Product Data Sheet

Cat# **SP-86870-1**

Description: Saposin C18 (AA: Val-Lys-Glu-Val-Thr-Lys-Leu-Ile-Asp-Asn-Asn-Lys-Thr-Glu-Lys-Glu-Ile-Leu) (MW: 2114.49)

Size: 1 mg

Purity: >95%

Store: Desiccated at -20oC.

Prosaposin also known as PSAP is a protein which in humans is encoded by the PSAP gene. This highly conserved glycoprotein is a precursor for 4 cleavage products: **saposins A, B, C, and D**. Saposin is an acronym for Sphingolipid Activator PrO[S]teINs. 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. Saposins A-D are required for the hydrolysis of certain sphingolipids by specific lysosomal hydrolases.

The neurotrophic activity of prosaposin resides in the saposin C domain. The active sequence pinpointed to a linear 12-mer is located in the NH2-terminal sequence of saposin C. Studies of the neuroblastoma line NS20Y using a radiolabeled 18-mer from the neurotrophic region identified a high-affinity (Kd = 70 pM) binding site indicative of receptor-ligand interaction.

Every saposin contains about 80 amino acid residues and has six equally placed cytesines, two prolines, and a glycosylation site (two in saposin A, one each in saposins B, C, and D). Since saposins characteristics of extreme heat-stability, adundance of disulfide linkages, and resistance to most proteases, they are assumed to be extremely compact and rigidly disulfide-linked molecules. Each saposin has an α-helical structure that is seen as being important for stimulation because this structure is maximal at a pH of 4.5; which is optimal for many lysosomal hydrolases.[3] This helical structure is seen in all (especially with the first region), but saposin has been predicted to have β-sheet configuration due to it first 24 amino acids of the N-end.

References: Morimoto S (1990) PNAS 87, 3493-3497; Kishimoto Y (1992) J. Lipid Res. 33, 1255-1267; O'Brien JS (1991) FAEB J. 5, 301-308; Hofmann K (1996) Trend Microbiol. 4, 91-94.

Related Items:

Catalog#	ProdDescription
SP-86869-1	Saposin C22 (AA: Cys-Glu-Phe-Leu-Val-Lys-Glu-Val-Thr-Lys-Leu-Ile-Asp-Asn-Asn-Lys-Thr-Glu-Lys-Glu-Ile-Leu) (MW: 2607.08)
SP-86870-1	Saposin C18 (AA: Val-Lys-Glu-Val-Thr-Lys-Leu-Ile-Asp-Asn-Asn-Lys-Thr-Glu-Lys-Glu-Ile-Leu) (MW: 2114.49)
SP-86871-5	Saposin C12 (AA: Leu-Ile-Asp-Asn-Asn-Lys-Thr-Glu-Lys-Glu-Ile-Leu) (MW: 1429.65)

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