

Resource Summary Report

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CutDB

RRID:SCR_013420

Type: Tool

Proper Citation

CutDB (RRID:SCR_013420)

Resource Information

URL: <http://cutdb.burnham.org>

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Description: The CutDB focuses on the annotation of individual proteolytic events, both actual and predicted. It offers searchable lists of proteases, Merops code, substrate, and diseases from which users can specify their desired queries in order to obtain more specific information. CutDB is one of the first systematic efforts to build an easily accessible collection of documented proteolytic events for natural proteins in vivo or in vitro. A CutDB entry is defined by a unique combination of these three attributes: protease, protein substrate and cleavage site. Currently, CutDB integrates 3070 proteolytic events for 470 different proteases captured from public archives (such as MEROPS and HPRD) and publications. CutDB supports various types of data searches and displays, including clickable network diagrams. Most importantly, CutDB is a community annotation resource based on a Wikipedia approach, providing a convenient user interface to input new data online. A recent contribution of 568 proteolytic events by several experts in the field of matrix metalloproteinases suggests that this approach will significantly accelerate the development of CutDB content.

Synonyms: CutDB

Resource Type: data or information resource, database

Keywords: predicted proteolytic event, protease, proteolysis

Resource Name: CutDB

Resource ID: SCR_013420

Alternate IDs: nif-0000-02706

Record Creation Time: 20220129T080316+0000

Record Last Update: 20260904T000328+0000

Ratings and Alerts

No rating or validation information has been found for CutDB.

No alerts have been found for CutDB.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 13 mentions in open access literature.

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

Bannaga AS, et al. (2020) Discovery, validation and sequencing of urinary peptides for diagnosis of liver fibrosis-A multicentre study. EBioMedicine, 62, 103083.

Gubina N, et al. (2020) Novel Apoptotic Mediators Identified by Conservation of Vertebrate Caspase Targets. Biomolecules, 10(4).

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.

Braga TT, et al. (2016) Early infiltration of p40IL12(+)CCR7(+)CD11b(+) cells is critical for fibrosis development. Immunity, inflammation and disease, 4(3), 300.

Kumar S, et al. (2015) CleavPredict: A Platform for Reasoning about Matrix Metalloproteinases Proteolytic Events. PloS one, 10(5), e0127877.

Frantzi M, et al. (2014) Discovery and validation of urinary biomarkers for detection of renal cell carcinoma. Journal of proteomics, 98, 44.

Nakayama K, et al. (2014) The C-terminal fragment of prostate-specific antigen, a 2331 Da peptide, as a new urinary pathognomonic biomarker candidate for diagnosing prostate cancer. PloS one, 9(9), e107234.

Cho JH, et al. (2013) Identification of the novel substrates for caspase-6 in apoptosis using proteomic approaches. BMB reports, 46(12), 588.

Siwy J, et al. (2012) Evaluation of the Zucker diabetic fatty (ZDF) rat as a model for human disease based on urinary peptidomic profiles. PloS one, 7(12), e51334.

Nilsson SC, et al. (2011) Complement factor I in health and disease. Molecular immunology, 48(14), 1611.

Nagata S, et al. (2010) Autoimmunity and the clearance of dead cells. Cell, 140(5), 619.

Jackson BC, et al. (2010) Update of human and mouse matrix metalloproteinase families. *Human genomics*, 4(3), 194.

Rawlings ND, et al. (2009) A large and accurate collection of peptidase cleavages in the MEROPS database. *Database : the journal of biological databases and curation*, 2009, bap015.