Resource Summary Report

Generated by dkNET on Apr 22, 2025

Protein Cross-Linking Database

RRID:SCR_021027
Type: Tool

Proper Citation

Protein Cross-Linking Database (RRID:SCR_021027)

Resource Information

URL: https://proxl-ms.org/

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

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: 20250422T060147+0000

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.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 5 mentions in open access literature.

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

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.

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.

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

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