

Human ACPL2 Protein (His Tag)

Catalog Number: 11243-H08H



Sino Biological Inc.
Biological Solution Specialist

General Information

Gene Name Synonym:

ACPL2; FLJ23751; UNQ370/PRO706

Protein Construction:

A DNA sequence encoding the human ACPL2 (NP_689495.1) (Met 1-Phe 480) precursor was fused with a polyhistidine tag at the C-terminus.

Source: Human

Expression Host: Human Cells

QC Testing

Purity: > 95 % 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: Leu 24

Molecular Mass:

The recombinant human ACPL2 consists of 468 amino acids after removal of the signal peptide and has a predicted molecular mass of 54 kDa. It migrates as an approximately 50 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:

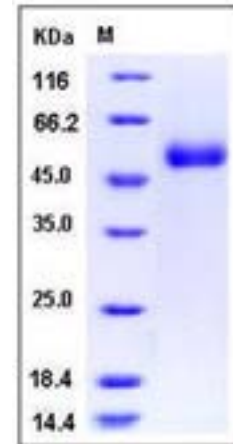
Store it under sterile conditions at -20°C to -80°C upon receiving. Recommend to aliquot the protein into smaller quantities for optimal storage.

Avoid repeated freeze-thaw cycles.

Reconstitution:

Detailed reconstitution instructions are sent along with the products.

SDS-PAGE:



Protein Description

acid phosphatase-like protein 2, also known as ACPL2, is a secreted protein which belongs to the histidine acid phosphatase family. A large-scale effort, termed the Secreted Protein Discovery Initiative (SPDI), was undertaken to identify novel secreted and transmembrane proteins. In the first of several approaches, a biological signal sequence trap in yeast cells was utilized to identify cDNA clones encoding putative secreted proteins. A second strategy utilized various algorithms that recognize features such as the hydrophobic properties of signal sequences to identify putative proteins encoded by expressed sequence tags (ESTs) from human cDNA libraries. A third approach surveyed ESTs for protein sequence similarity to a set of known receptors and their ligands with the BLAST algorithm. Finally, both signal-sequence prediction algorithms and BLAST were used to identify single exons of potential genes from within human genomic sequence.

References

1. Clark HF., et al., 2003, Genome Res. 13: 2265-70.
2. Ota T.et al., 2004, Nat. Genet. 36:40-5.

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Fax :+86-10-51029969 • Tel:+86-400-890-9989 • <http://www.sinobiological.com>