

LSUHSC Proteomics Core Facility

Applications Newsletter

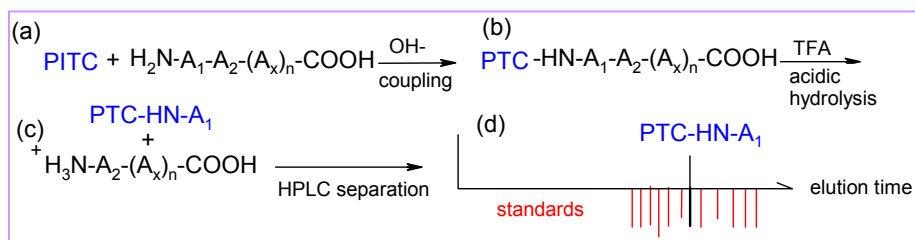
No.2 (June 1st, 2005)

Protein Identification by Peptide Mass Fingerprinting

The Facility currently provides **Protein Identification (ID) by Peptide Mass Fingerprinting (PMF)**, but does not yet offer **protein sequencing** by an automated Protein Sequencer. It is easy to confuse these two techniques. So in this issue we will clarify the principles behind protein sequencing and Protein ID by PMF.

Protein sequencing

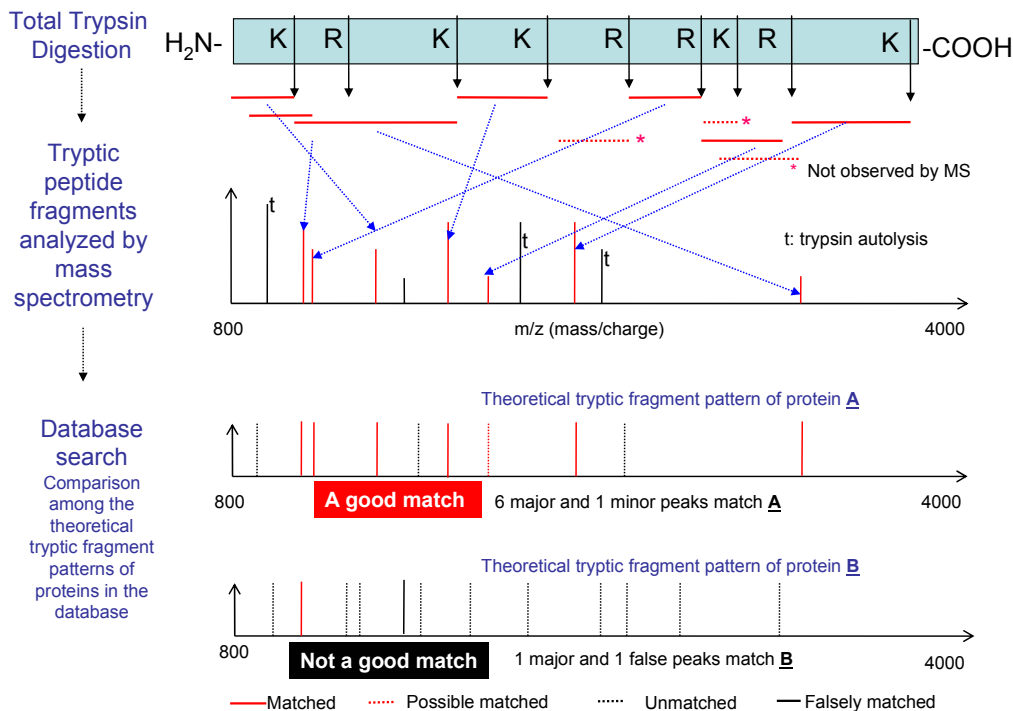
Protein sequencing is mostly done by amino-terminal sequencing. Edman Degradation is the most widely used method to obtain the *first 5-50 sequences of proteins/peptides at the unblocked N-terminal*. Each cycle can identify **one** sequence of the peptide/protein. The following scheme illustrates one cycle of Edman degradation (30-40 minutes/cycle):



The amino acid can be identified by comparing the elution time with those of the standards.

Protein Identification

Protein ID by PMF is the preferred technique for finding **the most probable candidates for unknown proteins**. PMF can find similar proteins in the current databases (gene and protein banks), which will suggest candidate proteins. The proteins (**mid ng level**) are subjected digestion by proteases, of which trypsin is the most commonly used for its very specific and active digestion at KX/RX (except KP/RP). The principle of protein ID is illustrated below:



See the Proteomics Core Web site for more information:
<http://www.medschool.lsuhs.edu/physiology/proteomics/>