

# Resource Summary Report

Generated by [nidm-terms](#) on Jul 31, 2026

## Protein Cross-Linking Database

RRID:SCR\_021027

Type: Tool

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### Proper Citation

Protein Cross-Linking Database (RRID:SCR\_021027)

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### Resource Information

**URL:** <https://proxl-ms.org/>

**Proper Citation:** Protein Cross-Linking Database (RRID:SCR\_021027)

**Description:** Web application and database designed for sharing, visualizing, and analyzing protein cross-linking mass spectrometry data with emphasis on structural analysis and quality control. Includes public and private data sharing capabilities, project based interface designed to ensure security and facilitate collaboration among multiple researchers. Used for private collaboration and public data dissemination.

**Abbreviations:** ProXL, proxl, Protein XL

**Synonyms:** Protein XL Database

**Resource Type:** data access protocol, software resource, web service, data or information resource, database

**Defining Citation:** [PMID:27302480](#)

**Keywords:** Protein cross-linking, mass spectrometry data, analysis, visualization, sharing, structural analysis, quality control, private collaboration, public data dissemination

**Funding:** NIGMS P41 GM103533;  
University of Washington Proteomics Resource

**Availability:** Free, Available for download, Freely available

**Resource Name:** Protein Cross-Linking Database

**Resource ID:** SCR\_021027

**Alternate URLs:** <https://github.com/yeastrc/proxl-web-app>

**License:** Apache License 2.0

**Record Creation Time:** 20220129T080353+0000

**Record Last Update:** 20260731T043054+0000

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## Ratings and Alerts

No rating or validation information has been found for Protein Cross-Linking Database.

No alerts have been found for Protein Cross-Linking Database.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 5 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [nidm-terms](#) .

Giannone C, et al. (2025) How J-chain ensures the assembly of immunoglobulin IgM pentamers. The EMBO journal, 44(2), 505.

Day M, et al. (2024) TopBP1 utilises a bipartite GINS binding mode to support genome replication. Nature communications, 15(1), 1797.

Klein BJ, et al. (2022) Taf2 mediates DNA binding of Taf14. Nature communications, 13(1), 3177.

Dahiya V, et al. (2022) The switch from client holding to folding in the Hsp70/Hsp90 chaperone machineries is regulated by a direct interplay between co-chaperones. Molecular cell, 82(8), 1543.

Brilot AF, et al. (2021) CM1-driven assembly and activation of yeast  $\gamma$ -tubulin small complex underlies microtubule nucleation. eLife, 10.