Viral Protein

HCV p7- Hepatitis C virus p7

Product specification

Acronym: HCV p7
Class: Transporter
Origin: Virus
Molecular weight: 7 kDa
Application: Screening & display technologies, vaccine development
Purity: >75%
Activity: Proven
Length: Full Length
TMD: 2
Biological function: Ion-channel activity and virus infection

Product description

Hepatitis C virus p7 (HCV p7) protein is involved in the viral life cycle including virus assembly and infectivity. It reveals a N-terminal α-helix and two transmembrane segments connected by a short hydrophilic cytosolic segment of 7 amino acids. The p7 protomer is able to oligomerize to a hexameric and heptameric state forming an ion channel.

Protein Source: HCV p7 wild type protein (serotype 1a):

Fig.1: AA sequence of HCV p7 protein

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        10          20          30
ALENLVILNA ASLAGTHGLV SFLVFFCFAW
        40          50          60
YLKGRWVPGA VYAFYGMWPL LLLLLALPQR
  63
AYA
```

Affinity Tag: Histidine tag fused to the N-terminal of the protein.

Production conditions: HCV p7 is expressed in a cell-free expression system in the presence of lipid vesicles. 100 µg can be produced and qualified in about 1 week.

Quality analysis

Purity: Typically > 75% as determined by SDS-Page and Coomassie Blue staining.

Purification procedure: As standard, HCV p7 proteoliposomes are purified on a sucrose gradient. Further purification steps can be added if required.

Activity: *Recombinant proteoliposomes containing HCV p7 have been shown to be active into liposomes using patch clamp recordings.*

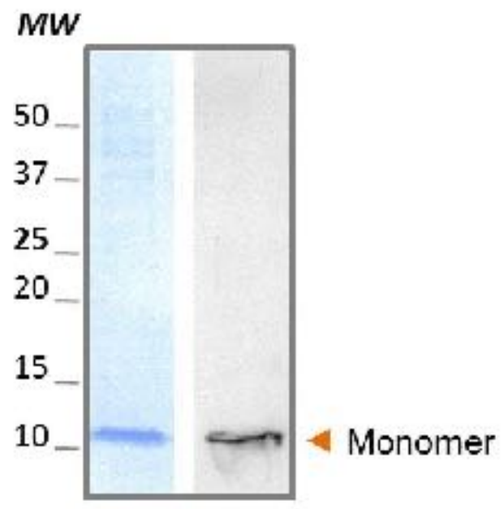

Fig.2: HCV p7 proteoliposome after purification (Coomassie Blue quantification and Western blot identification).

Quality Control

This process efficiency of expressing properly folded protein was measured using Fourier Transform InfraRed (FTIR) method. The 66% α-helix percentage obtained corresponds to the 69% predicted structure (CFSSP) and previous published data.

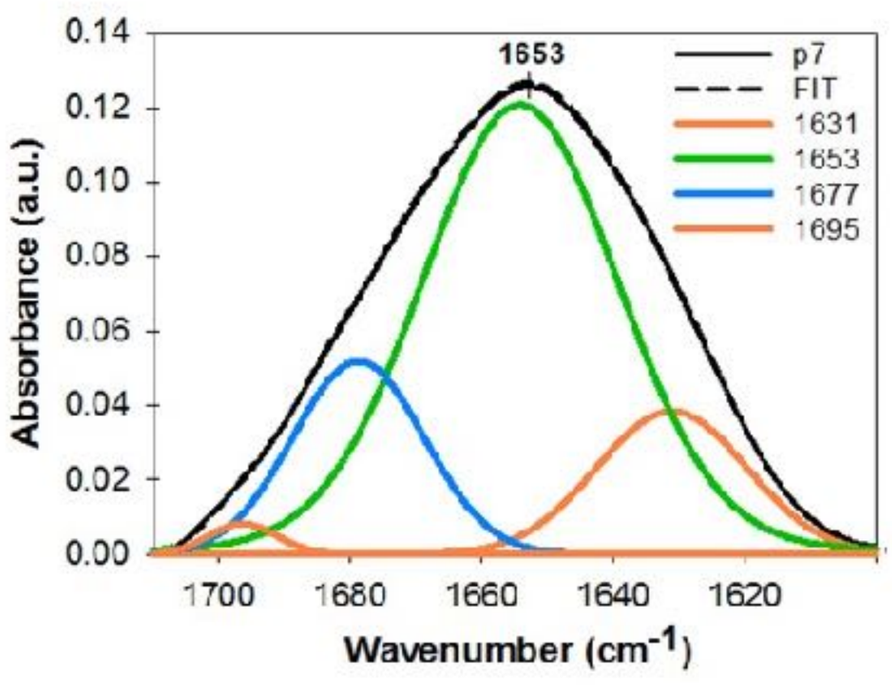

Fig.3: FTIR Spectra of p7 proteoliposomes.
Spectrum and fit of cell-free expressed p7 proteoliposomes (Fit: orange: β-sheets, green: α-helix, blue: β-turns).

Assessment of functionality

Cell-free expression systems provide a real alternative for membrane protein expression, enabling the study of structure and function of membrane proteins.

Methods: Patch clamp
The p7 viroporin from the hepatitis C virus was expressed in Synthelis' cell-free system as proteoliposome (via direct integration into the lipid bilayer of the liposomes). The functional activity of p7 proteoliposomes was measured by electrophysiology. To block this activity and further characterize the viroporin, we used HMA, compound that had been reported as a p7 inhibitor.

Results: We observed that p7 channel activity was decreasing immediately after addition of HMA. Ion channel activity was inhibited by HMA in a concentration dependent manner. At 1 mM HMA concentration (yellow), we noticed a full blockage of the channel.

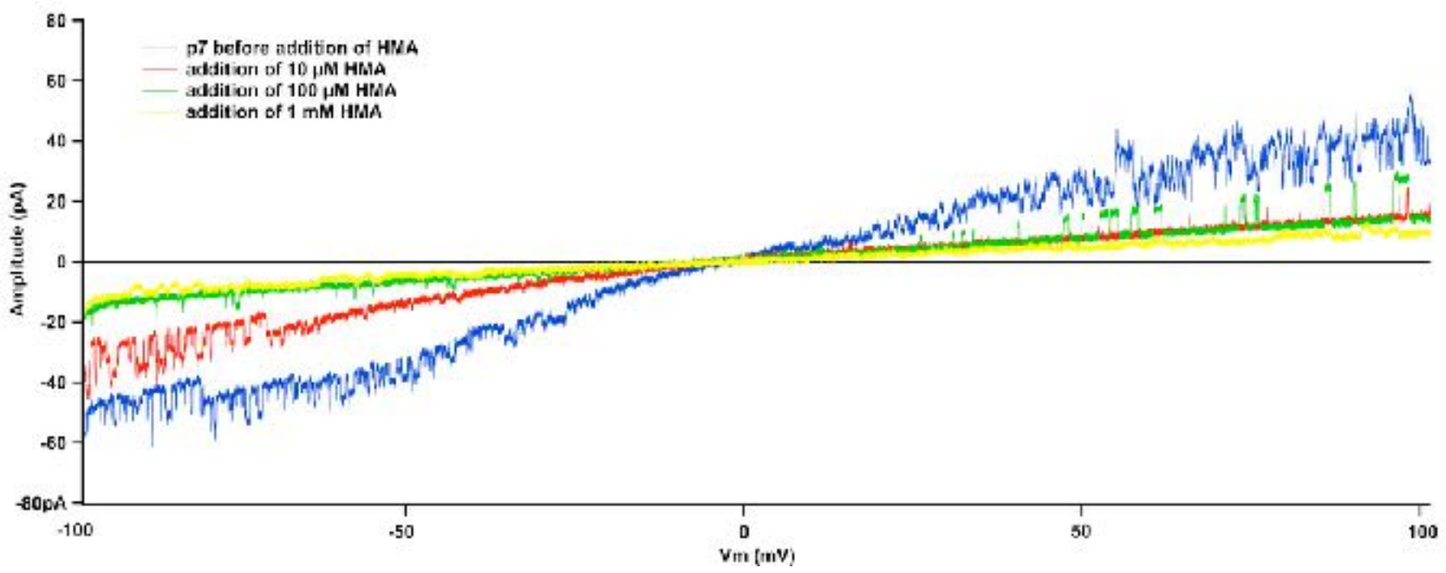

Fig.4: Effect of the HMA on p7 protein. Different concentrations of HMA were applied to the bilayer containing p7. The recordings were done using a ramp protocol from -100 mV to +100 mV during 2 s (100 mV/s ramp)

Formulation

Buffer: Available in Tris 50mM, pH 7.5. Others buffers or customized formulation can be provided upon request.

Customized Hydrophobic matrix: Customized formulation. Specific lipids can be used upon request.

Storage/Stability: Store at +4°C for up to one week or several months at -80°C. Aliquot for storage. Do not freeze-thaw after aliquoting.

Use restrictions: For life science research use only.

Available sizes: 25µg ,100 µg ,500 µg,bulk

Need a specific amount, a quote or any additional information?
Contact-us

Synthelis

T : +33 (0)4 76 54 95 35
E: contact@synthelis.fr
www.synthelis.com