Resource Summary Report

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TopFIND

RRID:SCR_008918
Type: Tool

Proper Citation

TopFIND (RRID:SCR_008918)

Resource Information

URL: http://clipserve.clip.ubc.ca/topfind

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Description: An integrated knowledgebase focused on protein termini, their formation by proteases and functional implications. It contains information about the processing and the processing state of proteins and functional implications thereof derived from research literature, contributions by the scientific community and biological databases. It lists more than 120,000 N- and C-termini and almost 10,000 cleavages. TopFIND is a resource for comprehensive coverage of protein N- and C-termini discovered by all available in silico, in vitro as well as in vivo methodologies. It makes use of existing knowledge by seamless integration of data from UniProt and MEROPS and provides access to new data from community submission and manual literature curating. It renders modifications of protein termini, such as acetylation and citrulination, easily accessible and searchable and provides the means to identify and analyse extend and distribution of terminal modifications across a protein. The data is presented to the user with a strong emphasis on the relation to curated background information and underlying evidence that led to the observation of a terminus, its modification or proteolytic cleavage. In brief the protein information, its domain structure, protein termini, terminus modifications and proteolytic processing of and by other proteins is listed. All information is accompanied by metadata like its original source, method of identification, confidence measurement or related publication. A positional cross correlation evaluation matches termini and cleavage sites with protein features (such as amino acid variants) and domains to highlight potential effects and dependencies in a unique way. Also, a network view of all proteins showing their functional dependency as protease, substrate or protease inhibitor tied in with protein interactions is provided for the easy evaluation of network wide effects. A powerful yet user friendly filtering mechanism allows the presented data to be filtered based on parameters like methodology used, in vivo relevance, confidence or data source (e.g. limited to a single laboratory or publication). This provides means to assess physiological relevant data and to deduce functional information and hypotheses

relevant to the bench scientist. TopFIND PROVIDES: * Integration of protein termini with proteolytic processing and protein features * Displays proteases and substrates within their protease web including detailed evidence information * Fully supports the Human Proteome Project through search by chromosome location CONTRIBUTE * Submit your N- or C-termini datasets * Contribute information on protein cleavages * Provide detailed experimental description, sample information and raw data

Abbreviations: TopFIND

Synonyms: Termini oriented protein Function Inferred Database

Resource Type: service resource, storage service resource, data or information resource, data repository, database

Defining Citation: PMID:22102574, PMID:21822272

Keywords: protein, n-termini, c-termini, protease, protein cleavage, proteomics, cleavage site, terminus, modification, proteolytic processing, protein function, domain structure, protein termini, terminus modification, protease, substrate, protease inhibitor, protein interaction, protein-protein interaction, interaction, bio.tools

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Availability: Public, Acknowledgement requested

Resource Name: TopFIND

Resource ID: SCR_008918

Alternate IDs: biotools:topfind, nlx_151607

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

Record Creation Time: 20220129T080250+0000

Record Last Update: 20250426T060048+0000

Ratings and Alerts

No rating or validation information has been found for TopFIND.

No alerts have been found for TopFIND.

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 FDI Lab - SciCrunch.org.

Germitsch N, et al. (2025) N-terminomics profiling of host proteins targeted by excretory-secretory proteases of the nematode Angiostrongylus vasorum identifies points of interaction with canine coagulation and complement cascade. PloS one, 20(1), e0316217.

de Vasconcellos Racorti N, et al. (2024) Mannose-6-Phosphate Isomerase Functional Status Shapes a Rearrangement in the Proteome and Degradome of Mannose-Treated Melanoma Cells. Journal of proteome research, 23(11), 5177.

Peng M, et al. (2024) Mapping Start Codons of Small Open Reading Frames by N-Terminomics Approach. Molecular & cellular proteomics : MCP, 23(11), 100860.

Mead TJ, et al. (2024) Combined genetic-pharmacologic inactivation of tightly linked ADAMTS proteases in temporally specific windows uncovers distinct roles for versican proteolysis and glypican-6 in cardiac development. Matrix biology : journal of the International Society for Matrix Biology, 131, 1.

Nandadasa S, et al. (2023) Degradomic Identification of Membrane Type 1-Matrix Metalloproteinase as an ADAMTS9 and ADAMTS20 Substrate. Molecular & cellular proteomics : MCP, 22(6), 100566.

Bayne AN, et al. (2023) MTSviewer: A database to visualize mitochondrial targeting sequences, cleavage sites, and mutations on protein structures. PloS one, 18(4), e0284541.

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Colombo EA, et al. (2023) Germline NUP98 Variants in Two Siblings with a Rothmund-Thomson-Like Spectrum: Protein Functional Changes Predicted by Molecular Modeling. International journal of molecular sciences, 24(4).

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Juurikka K, et al. (2021) MMP8 increases tongue carcinoma cell-cell adhesion and diminishes migration via cleavage of anti-adhesive FXYD5. Oncogenesis, 10(5), 44.

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Liberato T, et al. (2019) Proteomic profiling of the proteolytic events in the secretome of the transformed phenotype of melanocyte-derived cells using Terminal Amine Isotopic Labeling of Substrates. Journal of proteomics, 192, 291.

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Qi E, et al. (2019) Revealing favorable and unfavorable residues in cooperative positions in protease cleavage sites. Biochemical and biophysical research communications, 519(4), 714.

Mair B, et al. (2019) High-throughput genome-wide phenotypic screening via immunomagnetic cell sorting. Nature biomedical engineering, 3(10), 796.

Bienvenut WV, et al. (2017) EnCOUNTer: a parsing tool to uncover the mature N-terminus of organelle-targeted proteins in complex samples. BMC bioinformatics, 18(1), 182.

Yeom J, et al. (2017) Comprehensive analysis of human protein N-termini enables assessment of various protein forms. Scientific reports, 7(1), 6599.

Lazzarini N, et al. (2017) RGIFE: a ranked guided iterative feature elimination heuristic for the identification of biomarkers. BMC bioinformatics, 18(1), 322.

Anania VG, et al. (2016) Uncovering a Dual Regulatory Role for Caspases During Endoplasmic Reticulum Stress-induced Cell Death. Molecular & cellular proteomics : MCP, 15(7), 2293.