

Resource Summary Report

Generated by [kravitz2](#) on Sep 5, 2026

Kojak

RRID:SCR_021028

Type: Tool

Proper Citation

Kojak (RRID:SCR_021028)

Resource Information

URL: <http://www.kojak-ms.org/>

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Description: Software tool for identification of cross-linked peptides from mass spectra. Used for analysis of chemically cross-linked protein complexes. Used to analyze both novel and existing data sets.

Resource Type: data analysis software, data processing software, software application, software resource

Defining Citation: [PMID:25812159](#)

Keywords: Mass spectra, cross-linked peptides identification, protein complexes analysis, novel data analysis, existing data analysis

Funding: National Science Foundation MRI grant 0923536;
NCRR S10 RR027584;
NIGMS P41 GM103533;
NIGMS P50 GM076547;
NIGMS P50 GM08722150

Availability: Free, Available for download, Freely available

Resource Name: Kojak

Resource ID: SCR_021028

Record Creation Time: 20220129T080353+0000

Record Last Update: 20260903T235703+0000

Ratings and Alerts

No rating or validation information has been found for Kojak.

No alerts have been found for Kojak.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

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 γ -tubulin small complex underlies microtubule nucleation. eLife, 10.

Popov KI, et al. (2019) Insight into the Structure of the "Unstructured" Tau Protein. Structure (London, England : 1993), 27(11), 1710.

Miller MP, et al. (2019) Kinetochore-associated Stu2 promotes chromosome biorientation in vivo. PLoS genetics, 15(10), e1008423.