

Human PLBD2 Protein (His Tag)

Catalog Number: 13947-H08H



Sino Biological Inc.

Biological Solution Specialist

General Information

Gene Name Synonym:

P76; 1300012G16Rik; AU019810; P76

Protein Construction:

A DNA sequence encoding the human PLBD2 (Q8NHP8) (Met1-Asp589) was expressed with a polyhistidine tag at the C-terminus.

Source: Human

Expression Host: Human Cells

QC Testing

Purity: (69.5+23.3+6.5) % as determined by SDS-PAGE

Endotoxin:

< 1.0 EU per µg of the protein as determined by the LAL method

Stability:

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

Predicted N terminal: Ile 42

Molecular Mass:

The recombinant human PLBD2 consists of 559 amino acids and predicts a molecular mass of 62.7 KDa. It migrates as an approximately 68,46 and 34 KDa band in SDS-PAGE under reducing conditions.

Formulation:

Lyophilized from sterile PBS, pH 7.4.

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:

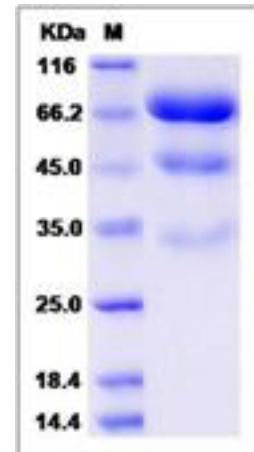
Store it under sterile conditions at -20°C to -80°C upon receiving. Recommend to aliquot the protein into smaller quantities for optimal storage.

Avoid repeated freeze-thaw cycles.

Reconstitution:

Detailed reconstitution instructions are sent along with the products.

SDS-PAGE:



Protein Description

PLBD2 localizes to the lysosome, as its absence could plausibly lead to a serious yet unrecognized lysosomal storage disease. PLBD1 and PLBD2 are semi-orphans in the sense of being probable phospholipases of B class but with uncertain physiological substrates and thus functionalities. PLBD1 and PLBD2 constitute a small gene family (sequence homology class) within vertebrates though one that occurs expanded in some early diverging eukaryotes. PLBD2 presents a special difficulty in that a sequence of post-translational steps are apparently necessary for its activation. Without these, potential substrates can hardly be assayed. These steps include removal of the signal peptide, mannosylation appropriate to the lysosome targeting receptor, and self-catalytic proteolytic activation to expose the substrate binding site as this becomes appropriate.

References

- 1.Morgan CP. et al., 2004), Biochem J. 382 (2): 441-9.
- 2.Kim W. et al., 2011, Mol Cell. 44 (2): 325-40.
- 3.Havugimana PC. et al., 2012. Cell. 150 (5): 1068-81.

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