

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 toolkit, software resource

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: 20260803T040657+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 569 mentions in open access literature.

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

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 γ -Conotoxins Targeting Muscle nAChRs. FASEB journal : official publication of the Federation of American Societies for Experimental Biology, 39(12), e70698.

Palla AM, et al. (2025) An Intrinsically Disordered Region of Histone Demethylase KDM5A Activates Catalysis Through Interactions With the Nucleosomal Acidic Patch and DNA. Journal of molecular biology, 437(19), 169301.

Neupert S, et al. (2025) Transcriptomics and Neuropeptidomics of the Cockroach Rhyparobia maderae to Characterize the Neuropeptide Landscape of the Cockroach's Circadian Clock. Journal of proteome research, 24(11), 5370.

Tulin F, et al. (2025) Mitotic entry is controlled by the plant-specific phosphatase BSL1 and cyclin-dependent kinase B. Nature plants, 11(11), 2395.

Remesal L, et al. (2025) Targeting iron-associated protein Ftl1 in the brain of old mice improves age-related cognitive impairment. Nature aging.

Woods CN, et al. (2025) Activation mechanism of small heat shock protein HSPB5 revealed by disease-associated mutants. *Proceedings of the National Academy of Sciences of the United States of America*, 122(20), e2425061122.

Braet SM, et al. (2025) Asymmetric isopeptide bond steers directional genomic RNA egress from icosahedral virus. *Science advances*, 11(50), eady4104.

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

Yang N, et al. (2025) FGF2 Mediated USP42-PPAR γ Axis Activation Ameliorates Liver Oxidative Damage and Promotes Regeneration. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 12(18), e2408724.

Schopfer LM, et al. (2025) Kinetic analysis suggests that malathion at low environmental exposures is not toxic to humans. *PloS one*, 20(10), e0335361.

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.

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*.

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

Chalkley RJ, et al. (2025) Improving the Depth and Reliability of Glycopeptide Identification Using Protein Prospector. *Molecular & cellular proteomics : MCP*, 24(2), 100903.

Sajjad A, et al. (2025) In-silico molecular analysis and blocking of the viral G protein of Nipah virus interacting with ephrin B2 and B3 receptor by using peptide mass fingerprinting. *Frontiers in bioinformatics*, 5, 1526566.

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

Landgraf AD, et al. (2025) Small-Molecule KRAS Inhibitors by Tyrosine Covalent Bond Formation. *ChemMedChem*, 20(12), e202400624.

Shi H, et al. (2025) Orthosteric Molecular Glue Inhibits COP9 Signalosome with Substrate-Dependent Potency. *bioRxiv : the preprint server for biology*.

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).