In-gel Tryptic digestion kit, Thermo Scientific Pierce

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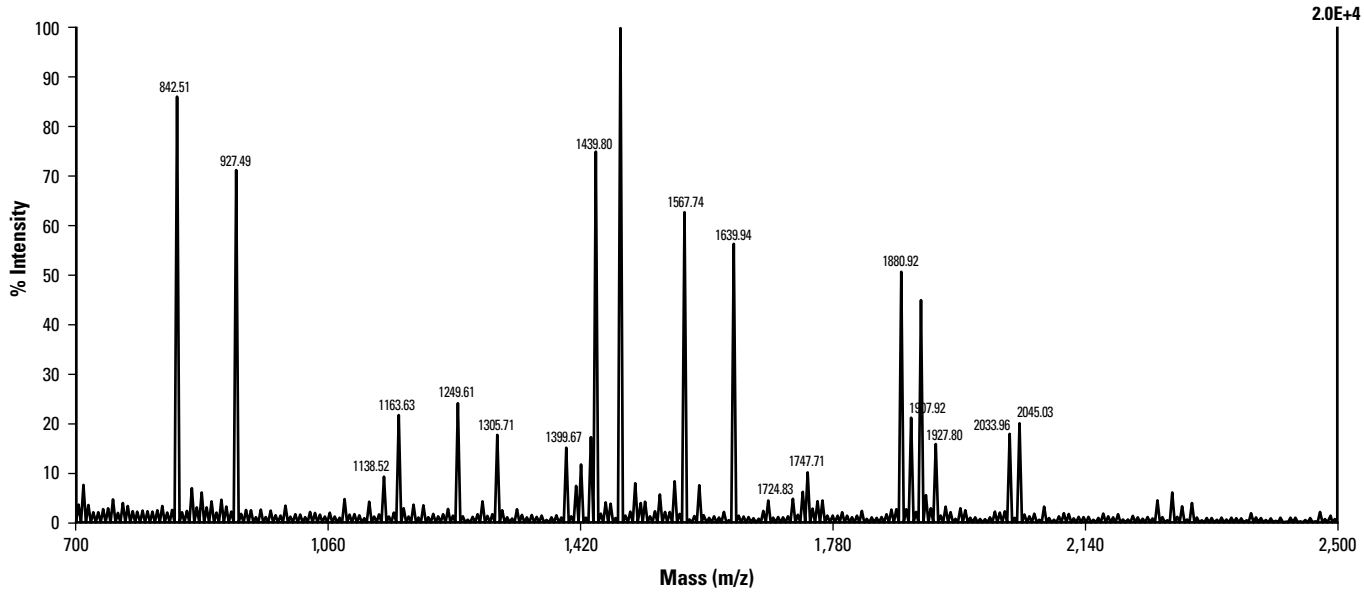

Catalogue No	Description
PN89871	**In-gel Tryptic digestion kit** Sufficient for approximately 150 in-gel digestions. Includes: Trypsin, modified, 20µg Trypsin storage solution, 40µL Acetonitrile, 70mL Ammonium Bicarbonate, 300mg Tris[2-carboxyethyl]phosphine (TCEP), 500µL Iodoacetamide, 500mg

MALDI-TOF MS analysis of bovine serum albumin (BSA) digest. Ten nanograms (150 fmol) of BSA was separated by SDS-PAGE and stained with Thermo Scientific GelCode Blue stain reagent and then processed with the in-gel Tryptic digestion kit. The resulting digest was treated with Thermo Scientific Pierce C-18 spin columns (**PN89870**) then subjected to analysis on an Applied Biosystems Voyager DE-PRO MALDI-MS in positive ion, linear, delayed-extraction mode. Database searches identified BSA with 47.0% sequence coverage.

In-solution Tryptic digestion and Guanidination kit, Thermo Scientific Pierce

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Analyse proteins by mass spec with confidence.

Trypsin specifically cleaves peptide bonds at the carboxyl side of arginine and lysine residues, generating a peptide map unique for each protein. Analysis of tryptic peptides by mass spectrometry (MS) provides a powerful tool for identifying proteins or analysing post-translational modifications. Reliable mass spectral analysis requires accurate and complete digestion of the target proteins as well as modification of peptides to optimise ionisation and detection. The in-solution Tryptic digestion and Guanidination kit contains optimised procedures and reagents for reduction, alkylation, digestion and guanidination to provide reliable MS analysis of approximately 90 protein samples containing 0.025 to 10µg of protein.

The in-solution Tryptic digestion and Guanidination kit contains a proteomics-grade modified trypsin that produces clean, complete digests with minimal autolysis products present. A reduction and alkylation protocol eliminates disulfide bonds, improving peptide identification and simplifying data analysis. Guanidination eliminates ionisation bias between peptides with C-terminal arginine residues over C-terminal lysine residues, improving detection and overall sequence coverage.

Proteins processed with the in-solution Tryptic digestion and Guanidination kit produce clean and reliable mass spectra with high sequence coverage (see table). Using the guanidination procedure to convert lysines to homoarginines enhances the overall signal intensity of lysine-containing peptides by an average of 1.5- to 4.0-times, eliminating the ionisation bias for peptides with a terminal arginine and improving sequence coverage and the reliability of data analysis.

Sequence coverage data for tryptic digestions with and without guanidination for three proteins

Protein	No Guanidination	With Guanidination[1]
Lysozyme (14,000 MW)	6/8 peptides 66/86aa 77%	8/8 peptides 86/86aa 100%
Myoglobin (17,000 MW)	6/12 peptides 78/134aa 58%	8/12 peptides 90/134aa 67%
BSA (66,000 MW)	25/44 peptides 318/489aa 65%	28/44 peptides 344/489aa 70%

[1]High levels of sequence coverage were obtained for all test proteins processed with the in-solution Tryptic digestion and Guanidination kit, especially when the guanidination procedure was used. Sequence coverage based only on those peptides expected to be identified based on scanning from 600 to 2,000m/z.

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