

# Resource Summary Report

Generated by [dkNET](#) on Aug 30, 2026

## Proteome Commons

RRID:SCR\_006234

Type: Tool

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### Proper Citation

Proteome Commons (RRID:SCR\_006234)

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### 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:** 20260829T182232+0000

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## Ratings and Alerts

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

No alerts have been found for Proteome Commons.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## 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.