

# 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 citrullination, 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:** data or information resource, data repository, database, service resource, storage service resource

**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, r3d100012721, nlx\_151607

**Alternate URLs:** <https://bio.tools/topfind>, <https://doi.org/10.17616/R3KB8J>,  
<https://doi.org/10.17616/R3KB8J>

**Record Creation Time:** 20220129T080250+0000

**Record Last Update:** 20260905T132630+0000

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## Ratings and Alerts

No rating or validation information has been found for TopFIND.

No alerts have been found for TopFIND.

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## Data and Source Information

## Usage and Citation Metrics

We found 29 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [PRECISE-TBI](#) .

Mead TJ, et al. (2025) ADAMTS7, a target in atherosclerosis, cooperates with its homolog ADAMTS12 to protect against myxomatous valve degeneration. *Journal of molecular and cellular cardiology plus*, 11, 100288.

Kapilan A, et al. (2025) N-terminomics and proteomics analysis of Calpain-2 reveal key proteolytic processing of metabolic and cell adhesion proteins. *Protein science : a publication of the Protein Society*, 34(5), e70144.

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.

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.

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

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.

Das N, et al. (2023) Tryptase ?? regulation of joint lubrication and inflammation via proteoglycan-4 in osteoarthritis. *Nature communications*, 14(1), 1910.

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).

Pablos I, et al. (2021) Mechanistic insights into COVID-19 by global analysis of the SARS-CoV-2 3CLpro substrate degradome. *Cell reports*, 37(4), 109892.

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.

Wunderli SL, et al. (2020) Tendon response to matrix unloading is determined by the patho-physiological niche. *Matrix biology : journal of the International Society for Matrix Biology*, 89, 11.

Bao Y, et al. (2019) Toward more accurate prediction of caspase cleavage sites: a comprehensive review of current methods, tools and features. *Briefings in bioinformatics*, 20(5), 1669.

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.

Lualdi M, et al. (2019) Exploring the Mitochondrial Degradome by the TAILS Proteomics Approach in a Cellular Model of Parkinson's Disease. *Frontiers in aging neuroscience*, 11, 195.

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.

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

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.