北京生夏蛋白
BEIJING LIFE PROTEOMIC

Product Information | Certification of Analysis

I Product Information

CAS: N/A

Lot No.

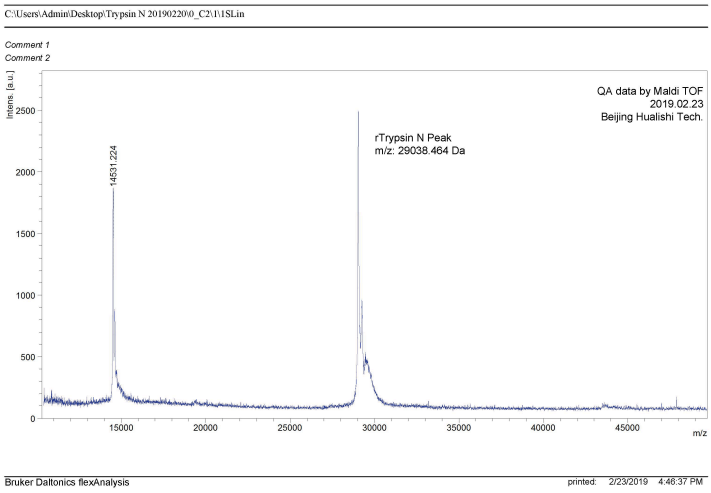
rTrypsin-N, Mass Spec Grade

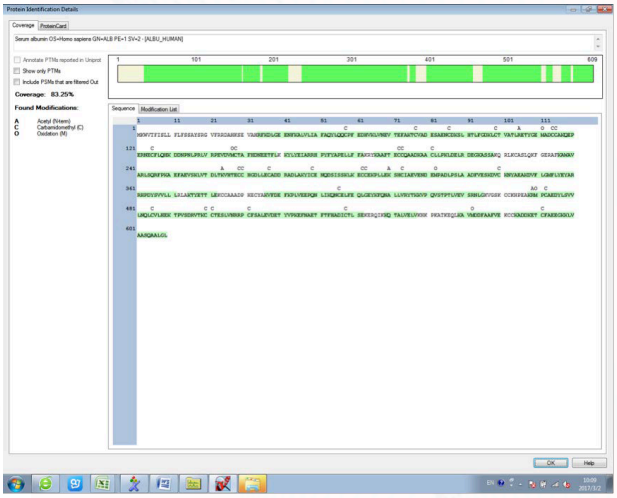
Part No.	Name	Size/pkg
HLS TRY001N	rTrypsin-N, Mass Spec Grade	20 μg

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.
Physical Appearance: Supplied by lyophilized powder with 0.47 mg HEPES; 0.05mg $CaCl_2$ per vial.
Molecular Weight: 29 kDa
Resuspension Buffer: 200 μL distilled water, pH 7.5
Storage Conditions: Store the lyophilized powder at –20°C, and reconstituted enzyme at –80 °C for up to 30 days.
Shelf life: 24 months at -80 °C
Stability: rTrypsin-N is maximally active at pH 7.5.
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 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 °C for 4 h.

I Quality Control

Purity: > 99.5% rTrypsin-N peak area analyzed by HPLC at 280 nm.
Specificity: < 5% nonspecific cleavage with Human Serum Albumin (HSA) sample. Digested products were incubated at 37 °C for 4 h, and was nonspecific cleavage was analyzed by LC-MS/MS.
Activity: 152 units/mg
Unit Definition: One unit is the amount of Mass spectrum Grade rTrypsin-N will hydrolyze per minutes at pH 10 at 25 °C, OD366, Light path = 1 cm.
MALDI-TOF Analysis: rTrysin-N is analyzed by MALDI-TOF, impurity peak is not found.
LC-MS/MS Analysis: HSA samples were dissolved and denatured for at 37 °C 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.





QA Manager Signature:

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