

Class: M-protein

**Attributes:**

**SARS-CoV specific**

**Accession #:** [NP\\_828855](#)

**Synonyms:** Orf 5, membrane protein

**Molecular weight:** unknown

**Number of amino acids:** 221

**Structure:**

- the three transmembrane helices were approximately located at residues 15-37, 50-72 and 77-99 within the 121 hydrophilic domain on the inside of the virus particle (1)
- contains one caveolin-binding site at amino acids 94 to 102 (YFVASFRLF) (2)

**Other Coronaviruses**

**Synonyms:** membrane protein

**Molecular weight:** 22-25 kDa (3)

**Number of amino acids:** 225-230

**Structure:**

- signal sequence is internal (4)
- MHV-2 strain has a Met-Asn-Ser-Thr-Thr and the Asn is N-glycosylated and Thr-5 was O-glycosylated (5)
- N-terminal**
  - approximately 25 residues (6)
  - plays no role in membrane integration
  - N terminal 20 residues are hydrophilic (3)
  - N-terminal on luminal side of the ER membrane, can enter the membrane at late stages of synthesis (140-150 aa), N terminal leader peptide not cleaved (7)
  - A single oligosaccharide side chain added at cluster of 4 hydroxylamino acids Ser-Ser-Thr-Thr at extreme N-term Thr-5 is the functional acceptor site (8)
    - this sequence is immediately adjacent to the initiator Met
    - proline at position 8 also needed
    - remainder of the N-term half forms three helical membrane-spanning domains / member of the group II proteins (6)
- C-terminal**
  - structure uncertain but within viral envelope
  - the C-term domain in combination the middle domain may direct the protein to the trans-Golgi
  - deletion of 18 amino acids from C-terminus causes M to be relocalized to the plasma membrane (6)
  - there may be an internal sorting signal (6)

**Processing:**

- not acetylated (11)
- small number of O-linked glycosylation sites (12)

**Location:**

- localized in the trans-Golgi complex
- hydrophobic domain I alone was sufficient to translocate the amino-terminal part of M to the luminal side (9)
- domains I and III could function as signal and stop transfer sequences (9)

**Functions:**

- essential for the production of coronavirus-like particles
- insertion of different amino acids at six-His stretch at very amino terminus prevents virion assembly (10)
- may play structural role in forming envelope and internal core of the virion

**Abundance:**

- most abundant protein

**Responsibilities:**

Interaction with M protein links ribonucleoprotein to viral membrane and might initiate tight N protein association

Interaction of M with membrane plays structural role in viral particle assembly

Oligomerization may be part of proteins retention mechanism

Complex with N and RNA to determine specificity and selective packaging of Positive Genomic RNA

Interaction between M and E is a key event for viral particle assembly

Functional consequence unknown

May use caveolin-1 as a scaffolding protein during the assembly and release of SARS-CoV

**Collaborators:**

N\_protein

Membrane

M\_protein

RNA

E\_protein

U274 (13) (**SARS-specific**)

caveolin-1 (2) (**SARS-specific**)

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- 9) Mayer, T., et al., (1988) Membrane integration and intracellular transport of the coronavirus glycoprotein E1, a class III membrane glycoprotein, *J. Biol. Chem.*, **263(29)**, 14956-14963.
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- 13) Tan, Y.J., et al., (2004) A novel severe acute respiratory syndrome coronavirus protein, U274, is transported to the cell surface and undergoes endocytosis, *J Virol*, **78(13)**, 6723-34.