Resource Summary Report

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ExPASy Aldente Peptide Mass Fingerprinting tool

RRID:SCR_008508
Type: Tool

Proper Citation

ExPASy Aldente Peptide Mass Fingerprinting tool (RRID:SCR_008508)

Resource Information

URL: http://www.expasy.org/tools/peptident.html

Proper Citation: ExPASy Aldente Peptide Mass Fingerprinting tool (RRID:SCR_008508)

Description: THIS RESOURCE IS NO LONGER IN SERVICE documented on June 4, 2013. Aldente is a tool to identify proteins from peptide mass fingerprinting data. This fast and powerful tool takes advantage of the Hough transform for spectra recalibration and outlier exclusion. The Aldente search form can be used in two modes: for a global view of all the search parameters on one page: click on the section tab All. This global view is useful to have a quick overview before sending the query. to have search parameters grouped into smaller logical sections: click on the corresponding section tab in the tabs banner. Note! Moving from one section to another keeps search parameter selections. For your convenience, you may view / hide the help during your search parameters selection. Use the Help or No help section tab accordingly.

Abbreviations: ExPASy

Resource Type: software resource

Keywords: mass spectroscopy

Funding:

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: ExPASy Aldente Peptide Mass Fingerprinting tool

Resource ID: SCR_008508

Alternate IDs: nif-0000-30539

Record Creation Time: 20220129T080247+0000

Record Last Update: 20250410T065722+0000

Ratings and Alerts

No rating or validation information has been found for ExPASy Aldente Peptide Mass Fingerprinting tool.

No alerts have been found for ExPASy Aldente Peptide Mass Fingerprinting tool.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 310 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Khaksar G, et al. (2019) Genome-wide analysis of the Dof gene family in durian reveals fruit ripening-associated and cultivar-dependent Dof transcription factors. Scientific reports, 9(1), 12109.

Knapik K, et al. (2019) Microbial diversity analysis and screening for novel xylanase enzymes from the sediment of the Lobios Hot Spring in Spain. Scientific reports, 9(1), 11195.

Aslam M, et al. (2019) Genome-Wide Identification and Expression Profiling of CBL-CIPK Gene Family in Pineapple (Ananas comosus) and the Role of AcCBL1 in Abiotic and Biotic Stress Response. Biomolecules, 9(7).

Chen X, et al. (2019) Amino acid substitutions in a polygalacturonase inhibiting protein (OsPGIP2) increases sheath blight resistance in rice. Rice (New York, N.Y.), 12(1), 56.

Ke F, et al. (2019) Ranaviruses Bind Cells from Different Species through Interaction with Heparan Sulfate. Viruses, 11(7).

Djoumbou-Feunang Y, et al. (2019) BioTransformer: a comprehensive computational tool for small molecule metabolism prediction and metabolite identification. Journal of cheminformatics, 11(1), 2.

Mendoza-Elizalde S, et al. (2019) Inference from the analysis of genetic structure of Helicobacter pylori strains isolates from two paediatric patients with recurrent infection. BMC

microbiology, 19(1), 184.

Niu X, et al. (2019) Genome-wide identification of GRAS genes in Brachypodium distachyon and functional characterization of BdSLR1 and BdSLRL1. BMC genomics, 20(1), 635.

Rice K, et al. (2019) The predominance of nucleotidyl activation in bacterial phosphonate biosynthesis. Nature communications, 10(1), 3698.

Li Y, et al. (2019) Molecular identification of the phosphate transporter family 1 (PHT1) genes and their expression profiles in response to phosphorus deprivation and other abiotic stresses in Brassica napus. PloS one, 14(7), e0220374.

Gevaert O, et al. (2019) Characterization of the First Bacterial and Thermostable GDP-Mannose 3,5-Epimerase. International journal of molecular sciences, 20(14).

Guo D, et al. (2019) Integrating molecular characterization and metabolites profile revealed CtCHI1's significant role in Carthamus tinctorius L. BMC plant biology, 19(1), 376.

Liu T, et al. (2019) Genomewide identification and analysis of heat-shock proteins 70/110 to reveal their potential functions in Chinese soft-shelled turtle Pelodiscus sinensis. Ecology and evolution, 9(12), 6968.

Pander B, et al. (2019) The carbonic anhydrase of Clostridium autoethanogenum represents a new subclass of ?-carbonic anhydrases. Applied microbiology and biotechnology, 103(17), 7275.

Li L, et al. (2019) Genome-wide identification, characterization and expression analysis of the HD-Zip gene family in the stem development of the woody plant Prunus mume. PeerJ, 7, e7499.

Muñoz González F, et al. (2019) The BtaF Adhesin Is Necessary for Full Virulence During Respiratory Infection by Brucella suis and Is a Novel Immunogen for Nasal Vaccination Against Brucella Infection. Frontiers in immunology, 10, 1775.

Kurotani A, et al. (2019) Localization-specific distributions of protein pI in human proteome are governed by local pH and membrane charge. BMC molecular and cell biology, 20(1), 36.

Wan X, et al. (2019) Genome-wide identification and classification of the Hsf and sHsp gene families in Prunus mume, and transcriptional analysis under heat stress. PeerJ, 7, e7312.

Hao Q, et al. (2019) Genome-Wide Analysis of the WOX Gene Family and Function Exploration of GmWOX18 in Soybean. Plants (Basel, Switzerland), 8(7).

Dey D, et al. (2019) The effect of amantadine on an ion channel protein from Chikungunya virus. PLoS neglected tropical diseases, 13(7), e0007548.