

Class: SARS-CoV nsp9

Attributes:

Accession #: NP_828867

Synonyms: none

Molecular weight: unknown

Number of amino acids: 112

Structure:

1) Homology:

- a new variant within the oligosaccharide/oligonucleotide fold-like fold family (1)
- the six-stranded closed beta-barrels have been identified in several proteins that interact with RNA
 - the small protein B (2)
 - the domain III of EF-Tu (3)

2) Domains:

- contains seven beta-strands, one alpha helix and are arranged into a single compact domain and form a cone-shaped beta-barrel flanked by the C-term alpha-helix (1)
- the C-term alpha-helix makes a 45o angle with the axis of the beta-barrel and has a high content of hydrophobic residues yielding 2 hydrophobic sides (1)

3) Dimer Information:

- crystals contain a dimer which provides a single, uninterrupted nucleic acid-binding site (1)
 - each ssRNA binds several nsp9 dimers and each nsp9 dimer can bind two distinct single-stranded segments (1)
 - nucleic acid binding activity is not sequence-specific (1)
 - ssRNA may wrap around nsp9 dimer (1)
 - one side of the C-term alpha-helix faces the beta barrel and the other interacts with the alpha helix of another monomer (1)
 - therefore, the dimer is assembled by hydrophobic interactions (1)
 - further stabilized by four long hydrogen bonds involving main-chain atoms (1)

4) Substrate Binding Information

- nsp9 binds substrates in the uM range (1)
- a network of positively charged amino acids defines a positive track suitable for binding the phosphate backbone to the protein surface (1)
- exposed aromatic residues might provide stacking interactions with nucleobases (1)
 - Arg-10, Lys-52, Trp-53, Arg-55, Arg-74, Phe-75, Lys-86, Tyr-87, Phe-90, Lys-92, Arg-99 and Arg-111 are conserved
- two extended loops L23 and L45 have weak electron density associated with high B factor values suggesting they are flexible and/or mobile (1)
- they line the positively charged track and may clamp nucleic acids on the nsp9 surface after conformational change(1)

Processing: unknown

Location: unknown

Function:

- single-stranded RNA/DNA-binding protein (1)
- nsp9 might stabilize nascent nucleic acid during replication or transcription, thus providing protection from nucleases (1)
- nsp9 could participate in a base-pairing-driven process such as RNA processing (1)

Abundance:

- nsp9 and other OTR1a encoded replicase subunits are produced in 3 to 5-fold excess relative to the core replicative enzymes such as polymerase, and helicase (1)

Responsibilities:

Dimerize

Might stabilize nascent nucleic acid during replication or transcription, thus providing protection from nucleases; could participate in RNA processing

Collaborators:

nsp9

ssRNA

- 1) Egloff, M.P., et al., (2004) The severe acute respiratory syndrome-coronavirus replicative protein nsp9 is a single-stranded RNA-binding subunit unique in the RNA virus world, *Proc Natl Acad Sci U S A*, **101(11)**, 3792-6.
- 2) Gutmann, S., et al., (2003) Crystal structure of the transfer-RNA domain of transfer-messenger RNA in complex with SmpB, *Nature*, **424(6949)**, 699-703.
- 3) Nissen, P., et al., (1996) The ternary complex of aminoacylated tRNA and EF-Tu-GTP. Recognition of a bond and a fold, *Biochimie*, **78(11-12)**, 921-33.