

# Recombinant Human ACPL2 Protein (His Tag)

Catalog Number:PKSH031183



**Note:** Centrifuge before opening to ensure complete recovery of vial contents.

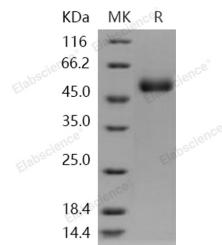
## Description

<b>Synonyms</b>	ACPL2;FLJ23751;UNQ370/PRO706
<b>Species</b>	Human
<b>Expression Host</b>	HEK293 Cells
<b>Sequence</b>	Met 1-Phe 480
<b>Accession</b>	NP_689495.1
<b>Calculated Molecular Weight</b>	54.0 kDa
<b>Observed molecular weight</b>	50 kDa
<b>Tag</b>	C-His

## Properties

<b>Purity</b>	> 95 % as determined by reducing SDS-PAGE.
<b>Endotoxin</b>	< 1.0 EU per $\mu$ g of the protein as determined by the LAL method.
<b>Storage</b>	Generally, lyophilized proteins are stable for up to 12 months when stored at -20 to -80°C. Reconstituted protein solution can be stored at 4-8°C for 2-7 days. Aliquots of reconstituted samples are stable at < -20°C for 3 months.
<b>Shipping</b>	This product is provided as lyophilized powder which is shipped with ice packs.
<b>Formulation</b>	Lyophilized from sterile PBS, pH 7.4 Normally 5 % - 8 % trehalose, mannitol and 0.01% Tween80 are added as protectants before lyophilization. Please refer to the specific buffer information in the printed manual.
<b>Reconstitution</b>	Please refer to the printed manual for detailed information.

## Data



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## Background

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

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