PRODUCT INFORMATION

Trypsin MS approved — Art. No. 37286

Product Description:

General

Trypsin MS approved is a serine endopeptidase which specifically cleaves at the carboxyl side of lysine, arginine and S-aminoethyl cysteine residues. There is little or no cleavage at arginyl-proline or lysyl-proline bonds. Cleavage may also be reduced when acidic residues are present on either side of a potentially susceptible bond[1].

Trypsin is used in proteomics for peptide mapping due to its highly specific cleavage resulting in a limited number of tryptic peptides.

Features

- Source: porcine pancreas
- Purity: > 90 %
- Tryptic activity: > 6000 U/g*
- No chymotryptic activity detectable
- Modified by reductive methylation
- Each lot qualified by in-gel digestion and mass spectrometric analysis
- Quantity: ≥ 100 µg/vial, determined by measuring A280.

Storage

Trypsin MS approved should be stored **in a dry state** at -15 °C to -25 °C.

Digestion of proteins in solution

Lyophilized Trypsin MS approved is reconstituted in 50 mM acetic acid to a final concentration of 1 µg/µl. For digestion of the target protein add Trypsin to a final protease:protein ratio of 1:100 to 1:20 (w/w).

In-gel protein digestion

Lyophilized Trypsin MS approved is reconstituted in 50 mM acetic acid to a final concentration of 1 µg/µl.. Then add 25 mM NH_4HCO_3, pH 8 to make a concentration of 50 µg/ml.

For the final use dilute Trypsin solution 1:2.5 with 25 mM NH_4HCO_3, pH 8 and use 10 to 20 µl for rehydration / digestion of each gel piece.

Optional: To avoid clogging of the LC system clear the solution from the In-gel digest by centrifugation of extract the peptides, e.g. with acetic acid and acetonitrile.

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Quality control

Each lot of Trypsin MS approved is qualified by in-gel digestion and mass spectrometric analysis. An example of a spectrogram is shown in figure 1. Lot specific generated spectrograms using bovine serum albumin (BSA) as substrate are available at tech.service@serva.de.

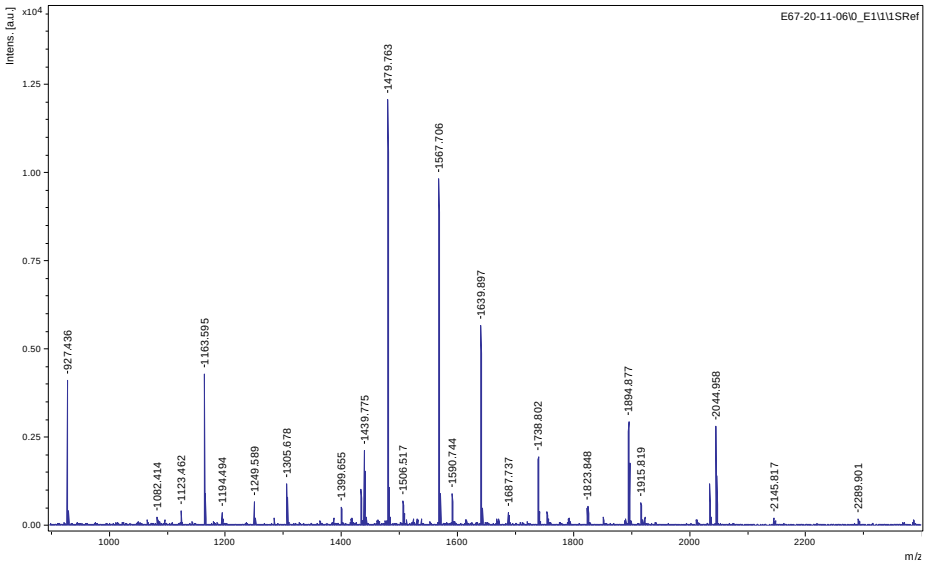

Fig. 1: Spectrogram of BSA digested with Trypsin MS approved. 300 ng BSA were separated by gel electrophoresis and digested with 10 ng/µl Trypsin MS approved in 50 mM NH_4HCO_3 at 37 °C overnight. The peptides generated were analyzed in reflectron mode using the Bruker Ultraflex MALDI-TOF/TOF mass spectrometer. Indicated mass values were identified as BSA protein using the Mascot search engine (Score >300). No tryptic autocatalytic digestion signals were identified (Ref. A. Pich, unpublished, Medical School Hanover (MHH)).

***Unit definition:** 1 U catalyzes the hydrolysis of 1 µmol Nα-Benzoyl-L-arginine-4-nitroanilide hydrochloride (BAPNA) per minute at 30 °C, pH 8.0.

[1]Wilkinson, J. M. (1986): Fragmentation of Polypeptides by Enzymatic Methods. In: *Practical Protein Chemistry: A Handbook*. A. Darbre, ed., John Wiley and Sons, New York, N.Y.

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