

Structural polyprotein Protein, Barmah forest virus (Cell-Free, His)

Cat. No.:	HY-P702454
Synonyms:	Structural polyprotein; p130
Species:	Virus
Source:	E. coli Cell-free
Accession:	P89946 (Y801-H1239)
Gene ID:	1489701
Molecular Weight:	50.7 kDa

PROPERTIES

AA Sequence	<pre> Y E H S T T M P N Q V G I P F K A L I E R P G Y A G L P L S L V V I K S E L V P S L V Q D Y I T C N Y K T V V P S P Y I K C C G G A E C S H K N E A D Y K C S V F T G V Y P F M W G G A Y C F C D T E N S Q M S E V Y V T R G E S C E A D H A I A Y Q V H T A S L K A Q V M I S I G E L N Q T V D V F V N G D S P A R I Q Q S K F I L G P I S S A W S P F D H K V I V Y R D E V Y N E D Y A P Y G S G Q A G R F G D I Q S R T V N S T D V Y A N T N L K L K R P A S G N V H V P Y T Q T P S G F S Y W K K E K G V P L N R N A P F G C I I K V N P V R A E N C V Y G N I P I S M D I A D A H F T R I D E S P S V S L K A C E V Q S C T Y S S D F G G V A S I S Y T S N K V G K C A I H S H S N S A T M K D S V Q D V Q E S G A L S L F F A T S S V E P N F V V Q V C N A R I T C H G K C E P P K D H I V P Y A A K H N D A E F P S I S T T A W Q W L A H T T S G P L T I L V V A I I V V V V V S I V V C A R H </pre>
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.
Reconstitution	It is not recommended to reconstitute to a concentration less than 100 µg/mL in ddH ₂ O. 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 plays a pivotal role in the formation of an icosahedral capsid with T=4 symmetry, comprising 240 copies of the capsid protein surrounded by a lipid membrane, featuring 80 spikes composed of E1-E2 heterodimeric trimers. Binding to the viral RNA genome, adjacent to a ribosome binding site, facilitates viral genome translation following release. The structural polyprotein possesses protease activity, leading to its autocatalytic cleavage from the nascent structural protein. Post-cleavage, it transiently associates with ribosomes, rapidly assembles into icosahedric core particles, and eventually associates with the spike glycoprotein E2 at the cell membrane, culminating in budding and mature virion formation. During infection, virions attach to target cells, undergo clathrin-mediated endocytosis, and fuse with the host endosomal membrane, releasing the nucleocapsid into the cytoplasm. This uncoating event, crucial for genomic RNA accessibility, may be triggered by the interaction of capsid proteins with ribosomes. The structural polyprotein also inhibits interleukin-1 receptor-associated kinase 1/IRAK1-dependent signaling during viral entry, potentially aiding the evasion of innate immune detection. Additionally, it provides the signal sequence for translocating the precursor of protein E3/E2 to the host endoplasmic reticulum. Furin-cleaved E3 remains associated with spike glycoprotein E1, ensuring pH protection during transport via the secretory pathway, with gradual release into the extracellular space upon virion release from the host cell.

Caution: Product has not been fully validated for medical applications. For research use only.

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