KRISHZYME™ Endoproteinase Lys-C

(Lysyl Endopeptidase / Achromobacter Lyticus Lys-c)

Catalog Number: KBENZ49

Description

The KRISHZYME™ Endoproteinase Glu-C (Lysyl-endopeptidase / (Lys-c)) was isolated from the Gramnegative soil bacterium Achromobacter lyticus. The protein hydrolyzes amide and peptide ester bonds at the carboxylic side of lysine and S-aminoethylcysteine residues making it an important tool for enzymatic protein sequencing and Lys-X compound synthesis. The enzyme functions optimally between 30 – 37oC and suffers from degradation when subjected to temperatures above 50oC. Lysyl-endopeptidase retains complete activity after incubation in 4M urea or in 0.1% SDS solution for up to 6 hours at 30oC. Conversely, the enzyme is inhibited by DFP, PMSF, TLCK. Lysyl endopeptidase is involved during the production of recombinant insulin and in proteomics research.

Source:

Achromobacter Lyticus

Expression Host:

E.coli

Purity:

>95% as determined by SDS-PAGE quantitative densitometry by Coomassie Blue Staining.

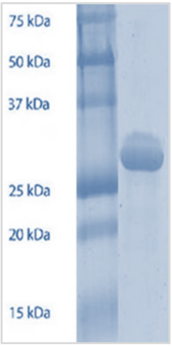
Endotoxin:

< 0.05 EU/1000 units as determined by the LAL method.

Molecular Mass:

The KRISHZYME™ Endoproteinase Lys C has a calculated molecular mass of 34 kDa

SDS-PAGE:
Fig.1.



KDa Marker

Fig. 1. Purity analysis by SDS-PAGE Detection

Activity:

~1.1 U/mg

Formulation:

KRISHZYME™ Endoproteinase Lys-C is supplied as a lyophilized product from buffer of 50 mM Tris-HCl, pH 8.0, 3% mannitol

Reconstitution:

Being an enzyme, the concentration may differ from lot to lot. We always recommend referring the accompanying data sheet to view the exact concentration and the recommended dilution schemata.

Centrifuge the vial at 4ºC before opening to recover the entire contents. Please contact us for any concerns or special requirements at +91-22-49198700 | Email: sales1@krishgen.com

Storage:

Store it under sterile conditions at -20ºC to -80ºC upon receiving for at least 12 months. It is recommended to aliquot the enzyme into smaller quantities for optimal storage. Avoid repeated freeze-thaw cycles.

Application:

- Protein Sequencing and Peptide Mapping
- Glu-C is commonly used to digest proteins into peptides for LC-MS/MS analysis, particularly when trypsin does not provide optimal coverage.
- Glu-C cleavage generates different peptide fragments than trypsin (which cleaves after Lys/Arg), enhancing sequence coverage in proteomic studies.
- Helps identify specific proteins based on their digestion pattern.
- When phosphorylation occurs near tryptic cleavage sites and limits trypsin effectiveness, Glu-C digestion provides an alternative cleavage pattern.
- Assists in structural characterization of glycoproteins by generating suitable peptides for MS.
- Used to determine functional domains of proteins by selective cleavage, helping identify epitope regions for antibody development.
- Helps truncate flexible or unstructured regions to improve crystallization success.
- Used in peptide mapping protocols to compare primary structures and modifications between innovator biologics and biosimilars.
- Enables middle-down or bottom-up proteomics workflows, particularly to identify disulfide bonds, sequence variants, or PTMs (post-translational modifications).
- Histones are highly basic proteins with modifications such as methylation and acetylation. Glu-C is valuable for generating peptides that retain these PTMs for downstream MS detection.

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