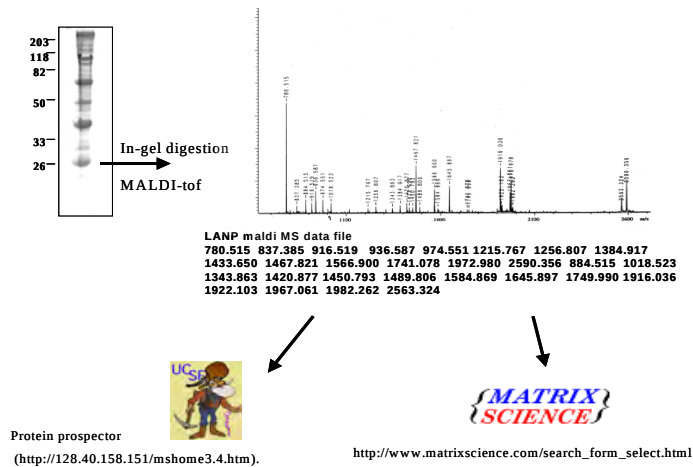


Peptide mass fingerprint analysis of an SDS PAGE band.



Protein prospector: (<http://128.40.158.151/mshome3.4.htm>).

http://www.matrixscience.com/search_form_select.html

LANP maldi MS 14B masses

780.515
837.385
916.519
936.587
974.551
1215.767
1256.807
1384.917
1433.650 keratin
1467.821(keratin)
1566.900
1741.078
1972.980
2590.356
884.515
1018.523
1343.863
1420.877
1450.793
1489.806
1584.869
1645.897
1749.990
1916.036
1922.103
1967.061
1982.262
2563.324

The image displays two screenshots of the Mascot search interface. The top screenshot shows the 'Mascot Search' page with a sidebar menu and a main content area. The bottom screenshot shows the 'Mascot Peptide Mass Fingerprint' search form with various input fields and options.

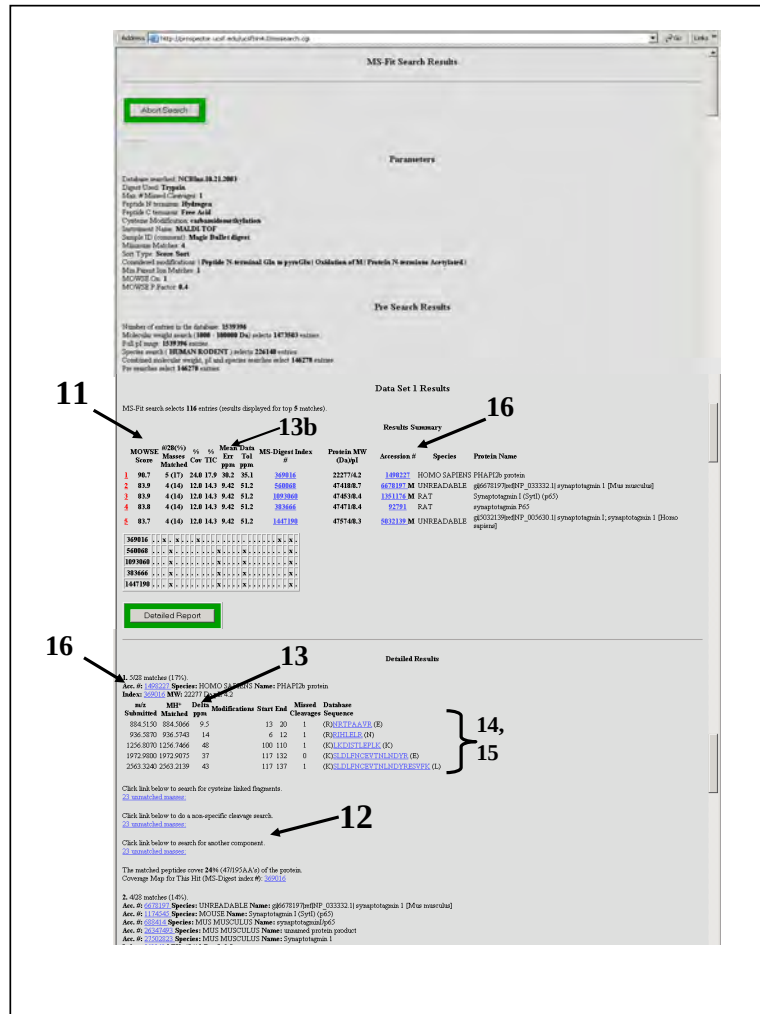
Mascot Search Page:

- Navigation Bar:** HOME WHAT'S NEW? MASCOT HELP PRODUCTS SUPPORT CONTACT Search Go
- Mascot Search:**
 - Peptide Mass Fingerprint:** The experimental data are a list of peptide mass values from an enzymatic digest of a protein.
 - Example of results report
 - More information
 - Sequence Query:** One or more peptide mass values associated with information such as partial or ambiguous sequence strings, amino acid composition information, MS/MS fragment ion masses, etc. & a subset of a sequence tag query.
 - Example of results report
 - More information
 - MS/MS (an Search):** Identification based on raw MS/MS data from one or more peptides.
 - Example of results report
 - More information
- Search Form Defaults:** Follow this link to save your preferred search form defaults as a browser cookie.

Mascot Peptide Mass Fingerprint Search Form:

- Navigation Bar:** HOME WHAT'S NEW? MASCOT HELP PRODUCTS SUPPORT CONTACT Search Go
- Mascot > Peptide Mass Fingerprint:**
- MASCOT Peptide Mass Fingerprint:**
 - Your name:** Mastar Aten **Email:** Mastar.Aten@ad.jku.at
 - Search title:** [Text field]
 - Database:** SwissProt
 - Taxonomy:** Mammalia (mammals)
 - Enzyme:** Trypsin
 - Fixed modifications:**
 - AB_016_1CAT00 (C)
 - AB_016_1CAT00 (C)
 - Acetyl (C)
 - Aspar (N-term)
 - Amide (C-term)
 - Variable modifications:**
 - Amide (C-term)
 - Aspar (N-term)
 - Carbamyl (N)
 - Protein mass:** [Text field] kDa
 - Mass values:**
 - ☒ NBr
 - ☐ M_r
 - Peptide tag:** [Text field] [cm] [cm]
 - Mass values:**
 - ☒ Monoisotopic
 - ☐ Average
 - Query:**
 - 780.515
 - 837.495
 - 884.515
 - 916.519
 - 956.537
 - 974.551
 - Overview:** ☐
 - Report top:** 5 hits
 - Start Search:** [Button]
 - Reset Form:** [Button]

[illegible]



MS-Fit Search Results

Press stop on your browser if you wish to abort this MS-Fit search prematurely.

Sample ID (comment): **nuceolin interaction**

Database searched: **SwissProt.2.26.2004**

Molecular weight search (1000 - 100000 Da) selects **136470** entries.

Full pl range: **144280** entries.

Species search (**HUMAN RODENT**) selects **20867** entries.

Combined molecular weight, pI and species searches select **18318** entries.

Pre searches select **18318** entries.

MS-Fit search selects **24** entries (results displayed for top **5** matches).

Parameters Used in Search

Considered modifications: | **Oxidation of M** | **Protein N-terminus Acetylated** |

Min. # Peptides to Match	Peptide Mass Tolerance (+/-)	Peptide Masses are	Digest Used	Max. # Missed Cleavages	Cysteines Modified by	Peptide N terminus	Peptide C terminus
4	50.000 ppm	monoisotopic	Trypsin	1	carbamidomethylation	Hydrogen (H)	Free Acid (OH)

Result Summary

Rank	MO WS E Score	# (%) Masses Matched	Protein MW (Da)/pI	Species	Accession #	Protein Name
1	240	5/28 (17.9%)	28787.9 / 5.2	HUMAN	Q92688	Acidic leucine-rich nuclear phosphoprotein 32 family member B (PHAPI2 protein) (Silver-stainable protein SSP29) (Acidic protein rich in leucines)