Resource Summary Report

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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/

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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

Funding:

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: 20250420T014505+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 27 mentions in open access literature.

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

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.

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.

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

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.

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.

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

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.

Vijaya Kumar S, et al. (2020) A carotenoid-deficient mutant of the plant-associated microbe Pantoea sp. YR343 displays an altered membrane proteome. Scientific reports, 10(1), 14985.

The M, et al. (2020) Focus on the spectra that matter by clustering of quantification data in shotgun proteomics. Nature communications, 11(1), 3234.

Mikulenkova E, et al. (2020) NANOG/NANOGP8 Localizes at the Centrosome and is Spatiotemporally Associated with Centriole Maturation. Cells, 9(3).

Buric F, et al. (2020) Parallel Factor Analysis Enables Quantification and Identification of Highly Convolved Data-Independent-Acquired Protein Spectra. Patterns (New York, N.Y.), 1(9), 100137.

Salih KJ, et al. (2020) The composition and turnover of the Arabidopsis thaliana 80S cytosolic ribosome. The Biochemical journal, 477(16), 3019.

Kong AT, et al. (2017) MSFragger: ultrafast and comprehensive peptide identification in mass spectrometry-based proteomics. Nature methods, 14(5), 513.

Peters JS, et al. (2016) Identification of Quantitative Proteomic Differences between Mycobacterium tuberculosis Lineages with Altered Virulence. Frontiers in microbiology, 7, 813.