

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: 20260912T200251+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 [SPARC SAWG](#) .

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 *Acyrtosiphon 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).

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.

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

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.

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*.

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 rolandi* 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.

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.

Machata S, et al. (2025) Identification of a fungal antibacterial endopeptidase that cleaves peptidoglycan. *EMBO reports*, 26(15), 3889.

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*.