

# Recombinant Human PSAP Protein(His Tag)

Catalog Number: PDMH100202



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

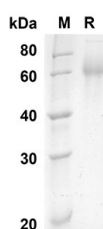
## Description

<b>Species</b>	Human
<b>Source</b>	Mammalian-derived Human PSAP protein Met1-Asn524, with an C-terminal His
<b>Mol_Mass</b>	57.5 kDa
<b>Accession</b>	P07602
<b>Bio-activity</b>	Not validated for activity

## Properties

<b>Purity</b>	> 90% as determined by reducing SDS-PAGE.
<b>Endotoxin</b>	< 1.0 EU/mg 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 a 0.2 µm filtered solution in PBS with 5% Trehalose and 5% Mannitol.
<b>Reconstitution</b>	It is recommended that sterile water be added to the vial to prepare a stock solution of 0.5 mg/mL. Concentration is measured by UV-Vis.

## Data



SDS-PAGE analysis of Human PSAP proteins, 2 µg/lane of Recombinant Human PSAP proteins was resolved with SDS-PAGE under reducing conditions, showing bands at 57.5 KD

## Background

This gene encodes a highly conserved preproprotein that is proteolytically processed to generate four main cleavage products including saposins A, B, C, and D. Each domain of the precursor protein is approximately 80 amino acid residues long with nearly identical placement of cysteine residues and glycosylation sites. Saposins A-D localize primarily to the lysosomal compartment where they facilitate the catabolism of glycosphingolipids with short oligosaccharide groups. The precursor protein exists both as a secretory protein and as an integral membrane protein and has neurotrophic activities. Mutations in this gene have been associated with Gaucher disease and metachromatic leukodystrophy. Alternative splicing results in multiple transcript variants, at least one of which encodes an isoform that is proteolytically processed.

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