

Resource Summary Report

Generated by [dkNET](#) on Sep 20, 2026

Proteome Commons

RRID:SCR_006234

Type: Tool

Proper Citation

Proteome Commons (RRID:SCR_006234)

Resource Information

URL: <https://proteomecommons.org/>

Proper Citation: Proteome Commons (RRID:SCR_006234)

Description: THIS RESOURCE IS NO LONGER IN SERVICE, documented on July 17, 2013. A public resource for sharing general proteomics information including data (Tranche repository), tools, and news. Joining or creating a group/project provides tools and standards for collaboration, project management, data annotation, permissions, permanent storage, and publication.

Abbreviations: Proteome Commons

Synonyms: ProteomeCommons.org, ProteomeCommons

Resource Type: community building portal, data or information resource, data repository, database, portal, service resource, software resource, storage service resource

Defining Citation: [PMID:20356086](#)

Keywords: proteomics, protein, peptide, data sharing, data, tool, news, annotation, proteome, genome

Funding: NCI ;
Clinical Proteomics Technologies for Cancer ;
NCRR P41-RR018627

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Proteome Commons

Resource ID: SCR_006234

Alternate IDs: nlx_151800

Record Creation Time: 20220129T080235+0000

Record Last Update: 20260919T195106+0000

Ratings and Alerts

No rating or validation information has been found for Proteome Commons.

No alerts have been found for Proteome Commons.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 12 mentions in open access literature.

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

Mellacheruvu D, et al. (2013) The CRAPome: a contaminant repository for affinity purification-mass spectrometry data. *Nature methods*, 10(8), 730.

LeRoy G, et al. (2012) Proteogenomic characterization and mapping of nucleosomes decoded by Brd and HP1 proteins. *Genome biology*, 13(8), R68.

Wang H, et al. (2012) Chromatin-Associated Proteins Revealed by SILAC-Proteomic Analysis Exhibit a High Likelihood of Requirement for Growth Fitness under DNA Damage Stress. *International journal of proteomics*, 2012, 630409.

Chen ZW, et al. (2012) Deep amino acid sequencing of native brain GABAA receptors using high-resolution mass spectrometry. *Molecular & cellular proteomics : MCP*, 11(1), M111.011445.

Riley CP, et al. (2011) A large, consistent plasma proteomics data set from prospectively collected breast cancer patient and healthy volunteer samples. *Journal of translational medicine*, 9, 80.

Ueda K, et al. (2011) A comprehensive peptidome profiling technology for the identification of early detection biomarkers for lung adenocarcinoma. *PloS one*, 6(4), e18567.

Beck M, et al. (2011) The quantitative proteome of a human cell line. *Molecular systems biology*, 7, 549.

Tran TN, et al. (2011) Classification of ancient mammal individuals using dental pulp MALDI-TOF MS peptide profiling. *PloS one*, 6(2), e17319.

Khan Z, et al. (2011) Accurate proteome-wide protein quantification from high-resolution 15N mass spectra. *Genome biology*, 12(12), R122.

González-Fernández R, et al. (2010) Proteomics of plant pathogenic fungi. *Journal of biomedicine & biotechnology*, 2010, 932527.

Langille MG, et al. (2010) BioTorrents: a file sharing service for scientific data. *PloS one*, 5(4), e10071.

Yuan J, et al. (2009) Metabolomics-driven quantitative analysis of ammonia assimilation in *E. coli*. *Molecular systems biology*, 5, 302.