

Resource Summary Report

Generated by [ASWG](#) on Aug 2, 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: data or information resource, data repository, storage service resource, portal, database, service resource, community building portal, software 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: 20260801T190306+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 [ASWG](#) .

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.

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

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

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.