

Name: Signal peptidase IB

Function: “Essential for cell viability.By similarity

Catalytic activity: Cleavage of hydrophobic, N-terminal signal or leader sequences from secreted and periplasmic proteins.”

Score 3 of 5

Subcellular location:

Cell membrane Curated; Single-pass type II membrane protein

Source: To analyse this protein, we did our blast against Swissprot database to confirm results and we obtained the accession number P0A067 and E_value:2.124e-11 and by the EC number we searched more information on BRENDA and in EXPASY, where we took the following quote:

” Signal peptidases (SPases) (also known as leader peptidases) remove the signal peptides from secretory proteins. In prokaryotes three types of SPases are known: type I (gene lepB) which is responsible for the processing of the majority of exported pre-proteins; type II (gene lsp) which only process lipoproteins, and a third type involved in the processing of pili subunits.

SPase I (EC 3.4.21.89) is an integral membrane protein that is anchored in the cytoplasmic membrane by one (in *B. subtilis*) or two (in *E. coli*) N-terminal transmembrane domains with the main part of the protein protruding in the periplasmic space. Two residues have been shown to be essential for the catalytic activity of SPase I: a serine and an lysine.

SPase I is evolutionary related to the yeast mitochondrial inner membrane protease subunit 1 and 2 (genes IMP1 and IMP2) which catalyze the removal of signal peptides required for the targeting of proteins from the mitochondrial matrix, across the inner membrane, into the inter-membrane space

In eukaryotes the removal of signal peptides is effected by an oligomeric enzymatic complex composed of at least five subunits: the signal peptidase complex (SPC). The SPC is located in the endoplasmic reticulum membrane. Two components of mammalian SPC, the 18 Kd (SPC18) and the 21 Kd (SPC21) subunits as well as the yeast SEC11 subunit have been shown to share regions of sequence similarity with prokaryotic SPases I and yeast IMP1/IMP2.

We have developed three signature patterns for these proteins. The first signature contains the putative active site serine, the second signature contains the putative active site lysine which is not conserved in the SPC subunits, and the third signature corresponds to a conserved region of unknown biological significance which is located in the C-terminal section of all these proteins.”

We obtained a of Score 3 out of 5 and also the information about the Subcellular location:

Cell membrane Curated; Single-pass type II membrane protein

On NCBI we have the information that we are dealing with a “Leader peptidase IB”.