

Resource Summary Report

Generated by [FDI Lab - SciCrunch.org](#) on Apr 22, 2025

xQuest

RRID:SCR_021006

Type: Tool

Proper Citation

xQuest (RRID:SCR_021006)

Resource Information

URL: <https://www.nature.com/articles/nmeth.1192>

Proper Citation: xQuest (RRID:SCR_021006)

Description: Resource no longer available. Documented on March 15, 2021. Software tool to identify cross-linked peptides from complex samples and large protein sequence databases by combining isotopically tagged cross-linkers, chromatographic enrichment, targeted proteomics. Reduces search space by upstream candidate peptide search before recombination step. Search engine for cross-linked peptides from complex samples.

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

Keywords: Cross-linked peptides identification, complex samples, protein sequence databases, candidate peptide search

Funding:

Availability: Resource no longer available. Documented on March 15, 2021

Resource Name: xQuest

Resource ID: SCR_021006

Old URLs: <http://www.xQuest.org>

Record Creation Time: 20220129T080353+0000

Record Last Update: 20250421T054328+0000

Ratings and Alerts

No rating or validation information has been found for xQuest.

No alerts have been found for xQuest.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 3 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

Uliana F, et al. (2023) Phosphorylation-linked complex profiling identifies assemblies required for Hippo signal integration. Molecular systems biology, 19(4), e11024.

Gorbovytska V, et al. (2022) Enhancer RNAs stimulate Pol II pause release by harnessing multivalent interactions to NELF. Nature communications, 13(1), 2429.

Cho C, et al. (2019) Structural basis of nucleosome assembly by the Abo1 AAA+ ATPase histone chaperone. Nature communications, 10(1), 5764.