRID on Aug 6, 2026

Proteomic Data Commons

RRID:SCR_018273
Type: Tool

Proper Citation

Proteomic Data Commons (RRID:SCR_018273)

Resource Information

URL: https://pdc.cancer.gov/pdc/

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Description: Portal to make cancer related proteomic datasets easily accessible to public. Facilitates multiomic integration in support of precision medicine through interoperability with other resources. Developed to advance our understanding of how proteins help to shape risk, diagnosis, development, progression, and treatment of cancer. One of several repositories within NCI Cancer Research Data Commons which enables researchers to link proteomic data with other data sets (e.g., genomic and imaging data) and to submit, collect, analyze, store, and share data throughout cancer data ecosystem. PDC provides access to highly curated and standardized biospecimen, clinical, and proteomic data, intuitive interface to filter, query, search, visualize and download data and metadata. Provides common data harmonization pipeline to uniformly analyze all PDC data and provides advanced visualization of quantitative information. Cloud based (Amazon Web Services) infrastructure facilitates interoperability with AWS based data analysis tools and platforms natively. Application programming interface (API) provides cloud-agnostic data access and allows third parties to extend functionality beyond PDC. Structured workspace that serves as private user data store and also data submission portal. Distributes controlled access data, such as patient-specific protein fasta sequence databases, with dbGaP authorization and eRA Commons authentication.

Abbreviations: PDC

Resource Type: data or information resource, data repository, database, storage service resource, production service resource, service resource, analysis service resource

Keywords: Cancer, proteomic, data, precision medicine, diagnosis, treatment, analysis, biospeciment, clinical data, metadata

Related Condition: cancer

Availability: Restricted

Resource Name: Proteomic Data Commons

Resource ID: SCR_018273

Record Creation Time: 20220129T080339+0000

Record Last Update: 20260806T054701+0000

Ratings and Alerts

No rating or validation information has been found for Proteomic Data Commons.

No alerts have been found for Proteomic Data Commons.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 66 mentions in open access literature.

Listed below are recent publications. The full list is available at RRID .

Zhang J, et al. (2025) TRIM22 promotes glioblastoma development by ubiquitinating Bcl-2. Molecular & cellular oncology, 12(1), 2518679.

Wei X, et al. (2025) Knockdown of ACC1 promotes migration and invasion of U251 glioma cells by epigenetically suppressing SDH. International journal of oncology, 67(3).

Wang Y, et al. (2025) iDDN: determining trans-omics network structure and rewiring with integrative differential dependency networks. Bioinformatics advances, 5(1), vbaf086.

Tran D, et al. (2025) DSCC: disease subtyping using spectral clustering and community detection from consensus networks. Briefings in bioinformatics, 26(6).

Wen B, et al. (2025) DeepMVP: deep learning models trained on high-quality data accurately predict PTM sites and variant-induced alterations. Nature methods, 22(9), 1857.

Hyeon DY, et al. (2025) Proteogenomic characterization of molecular and cellular targets for treatment-resistant subtypes in locally advanced cervical cancers. Molecular cancer, 24(1), 77.

Li D, et al. (2025) Integrative pan-cancer analysis and experiment validation identified GLS as a biomarker in tumor progression, prognosis, immune microenvironment, and immunotherapy. Scientific reports, 15(1), 525.

Meng K, et al. (2025) The cryptic lncRNA-encoded microprotein TPM3P9 drives oncogenic RNA splicing and tumorigenesis. Signal transduction and targeted therapy,

10(1), 43.

Ivanisenko NV, et al. (2025) Oligomerised RIPK1 is the main core component of the CD95 necrosome. The EMBO journal, 44(11), 3231.

Wang F, et al. (2025) Identification of SURF4 and RALGAPA1 as promising therapeutic targets in glioblastoma and pan-cancer through integrative multi-omics, CRISPR-Cas9 screening and prognostic meta-analysis. Cancer immunology, immunotherapy : CII, 74(6), 175.

Chang HY, et al. (2025) Analysis of isobaric quantitative proteomic data using TMT-Integrator and FragPipe computational platform. bioRxiv : the preprint server for biology.

Ren Y, et al. (2025) A multi-omics atlas of CAF subtypes reveals apCAF-M2 macrophage interactions driving immune resistance in glioma. PloS one, 20(8), e0329801.

Li H, et al. (2025) A Pan-Cancer Study of Tumour-Associated Efferocytosis Core Genes and Preliminary Exploration of TIMD4 in Renal Cell Carcinoma. Journal of cellular and molecular medicine, 29(12), e70671.

Lee DKC, et al. (2025) ITGAV and SMAD4 influence the progression and clinical outcome of pancreatic ductal adenocarcinoma. Molecular oncology.

Xie H, et al. (2025) Development of a novel 4-protein signature for prognostic prediction in hepatitis B virus-induced hepatocellular carcinoma. Discover oncology, 16(1), 1835.

Ma L, et al. (2025) Bioinformatics approaches to multi-omics analysis of the potential of CDKN2A as a biomarker and therapeutic target for uterine corpus endometrial carcinoma. Scientific reports, 15(1), 895.

Hu GS, et al. (2025) Integrated Analysis of Proteome and Transcriptome Profiling Reveals Pan-Cancer-Associated Pathways and Molecular Biomarkers. Molecular & cellular proteomics : MCP, 24(3), 100919.

Zhang H, et al. (2025) Glycoprotein-Notebook: A Pan-Cancer Glycoproteomic Database and Toolkit for Analysis of Protein Glycosylation Changes Associated With Cancer Phenotypes. Molecular & cellular proteomics : MCP, 24(11), 101089.

Lin Q, et al. (2025) Cancer Biology of GSPT1: Mechanisms and Targeted Therapy Opportunities of Molecular Glue Degraders. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(47), e11789.

Luo X, et al. (2025) IGF2BP3 recruits NUDT21 to regulate SPTBN1 alternative polyadenylation and drive ovarian cancer progression. Communications biology, 8(1), 680.