

Human ABHD4 Protein (His Tag)

Catalog Number: 11097-H07B



Sino Biological Inc.

Biological Solution Specialist

General Information

Gene Name Synonym:

ABHD4, ABH4, FLJ12816

Protein Construction:

A DNA sequence encoding the full length of human ABHD4 (NP_071343.2) (Met 1-Asp 342) was expressed, with a polyhistidine tag at the N-terminus.

Source: Human

Expression Host: Baculovirus-Insect Cells

QC Testing

Purity: > 82 % 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: His

Molecular Mass:

The recombinant human ABHD4 consists of 360 amino acids and predicts a molecular mass of 41 kDa. It migrates as an approximately 40 kDa band in SDS-PAGE under reducing conditions.

Formulation:

Lyophilized from sterile 50mM Tris, 100mM NaCl, pH 8.0

Normally 5 % - 8 % trehalose and mannitol are added as protectants before lyophilization. Specific concentrations are included in the hardcopy of COA. Please contact us for any concerns or special requirements.

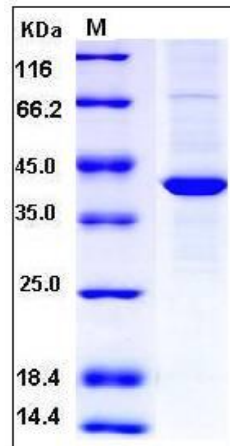
Usage Guide

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.

SDS-PAGE:



Reconstitution:

Detailed reconstitution instructions are sent along with the products.

Protein Description

Abhydrolase domain-containing protein 4, also known as Lyso-N-acylphosphatidylethanolamine lipase, Alpha/beta-hydrolase 4 and ABHD4, is a protein which belongs to the peptidase S33 family and ABHD4 / ABHD5 subfamily. The alpha/beta hydrolase fold is common to a number of hydrolytic enzymes of widely differing phylogenetic origin and catalytic function. The core of each enzyme is an alpha/beta-sheet (rather than a barrel), containing 8 strands connected by helices. The enzymes are believed to have diverged from a common ancestor, preserving the arrangement of the catalytic residues. All have a catalytic triad, the elements of which are borne on loops, which are the best-conserved structural features of the fold. ABHD4 lysophospholipase selective for N-acyl phosphatidylethanolamine (NAPE). ABHD4 contributes to the biosynthesis of N-acyl ethanolamines, including the endocannabinoid anandamide by hydrolyzing the sn-1 and sn-2 acyl chains from N-acyl phosphatidylethanolamine (NAPE) generating glycerophospho-N-acyl ethanolamine (GP-NAE), an intermediate for N-acyl ethanolamine biosynthesis. ABHD4 hydrolyzes substrates bearing saturated, monounsaturated, polyunsaturated N-acyl chains.

References

1. Ollis, D L. et al., 1992, Protein Eng.5 (3): 197-211.
2. Liu, J. et al., 2008, Neuropharmacology. 54 (1):1-7.
3. Katz-Jaffe, M.G. et al., 2009, Theriogenology.71 (6): 939-46.

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