

Human OTUB2 Protein (His Tag)

Catalog Number: 13177-H07E



Sino Biological Inc.
Biological Solution Specialist

General Information

Gene Name Synonym:

C14orf137; OTB2; OTU2; 2010015L18Rik; 4930586I02Rik; AI413508; AW557219; OTB2; OTU2

Protein Construction:

A DNA sequence encoding the human OTUB2 (Q96DC9-1) (Met 1-His 234) was expressed, with a polyhistidine tag at the N-terminus.

Source: Human

Expression Host: E. coli

QC Testing

Purity: > 97 % as determined by SDS-PAGE

Endotoxin:

Please contact us for more information.

Stability:

Samples are stable for up to twelve months from date of receipt at -70 °C

Predicted N terminal: Met

Molecular Mass:

The recombinant human OTUB2 consisting of 249 amino acids and has a calculated molecular mass of 29 kDa. It migrates as an approximately 30 kDa band in SDS-PAGE under reducing conditions.

Formulation:

Lyophilized from sterile PBS, 10% glycerol, pH 7.5

Normally 5 % - 8 % trehalose, mannitol and 0.01% Tween80 are added as protectants before lyophilization. Specific concentrations are included in the hardcopy of COA. Please contact us for any concerns or special requirements.

Usage Guide

Storage:

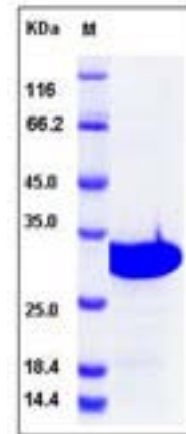
Store it under sterile conditions at -20°C to -80°C upon receiving. Recommend to aliquot the protein into smaller quantities for optimal storage.

Avoid repeated freeze-thaw cycles.

Reconstitution:

Detailed reconstitution instructions are sent along with the products.

SDS-PAGE:



Protein Description

Otubain 2 (OTUB2) is a member of DUBs that belong to the ovarian tumour (OTU) superfamily of proteins which consists of a five-stranded β -sheet sandwiched in between a small helical amino-terminal region consisting of α 1 and α 2, and a large helical region comprised of α 3- α 10. Like other DUBs, otubain 2 (OTUB2) cleaves proteins precisely at the ubiquitin-protein bond so that ubiquitylation process can be reversed and regulated. Otubain 2 (OTUB2)'s active-site cleft is sterically occluded by a novel loop conformation resulting in an oxyanion hole, which consists uniquely of backbone amides. Furthermore, the residues that orient and stabilize the active-site histidine of otubain 2 (OTUB2) are different from other cysteine proteases. This reorganization of the active-site topology provides a possible explanation for the low turnover and substrate specificity of the otubains.

References

1. Balakirev MY, et al. (2003) Otubains: a new family of cysteine proteases in the ubiquitin pathway. EMBO Rep 4 (5): 517-22.
2. Nanao MH. (2004) Crystal structure of human otubain 2. EMBO reports. 5: 783-8.

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