Recombinant Human ACPL2 Protein (His Tag)

Catalog Number:PKSH031183

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

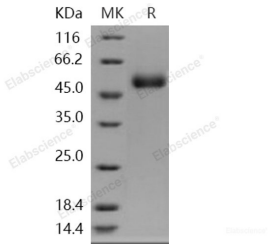
Description

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

Properties

Purity	> 95 % as determined by reducing SDS-PAGE.
Endotoxin	< 1.0 EU per μg of the protein as determined by the LAL method.
Storage	Generally, lyophilized proteins are stable for up to 12 months when stored at -20 to -80℃. Reconstituted protein solution can be stored at 4-8℃ for 2-7 days. Aliquots of reconstituted samples are stable at < -20℃ for 3 months.
Shipping	This product is provided as lyophilized powder which is shipped with ice packs.
Formulation	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.
Reconstitution	Please refer to the printed manual for detailed information.

Data



> 95 % as determined by reducing SDS-PAGE.

Background

acid phosphatase-like protein 2, also known as ACPL2, is a secreted protein which belongs to thehistidine 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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