Resource Summary Report

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Protein Prospector

RRID:SCR_014558
Type: Tool

Proper Citation

Protein Prospector (RRID:SCR_014558)

Resource Information

URL: http://prospector.ucsf.edu

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Description: A package of over twenty mass spectrometry-based tools primarily geared toward proteomic data analysis and database mining. It can be run from the command line, but is primarily used through a web browser, and there is a public website that allows anyone to use the software without local installation. Tandem mass spectrometry analysis tools are used for database searching and identification of peptides, including post-translationally modified peptides and cross-linked peptides. Support for isotope and label-free quantification from this type of data is provided. MS-Viewer software allows sharing and displaying of annotated spectra from many different tandem mass spectrometry data analysis packages. Other tools include software for analyzing peptide mass fingerprinting data (MS-Fit); prediction of theoretical fragmentation of peptides (MS-Product); theoretical chemical or enzymatic digestion of proteins (MS-Digest); and theoretical modeling of the isotope distribution of any chemical, including peptides (MS-Isotope). Searches using amino acid sequence can be used to identify homologous peptides in a database (MS-Pattern); the use of the combination of amino acid sequence and masses can be used for homologous peptide and protein identification using MS-Homology. Tandem mass spectrometry peak list files can be filtered for the presence of certain peaks or neutral losses using MS-Filter. Given a list of proteins, MS-Bridge can report all potential cross-linked peptide combinations of a specified mass. Given a precursor peptide mass and information about known amino acid presence, absence, or modifications, MS-Comp can report all amino acid combinations that could lead to the observed mass.

Synonyms: ProteinProspector

Resource Type: software resource, software toolkit

Keywords: database search program, database search, database management, peptide, protein, mass spectrometry, ms, utility program, batch msms, bio.tools, FASEB list

Availability: Open source, Freely available to academic researchers

Resource Name: Protein Prospector

Resource ID: SCR_014558

Alternate IDs: biotools:proteinprospector

Alternate URLs: https://bio.tools/proteinprospector

Record Creation Time: 20220129T080321+0000

Record Last Update: 20260919T195812+0000

Ratings and Alerts

No rating or validation information has been found for Protein Prospector.

No alerts have been found for Protein Prospector.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 595 mentions in open access literature.

Listed below are recent publications. The full list is available at nidm-terms .

Yogo T, et al. (2026) A Pilot Proteomic Analysis of Tear Fluid in Domestic Cats with and Without Conjunctivitis Using MALDI-TOF/TOF Mass Spectrometry. Animals : an open access journal from MDPI, 16(6).

Colizzi FS, et al. (2026) Clock-related neuropeptides in Acyrthosiphon pisum. Frontiers in genetics, 17, 1818975.

Wang Y, et al. (2026) A 15-layer multi-omics analysis of gastric cancer ecotypes provides therapeutic insights. Cell reports. Medicine, 7(5), 102756.

Dunshee EB, et al. (2026) Human pumilio proteins use fuzzy multivalent hydrophobic interactions to recruit the CCR4-NOT deadenylase complex to repress mRNAs. The Journal of biological chemistry, 302(4), 111281.

Prertprawnon S, et al. (2026) Assessment of Protein Conformation via Diazirine-Promoted Oxidation of Methionine and Tryptophan Residues. Analytical chemistry, 98(20), 14841.

Nashed A, et al. (2026) An in vitro approach for simulating divergent Golgi O-glycosylation of tumor-associated MUC1 from normal MUC1. Nature communications, 17(1).

Sun J, et al. (2026) Mapping the vRNA Interaction with HIV-1 Integrase. bioRxiv : the preprint server for biology.

Sun J, et al. (2026) Mapping the TAR vRNA Interaction with HIV-1 Integrase. Viruses, 18(6).

Duan R, et al. (2026) Single-atom substitution redirects KatG reactivity from cofactor biogenesis to stereoselective sulfoxidation. Nature communications, 17(1).

Aljedani SS, et al. (2026) SH3 domains selectively activate the PI3 kinase through non-conventional tertiary contacts. Communications biology, 9(1).

Zhang Z, et al. (2026) Protocol for identifying the BZR1 interactome under starvation in Arabidopsis by metabolic stable isotope labeling quantitative IP-MS. STAR protocols, 7(1), 104343.

Shi H, et al. (2026) CSN5i-3 is an orthosteric molecular glue inhibitor of COP9 signalosome. Nature, 652(8112), 1375.

Bae W, et al. (2026) Enhanced oxidative stress resilience in C. elegans acox-1.1 mutants through CTL-3 and proteasomal regulation. Experimental biology and medicine (Maywood, N.J.), 251, 10796.

Cervantes M, et al. (2026) Function within Disorder: Small heat shock proteins use different functional regions to chaperone tau aggregation. bioRxiv : the preprint server for biology.

Close R, et al. (2026) A sulfotransferase from a gut microbe acts on diverse phenolic sulfate compounds, including acetaminophen sulfate. PNAS nexus, 5(1), pgaf403.

Zahavi EE, et al. (2025) Repeat-element RNAs integrate a neuronal growth circuit. Cell, 188(16), 4350.

Giglio ML, et al. (2025) An N-Terminally Elongated Peptide From Conus rolani Defines a New Class of Ribbon ??-Conotoxins Targeting Muscle nAChRs. FASEB journal : official publication of the Federation of American Societies for Experimental Biology, 39(12), e70698.

Williams RV, et al. (2025) The cysteine-rich domain of SEP15, a selenoprotein co-chaperone of the ER chaperone, UDP-glucose:glycoprotein glucosyltransferase, adopts a novel fold. bioRxiv : the preprint server for biology.

Asahi K, et al. (2025) Cryo-EM structure of the bacterial intramembrane metalloprotease RseP in the substrate-bound state. Science advances, 11(9), eadu0925.

Detomasi TC, et al. (2025) Structure-based discovery of highly bioavailable, covalent, broad-spectrum coronavirus MPro inhibitors with potent in vivo efficacy. Science advances, 11(17), eadt7836.