Trypsin-digested BSA
MS Standard (CAM-modified)

500 pmol Lot: 0051408 Exp: 8/16
freeze dried Store at –20°C

Description: A complex mixture of peptides produced by Trypsin digestion of Bovine Serum Albumin (BSA) that was reduced and alkylated with iodoacetamide (CAM modified). This peptide mixture can be used to test a Matrix-Assisted Laser Desorption/Ionization Time-Of-Flight (MALDI-TOF) or Electrospray Ionization (ESI) mass spectrometer (TOF, Q-TOF or Ion Trap).

Source: BSA (GENBANK P02769) was digested using Modified Trypsin (TPCK-treated).

Useful Range: 500 to 3000 Daltons.

Quality Assurance: Peptides are free of salts, glycerol and detergents.

Quality Controls
Nanoc-L-ESI MS/MS: One hundred fmol of the peptide mixture was subjected to nano-reverse-phase liquid chromatography on an Agilent Nanoc LC C18/Chip 6330 Ion Trap and developed with a water to acetonitrile gradient with both solvents containing 0.1% formic acid. The MS/MS data were analyzed with Mascot, 250 spectra were selected for analysis and a score of 600 or greater was obtained.

MALDI-TOF MS: 0.1 to 1 µl of each of the peptide mixture was subjected to MALDI analysis using Matrix-Assisted Laser Desorption/Ionization MS/MS analysis on Waters Micro MX MALDI-TOF MS. The spectra obtained contains more than 15 resolved peaks which match the theoretical peaks.

Notes: Suggested volume to resuspend: 500 µl. Avoid repeated freeze/thaw cycles once in solution.

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MALDI-TOF MS: 0.1 to 1 µl of each of the peptide mixture (0.5 to 5 pmol) was mixed with 1 µl of α-cyano-4-hydroxycinnamic acid matrix solution, air-dried and subjected to MALDI-TOF MS analysis on a Waters Micro MX MALDI-TOF MS. The spectra obtained contains more than 15 resolved peaks which match the theoretical peaks.

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Online Analysis of BSA Digest: The BSA digest solution was diluted to 100 fmol/μl with 0.1% formic acid. Ten μl (1 pmol) of the digest solution was injected via an Easy-nanoLC II (Proxeon) onto a self-packed reverse phase C18 nano column (Phenomenex packing material, 5 cm, 150 μm), washed, and loaded onto a self-packed C18 analytical column with an integrated tip (New Objective Picofrit, 15 cm, 100 μm, Phenomenex packing material). Peptides were separated using a 60 min 5-100%B linear gradient (A = 0.1% formic acid, B = CH3CN, 0.1% formic acid) at a flow rate of 500 nl/min. Eluting peptides were analyzed online by an LTQ Orbitrap XL mass spectrometer (Thermo Scientific) with an electrospray ion source. MS/MS spectra were acquired by CID using an acquisition range of 400 to 1600 m/z.