Resource Summary Report

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Mammalian Degradome Database

RRID:SCR_007624
Type: Tool

Proper Citation

Mammalian Degradome Database (RRID:SCR_007624)

Resource Information

URL: http://degradome.uniovi.es

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Description: A database of human, chimpanzee, mouse, and rat proteases and protease inhibitors, as well as as the growing number of hereditary diseases caused by mutations in protease genes. Analysis of the human and mouse genomes has allowed us to annotate 581 human, 580 chimpanzee, 667 mouse, and 655 rat protease genes. Proteases are classified in five different classes according to their mechanism of catalysis. Proteases are a diverse and important group of enzymes representing >2% of the human, chimpanzee, mouse and rat genomes. This group of enzymes is implicated in numerous physiological processes. The importance of proteases is illustrated by the existence of 99 different hereditary diseases due to mutations in protease genes. Furthermore, proteases have been implicated in multiple human pathologies, including vascular diseases, rheumatoid arthritis, neurodegenerative processes, and cancer. During the last ten years, our laboratory has identified and characterized more than 60 human protease genes. Due to the importance of proteolytic enzymes in human physiology and pathology, we have recently introduced the concept of Degradome, as the complete repertoire of proteases expressed by a tissue or organism. Thanks to the recent completion of the human, chimpanzee, mouse, and rat genome sequencing projects, we were able to analyze and compare for the first time the complete protease repertoire in those mammalian organisms, as well as the complement of protease inhibitor genes. This webpage also contains the Supplementary Material of Human and mouse proteases: a comparative genomic approach Nat Rev Genet (2003) 4: 544-558, Genome sequence of the brown Norway rat yields insights into mammalian evolution Nature (2004) 428: 493-521, A genomic analysis of rat proteases and protease inhibitors Genome Res. (2004) 14: 609-622, and Comparative genomic analysis of human and chimpanzee proteases Genomics (2005) 86: 638-647.

Abbreviations: Degradome Database

Synonyms: Mammalian Degradome Database

Resource Type: data or information resource, database

Defining Citation: PMID:18776217

Keywords: degradome, mammalian, protease inhibitor, protease, gene, protease gene, genetic disease, proteolysis, protease structure, ancillary domain, genomic, genome

Related Condition: Disease of proteolysis

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Obra Social Cajastur

Resource Name: Mammalian Degradome Database

Resource ID: SCR_007624

Alternate IDs: nif-0000-02746

Record Creation Time: 20220129T080242+0000

Record Last Update: 20250404T060614+0000

Ratings and Alerts

No rating or validation information has been found for Mammalian Degradome Database.

No alerts have been found for Mammalian Degradome Database.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 10 mentions in open access literature.

Listed below are recent publications. The full list is available at RRID.

Mótyán JA, et al. (2024) The human retroviral-like aspartic protease 1 (ASPRV1): From in vitro studies to clinical correlations. The Journal of biological chemistry, 300(9), 107634.

Mjokane N, et al. (2021) The Possible Role of Microbial Proteases in Facilitating SARS-CoV-2 Brain Invasion. Biology, 10(10).

Dong Z, et al. (2021) Bioinformatic mapping of a more precise Aspergillus niger degradome. Scientific reports, 11(1), 693.

Pérez-Silva JG, et al. (2016) The Degradome database: expanding roles of mammalian proteases in life and disease. Nucleic acids research, 44(D1), D351.

, et al. (2014) The common marmoset genome provides insight into primate biology and evolution. Nature genetics, 46(8), 850.

Pollheimer J, et al. (2014) Review: the ADAM metalloproteinases - novel regulators of trophoblast invasion? Placenta, 35 Suppl, S57.

Saboti? J, et al. (2012) Microbial and fungal protease inhibitors--current and potential applications. Applied microbiology and biotechnology, 93(4), 1351.

Mashiyama ST, et al. (2012) A global comparison of the human and T. brucei degradomes gives insights about possible parasite drug targets. PLoS neglected tropical diseases, 6(12), e1942.

Radisky ES, et al. (2010) Matrix metalloproteinase-induced epithelial-mesenchymal transition in breast cancer. Journal of mammary gland biology and neoplasia, 15(2), 201.

Quesada V, et al. (2009) The Degradome database: mammalian proteases and diseases of proteolysis. Nucleic acids research, 37(Database issue), D239.