

Product Information | Certification of Analysis

I Product Information

CAS: 66676-43-5 Lot No.

rGiu-C I mass Spec Grade					
Part No.	Name	Size/pkg			
HLS GLU001C	rGlu-C, Mass Spec Grade	50µg			

Description: Endoproteinase rGlu-C, Mass Spec Grade, is a serine proteinase that specifically cleaves peptide bonds at C-terminal to glutamic acid residues. Enzyme specificity to glutamic acid is high in ammonium bicarbonate and ammonium acetate. In phosphate buffers, cleavage occurs at both aspartic and glutamic residues. rGlu-C activity is optimal in the pH range of 4.0 - 9.0. This mass spec grade enzyme can be used alone or in combination with other proteases to generate protein digests.

Physical form: Lyophilized in the presence of trehalose (1.65mg/vial)

Molecular Weight: 24 kDa

Resuspension Buffer: Resuspend rGlu-C powder in double-distilled water from user.

Storage Conditions: Store the lyophilized powder at -4 °C or 20 °C; store reconstituted enzyme solution at -20 °C for up to 8 weeks.

Shelf life: 36 months at -20 °C

Stability: Maximally active in the pH range of 4-9

In-Solution Protein Digestion Protocol (recommended):

- 1. For maximum activity, resuspend Mass Spectrum Grade rGlu-C with the double-distilled from user.
- 2. Dissolve protein samples with Tris-HCI (pH 8) buffer to a final protein concentration of 50 mM prior to digestion.
- 3. Add rGlu-C proteinase to a protein : proteinase ratio of 20 : 1(w/w). Mix well and incubate at 37 °C for 4 h.

I Quality Control

Purity: > 99.5% peak area of rGlu-C, analyzed by HPLC at 280 nm.

Specificity : No prominent nonspecific peaks are observed by HPLC analysis after 16 hours of incubation of HSA with Glu-C compared to the 1-hour digestion

Activity: 800 U/min/mg.

Unit Definition: One unit is the amount of Mass spectrum Grade rGlu-C will hydrolyze 1.0 µmol of N-t-Boc--Lglutamic acid a-phenyl easter per minute at pH 7.8 at 37 °C, A270, and Light path=1 cm

MALDI-TOF Analysis: Impurity is not found in rGlu-C proteinase analyzed by MALDI-TOF.

LC-MS/MS Analysis: Human Serum Albumin (HSA) was dissolved, denatured at 37 °C for 1 h, diluted at pH 8.0, and incubated with rGlu-C for 4 h. The digest was analyzed by LC-MS/MS, and peptide results matched the peptides generated in a theoretical digests of HSA by rGlu-C.





(MATRIX) SCIENCE Mascot Search Results

Protein View

Match to: D6RHD5 Score: 11617 Serum albumin OS-Homo sapiens GN=ALB PE=1 SV=1 Found in search of HSA-TEST-GLU-C_20151119-mgf.mgf

Nominal mass (M_z) : 53565; Calculated pI value: 6.45 NCBI BLAST search of <u>D6RHD5</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Fixed modifications: Carbamidomethyl (C) Variable modifications: Acetyl (N-term),Oxidation (M) Cleavage by V8-DE: cuts C-term side of BDEZ unless next residue is P Sequence Coverage: 82%

Matched peptides shown in Bold Red

1	MSQLKIVTNH	LYLYEIARRH	PYFYAPELLF	FARRYRAAFT	ECCQAADRAA
51	CLLPKLDELR	DEGRASSARQ	RLRCASLORP	GERAFRAWAV	ARLSQRPPKA
101	EFAEVSKLVT	DLTRVHTECC	HGDLLECADD	RADLARYICE	NQDSISSKLK
151	ECCERPLLEK	SHCIAEVEND	EMPADLPSLA	ADFVE SKDVC	KNYAEARDVF
201	LOMPLYEYAR	RHPDYSVVLL	LRLARTYETT	LERCCAAADP	HECYARVFDE
251	FRPLVEEPQN	LIRQNCELFE	QLGE YKFQNA	LLVRYTKKVP	QVSTPTLVEV
301	SRNLGRVGSR	CCRHPEARRM	PCAEDYLSVV	LNQLCVLHER	TPVSDRVTRC
351	CTESLVNRRP	CFSALEVDET	YVPREFNAET	FTFHADICTL	SEKERQIKKQ
401	TALVELVKHK	PKATKEQLKA	VMDDFAAFVE	KCCKADDKET	CFAEEGKKLV
451	AASQAALGL				

QA Manager Signature:

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