Resource Summary Report

Generated by RRID on May 21, 2025

Protein Prospector

RRID:SCR_014558 Type: Tool

Proper Citation

Protein Prospector (RRID:SCR_014558)

Resource Information

URL: http://prospector.ucsf.edu

Proper Citation: Protein Prospector (RRID:SCR_014558)

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

Funding:

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: 20250519T204956+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: <u>SciCrunch Registry</u>

Usage and Citation Metrics

We found 339 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>RRID</u>.

Markovich SW, et al. (2025) Dehydroamino acids and their crosslinks in Alzheimer's disease aggregates. Brain communications, 7(1), fcaf019.

Döring S, et al. (2025) Challenges and Insights in Absolute Quantification of Recombinant Therapeutic Antibodies by Mass Spectrometry: An Introductory Review. Antibodies (Basel, Switzerland), 14(1).

Zhang T, et al. (2024) Comparison of Shared Class I HLA-bound Non-canonical Neoepitopes between Normal and Neoplastic Tissues of Pancreatic Adenocarcinoma. Clinical cancer research : an official journal of the American Association for Cancer Research.

Aljedani SS, et al. (2024) Functional selection in SH3-mediated activation of the PI3 kinase. bioRxiv : the preprint server for biology.

Challen B, et al. (2024) Liquid Atmospheric Pressure Matrix-Assisted Laser Desorption/Ionization Mass Spectrometry Using a Commercial Ion Source and Orbitrap Mass Analyzer. Analytical chemistry, 96(40), 15865.

Takahashi Y, et al. (2024) GlyComb: A novel glycoconjugate data repository that bridges glycomics and proteomics. The Journal of biological chemistry, 300(2), 105624.

Mun BG, et al. (2024) The PGPR Bacillus aryabhattai promotes soybean growth via nutrient and chlorophyll maintenance and the production of butanoic acid. Frontiers in plant science, 15, 1341993.

Fenoglio I, et al. (2024) Molecular insights into the interaction between cytochrome c and carbon nanomaterials. Heliyon, 10(23), e40587.

Burggraef MJ, et al. (2024) Exactly defined molecular weight poly(ethylene glycol) allows for facile identification of PEGylation sites on proteins. Nature communications, 15(1), 9814.

Schopfer LM, et al. (2024) Mass Spectrometry of Putrescine, Spermidine, and Spermine Covalently Attached to Francisella tularensis Universal Stress Protein and Bovine Albumin. Biochemistry research international, 2024, 7120208.

Damm M, et al. (2024) Venomics and Peptidomics of Palearctic Vipers: A Clade-Wide Analysis of Seven Taxa of the Genera Vipera, Montivipera, Macrovipera, and Daboia across Türkiye. Journal of proteome research, 23(8), 3524.

Anderson LC, et al. (2024) The Hunt Lab Guide to De Novo Peptide Sequence Analysis by Tandem Mass Spectrometry. Molecular & cellular proteomics : MCP, 23(12), 100875.

Qiu C, et al. (2024) Stub1 promotes degradation of the activated Diaph3: A negative feedback regulatory mechanism of the actin nucleator. The Journal of biological chemistry, 300(10), 107813.

Mikawy NN, et al. (2024) Are Internal Fragments Observable in Electron Based Top-Down Mass Spectrometry? Molecular & cellular proteomics : MCP, 23(9), 100814.

Roychowdhury T, et al. (2024) Phosphorylation-driven epichaperome assembly is a regulator of cellular adaptability and proliferation. Nature communications, 15(1), 8912.

Joglekar I, et al. (2023) Sequential Unfolding Mechanisms of Monomeric Caspases. Biochemistry, 62(12), 1878.

Wiebach V, et al. (2023) "What I wish I had known before starting my PhD". Analytical science advances, 4(1-2), 6.

Liu Y, et al. (2023) In-Cell Chemical Crosslinking Identifies Hotspots for SQSTM-1/p62-I?B?

Interaction That Underscore a Critical Role of p62 in Limiting NF-?B Activation Through I?B? Stabilization. Molecular & cellular proteomics : MCP, 22(2), 100495.

Spinck M, et al. (2023) Genetically programmed cell-based synthesis of non-natural peptide and depsipeptide macrocycles. Nature chemistry, 15(1), 61.

Baquer G, et al. (2023) rMSIfragment: improving MALDI-MSI lipidomics through automated in-source fragment annotation. Journal of cheminformatics, 15(1), 80.