KRISHGEN BioSystems
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KRISHZYME™ Endoproteinase Glu-C

Catalog Number: KBENZ48

Protein Description

The KRISHZYME™ Endoproteinase Glu-C (Protease S. aureus V8) specifically cleaves peptide bonds on the COOH-terminal side of either aspartic or glutamic acids. In the presence of ammonium, the enzyme specificity is limited to glutamic sites. It has a molecular weight of 27,000 daltons and optimum pH's of 4.0 and 7.8 with hemoglobin as the substrate. Protease S. aureus V8 is inhibited by diisopropylfluorophosphate and monovalent anions such as F-, Cl-, CH3COO- and NO3.

Source:

Staphylococcus aureus V8

Expression Host:

E.coli

Purity:

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

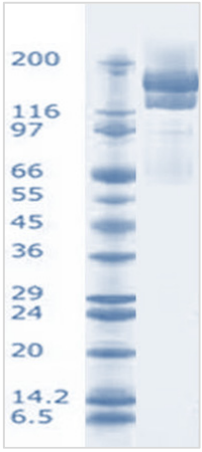
Endotoxin:

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

Molecular Mass:

The KRISHZYME™ Endoproteinase Glu C has a calculated molecular mass of 27 kDa

SDS-PAGE:
Fig.1.



KDa Marker

Fig. 1. Purity analysis by SDS-PAGE Detection

Concentration:

500 U/mg

Unit Definition:

One Unit causes a change of 0.001 A280 nm per minute at 37°C, pH 7.8 using casein as the substrate.

Formulation:

KRISHZYME™ Endoproteinase Glu-C is supplied as a lyophilized product from buffer of 25 mM Tris-HCl, 50 mM NaCl, 1 mM EDTA, 50% glycerol.

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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