

Recombinant Trypsin-N, Mass Spec Grade

Cat. No. Trypsin-N-39 **Lot. No.** (See product label)

SPECIFICATION

Product Overview

Description	rTrypsin-N, Mass Spec Grade, is an innovative protease that specifically hydrolyzes peptide bonds at the amino side of lysine and arginine residues. rTrypsin-N can be applied for post-translational modification (PTM) proteins research and is beat for protein sequencing. Peptides produced more b ions than y ions in the mass spectrometer.
Form	Supplied by lyophilized powder with 0.47 mg HEPES; 0.05 mg CaCl ₂ per vial.
Bio-activity	152 units/mg
Molecular Mass	29 kDa
Purity	> 99.5 % rTrypsin-N peak area analyzed by HPLC at 280 nm.
Storage	Store the lyophilized powder at -20 centigrade, and reconstituted enzyme at -80 centigrade for up to 30 days.
Shelf life	24 months at -80 centigrade
Stability	rTrypsin-N is maximally active at pH 7.5.
Usage Notes	In-Solution Protein Digestion Protocol: 1. For maximum activity, resuspend Mass Spec Grade rTrypsin-N in 200 µL distilled water, pH 7.5. 2. Use 20-50 mM HEPES

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	solution, 0.1 % BT Surfactant, or Tris-HCl (pH 7.5) for the protein mixture cleavage (recommended). 3. Add 0.5µg/µL rTrypsin-N to a final enzyme : substrate ratio of 1: 30. Mix well and incubated at 37 centigrade for 4 h.
Specificity	< 5 % nonspecific cleavage with Human Serum Albumin (HSA) sample. Digested products were incubated at 37 centigrade for 4 h, and was nonspecific cleavage was analyzed by LC-MS/MS.
Unit Definition	One unit is the amount of Mass spectrum Grade rTrypsin-N will hydrolyze per minutes at pH 10 at 25 centigrade, OD366, Light path = 1 cm.
LC-MS/MS Analysis	HSA samples were dissolved and denatured for at 37 centigrade for 1 h. The denatured HSA was diluted at pH 7.5 and incubated with rTrypsin-N for 4 h. The digest was analyzed by LC-MS/MS, and the peptides results matched the peptides generated in a theoretical digestion results of HSA by rTrypsin-N.
Resuspension Buffer	200 µL distilled water, pH 7.5
MALDI-TOF Analysis	rTrysin-N is analyzed by MALDI-TOF, impurity peak is not found.