Structural polyprotein Protein, Sindbis virus (Cell-Free, His, SUMO)

Cat. No.:	HY-P702456
Synonyms:	Structural polyprotein; p130
Species:	Virus
Source:	E. coli Cell-free
Accession:	P03316 (Y807-R1245)
Gene ID:	/
Molecular Weight:	65.9 kDa

PROPERTIES

AA Sequence	Y E H A T T V P N V P Q I P Y K A L V E R A G Y A P L N L E I T V M S S E V L P S T N Q E Y I T C K F T T V V P S P K I K C C G S L E C Q P A A H A D Y T C K V F G G V Y P F M W G G A Q C F C D S E N S Q M S E A Y V E L S A D C A S D H A Q A I K V H T A A M K V G L R I V Y G N T T S F L D V Y V N G V T P G T S K D L K V I A G P I S A S F T P F D H K V V I H R G L V Y N Y D F P E Y G A M K P G A F G D I Q A T S L T S K D L I A S T D I R L L K P S A K N V H V P Y T Q A S S G F E M W K N N S G R P L Q E T A P F G C K I A V N P L R A V D C S Y G N I P I S I D I P N A A F I R T S D A P L V S T V K C E V S E C T Y S A D F G G M A T L Q Y V S D R E G Q C P V H S H S S T A T L Q E S T V H V L E K G A V T V H F S T A S P Q A N F I V S L C G K K T T C N A E C K P P A D H I V S T P H K N D Q E F Q A A I S K T S W S W L F A L F G G A S S L L I I G L M I F A C S M M L T S T R R
Appearance	Lyophilized powder.
Formulation	Lyophilized from a 0.22 μm filtered solution of Tris/PBS-based buffer, 6% Trehalose, pH 8.0.
Endotoxin Level	<1 EU/μg, determined by LAL method.
Reconsititution	It is not recommended to reconstitute to a concentration less than 100 μg/mL in ddH_2O. For long term storage it is recommended to add 5-50% of glycerol (final concentration). Our default final concentration of glycerol is 50%. Customers could use it as reference.
Storage & Stability	Stored at -20°C for 2 years. After reconstitution, it is stable at 4°C for 1 week or -20°C for longer (with carrier protein). It is recommended to freeze aliquots at -20°C or -80°C for extended storage.
Shipping	Room temperature in continental US; may vary elsewhere.

DESCRIPTION

Background	The Structural polyprotein Protein orchestrates the formation of an icosahedral capsid with T=4 symmetry, comprising 240 copies of the capsid protein enveloped by a lipid membrane, and featuring 80 spikes composed of E1-E2 heterodimeric trimers. This protein binds to the viral RNA genome adjacent to a ribosome binding site, facilitating viral genome translation post-release. With protease activity causing autocatalytic cleavage, the capsid protein transiently associates with ribosomes, rapidly assembling into icosahedral core particles after self-cleavage. The resulting nucleocapsid associates with the cytoplasmic domain of the spike glycoprotein E2 at the cell membrane, driving budding and mature virion formation. In infection, new virions attach to target cells, undergo clathrin-mediated endocytosis, and fuse with the host endosomal membrane, releasing the nucleocapsid into the cytoplasm. This initiates an uncoating event crucial for genomic RNA accessibility, possibly triggered by capsid protein interaction with ribosomes. The protein specifically inhibits interleukin-1 receptor-associated kinase 1/IRAK1-dependent signaling during viral entry, evading innate immune detection before viral gene expression. Additionally, it provides a signal sequence for translocating the precursor of protein E3/E2 to the host endoplasmic reticulum. Furin-cleaved E3, associated with spike glycoprotein E1, mediates pH protection during transport through the secretory pathway, gradually releasing in the extracellular space after virion release from the host cell.

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