

Resource Summary Report

Generated by [SPARC SAWG](#) on Sep 18, 2026

Crux tandem mass spectrometry analysis software

RRID:SCR_010648

Type: Tool

Proper Citation

Crux tandem mass spectrometry analysis software (RRID:SCR_010648)

Resource Information

URL: <http://noble.gs.washington.edu/proj/crux/>

Proper Citation: Crux tandem mass spectrometry analysis software (RRID:SCR_010648)

Description: A software toolkit for tandem mass spectrometry analysis, with a focus on peptide identification. Crux analyzes shotgun proteomics tandem mass spectra, associating peptides with observed spectra. This software toolkit for tandem mass spectrometry analysis, with a focus on peptide identification is provided as a single executable. Crux is implemented in C and is distributed with source code freely to noncommercial users. Mass spectrometry, the core technology in the field of proteomics, promises to enable scientists to identify and quantify the entire complement of proteins in a complex biological sample. Currently, the primary bottleneck in this type of experiment is computational. Existing algorithms for interpreting mass spectra are slow and fail to identify a large proportion of the given spectra. We describe a database search program called Crux that reimplements and extends the widely used database search program Sequest. For speed, Crux uses a peptide indexing scheme to rapidly retrieve candidate peptides for a given spectrum. For each peptide in the target database, Crux generates shuffled decoy peptides on the fly, providing a good null model and, hence, accurate false discovery rate estimates. Crux also implements two recently described postprocessing methods: a p value calculation based upon fitting a Weibull distribution to the observed scores, and a semisupervised method that learns to discriminate between target and decoy matches. Both methods significantly improve the overall rate of peptide identification.

Synonyms: Crux

Resource Type: software resource

Defining Citation: [PMID:18505281](#), [DOI:10.1021/pr500741y](#)

Keywords: proteomics, software toolkit, source code, bio.tools

Resource Name: Crux tandem mass spectrometry analysis software

Resource ID: SCR_010648

Alternate IDs: nlx_66678, biotools:crux

Alternate URLs: <https://bio.tools/crux>

Old URLs: <https://sources.debian.org/src/crux-toolkit/>

Record Creation Time: 20220129T080259+0000

Record Last Update: 20260912T195721+0000

Ratings and Alerts

No rating or validation information has been found for Crux tandem mass spectrometry analysis software.

No alerts have been found for Crux tandem mass spectrometry analysis software.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 34 mentions in open access literature.

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

Tariq U, et al. (2026) End-to-end deep attention-based multitask pipeline for predicting uncertainty-quantified peptide properties from mass spectrometry data. Scientific reports, 16(1).

Soo TCC, et al. (2026) Deployment of non-canonical splicing in tunicate genomes is mediated by divergent U2AF function and changing m6A modification in U1 and U6 snRNA. Nucleic acids research, 54(12).

Wen B, et al. (2025) Assessment of false discovery rate control in tandem mass spectrometry analysis using entrapment. Nature methods, 22(7), 1454.

Madej D, et al. (2025) PyViscount: Validating False Discovery Rate Estimation Methods via Random Search Space Partition. Journal of proteome research, 24(3), 1118.

Liao SC, et al. (2025) CHCHD2 mutant mice link mitochondrial deficits to PD pathophysiology. Science advances, 11(46), eadu0726.

Kumarathanan P, et al. (2025) In Vitro Exposure of A549 and J774A.1 Cells to SiO₂ and TiO₂ Nanoforms and Related Cellular- and Molecular-Level Effects: Application of Proteomics. Journal of proteome research, 24(4), 1672.

Ichikawa K, et al. (2025) CGC1, a new reference genome for *Caenorhabditis elegans*. *Genome research*, 35(8), 1902.

Pandi B, et al. (2024) Tissue Usage Preference and Intrinsically Disordered Region Remodeling of Alternative Splicing Derived Proteoforms in the Heart. *Journal of proteome research*, 23(8), 3161.

Yilmaz M, et al. (2024) Sequence-to-sequence translation from mass spectra to peptides with a transformer model. *Nature communications*, 15(1), 6427.

Hollin T, et al. (2024) Proteome-Wide Identification of RNA-dependent proteins and an emerging role for RNAs in *Plasmodium falciparum* protein complexes. *Nature communications*, 15(1), 1365.

Bielow C, et al. (2024) Communicating Mass Spectrometry Quality Information in mzQC with Python, R, and Java. *Journal of the American Society for Mass Spectrometry*, 35(8), 1875.

Wen B, et al. (2024) Assessment of false discovery rate control in tandem mass spectrometry analysis using entrapment. *bioRxiv : the preprint server for biology*.

Ichikawa K, et al. (2024) CGC1, a new reference genome for *Caenorhabditis elegans*. *bioRxiv : the preprint server for biology*.

Liao SC, et al. (2024) CHCHD2 mutant mice display mitochondrial protein accumulation and disrupted energy metabolism. *bioRxiv : the preprint server for biology*.

Ananth V, et al. (2024) A learned score function improves the power of mass spectrometry database search. *Bioinformatics (Oxford, England)*, 40(Suppl 1), i410.

Higgins L, et al. (2023) Principles of phosphoproteomics and applications in cancer research. *The Biochemical journal*, 480(6), 403.

Volkening JD, et al. (2023) Viral proteogenomic and expression profiling during productive replication of a skin-tropic herpesvirus in the natural host. *PLoS pathogens*, 19(6), e1011204.

Pandi B, et al. (2023) Tissue Usage Preference and Intrinsically Disordered Region Remodeling of Alternative Splicing Derived Proteoforms in the Heart. *bioRxiv : the preprint server for biology*.

Mao Z, et al. (2022) Physical and in silico immunopeptidomic profiling of a cancer antigen prostatic acid phosphatase reveals targets enabling TCR isolation. *Proceedings of the National Academy of Sciences of the United States of America*, 119(31), e2203410119.

Tariq MU, et al. (2021) SpeCollate: Deep cross-modal similarity network for mass spectrometry data based peptide deductions. *PloS one*, 16(10), e0259349.