Data Sheet (Cat.No.TMPY-01586)

TargetMol

ACPL2 Protein, Human, Recombinant (His)

General Information

Synonyms:	ACPL2;UNQ37/PRO76;FLJ23751
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. Predicted N terminal: Leu 24
Species:	Human
Expression Host:	HEK293 Cells
Accession:	Q8TE99-1
Molecular Weight:	54 kDa (predicted); 50 kDa (reducing conditions)

QC Testing

Biological Activity:	Activity testing is in progress. It is theoretically active, but we cannot guarantee it. If you require protein activity, we recommend choosing the eukaryotic expression version first.
Purity:	> 95 % as determined by SDS-PAGE
Endotoxin:	< 1.0 EU/μg of the protein as determined by the LAL method.
Formulation:	Lyophilized from a solution filtered through a 0.22 μm filter, containing PBS, pH 7.4. Typically, a mixture containing 5% to 8% trehalose, mannitol, and 0.01% Tween 80 is incorporated as a protective agent before lyophilization.

Preparation and Storage

Reconstitution:

A Certificate of Analysis (CoA) containing reconstitution instructions is included with the products. Please refer to the CoA for detailed information.

Stability & Storage:

It is recommended to store recombinant proteins at -20°C to -80°C for future use. Lyophilized powders can be stably stored for over 12 months, while liquid products can be stored for 6-12 months at -80°C. For reconstituted protein solutions, the solution can be stored at -20°C to -80°C for at least 3 months. Please avoid multiple freeze-thaw cycles and store products in aliquots.

Actual storage temperature shall be subject to the COA.

Shipping:

In general, lyophilized powders are shipped with blue ice, while solutions are shipped with dry ice.

Protein 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 sequence.

Reference

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