Resource Summary Report

Generated by NIF on Aug 9, 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, production service resource, database, analysis service resource, service resource, storage service resource, data repository

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: 20260808T190102+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 102 mentions in open access literature.

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

Shi X, et al. (2026) Integrative proteomic characterization of human lung adenocarcinoma with KRAS G12 mutations reveals molecular pathogenesis. Journal of advanced research, 84, 675.

Shi H, et al. (2026) Multi-Omics Analysis of TYMS as a Prognostic Biomarker and Therapeutic Target for Lung Adenocarcinoma. Cancer medicine, 15(4), e71814.

Wang Y, et al. (2026) Stromal NNMT overexpression as an independent prognostic biomarker in lung adenocarcinoma and breast carcinoma. Carcinogenesis, 47(2).

Deng R, et al. (2026) Integrated multi-omics analysis and functional validation reveal the role of TRIM2 as a potential novel biomarker in breast cancer. Breast cancer research : BCR, 28(1).

Liu C, et al. (2026) Identifying diagnostic markers and constructing a prognostic model for pancreatic cancer based on microarray and bioinformatic analysis. Discover oncology, 17(1).

Tran D, et al. (2026) CSIE: cancer subtyping via inference and ensemble. Briefings in bioinformatics, 27(3).

Yu Y, et al. (2026) NUDT21-mediated Alternative Polyadenylation of CDK19 Reprograms Cholesterol Biosynthesis to Drive Colorectal Cancer Progression. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 13(7), e18346.

Chen F, et al. (2026) Global impact of germline structural variation on the cancer proteome. Nature communications, 17(1).

Chen B, et al. (2026) Explainable multi-omics modeling for risk stratification in pancreatic ductal adenocarcinoma. Gland surgery, 15(4), 91.

Xue Z, et al. (2026) IRAK4 Regulates NF-?B signaling to suppress CD8 + T cell activity and promote immune evasion in glioblastoma development. Cancer immunology, immunotherapy : CII, 75(2), 53.

Xing L, et al. (2026) Transcriptional activation of PPP1R14C by KLF7 unleashes CDK1 activity to promote lung squamous cell carcinoma. Scientific reports, 16(1).

Chang HY, et al. (2026) Analysis of isobaric quantitative proteomic data using TMT-Integrator and FragPipe computational platform. Nature communications, 17(1).

Savani MR, et al. (2026) Nitrogen metabolism profiling reveals cell state-specific pyrimidine synthesis pathway choice. Nature metabolism, 8(5), 1124.

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

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

Lu D, et al. (2025) Comprehensive analysis reveals cholesterol metabolism-related signature for predicting prognosis and guiding individualized treatment of glioma. Heliyon, 11(1), e41601.

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).

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.

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