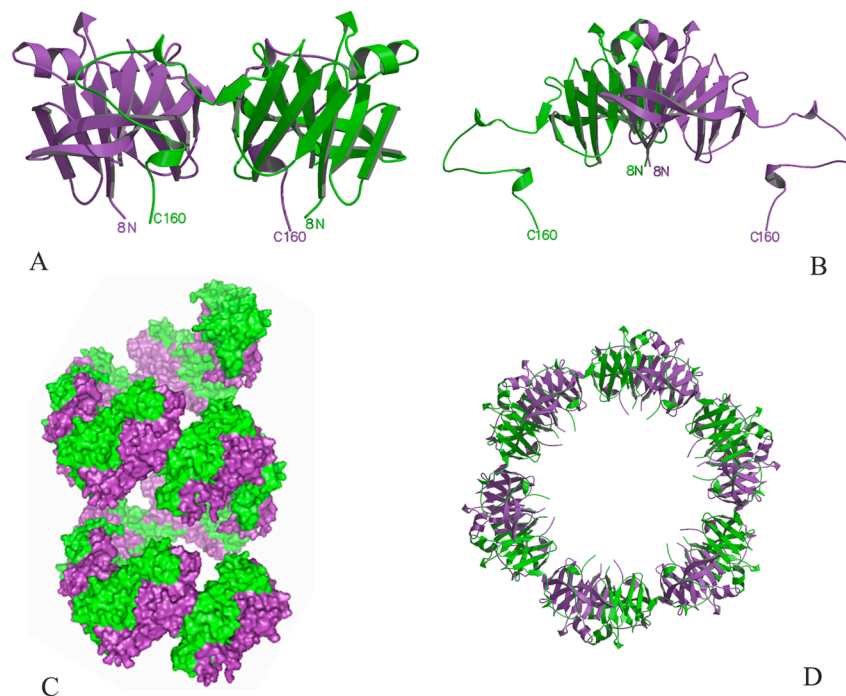


Bluetongue virus (BTV) non-structural protein 2 (NS2) belongs to a class of highly conserved proteins found in Orbiviruses of the Reoviridae family. NS2 forms large multimeric complexes, localizes to cytoplasmic inclusions in the infected cells and binds non-specifically single-stranded RNA (ssRNA). Due to its ability to bind ssRNA, it has been suggested that the protein is involved in the selection and condensation of the BTV ssRNA segments prior to genome encapsidation.

We determined the crystal structure of the 177 amino acid N terminal domain, sufficient for the ssRNA binding ability of NS2, to 2.4 Å resolution using anomalous scattering methods. We have found that the NS2₁₋₁₇₇ monomer is folded as a β sandwich with a unique topology. The structure reveals strong NS2₁₋₁₇₇ - NS2₁₋₁₇₇ contacts, that explain the ability of the protein to self assemble into large homomultimeric complexes. Of the entire surface area of the NS2₁₋₁₇₇ monomer, one third is used to create the interfaces of the curved multimeric assembly observed in the crystal structure. The structure reported here shows how the N-terminal domain would be able to bind ssRNA non-specifically protecting the bound regions in a heterogeneous multimeric, but not polymeric, complex.



Ribbon representation of the NS2₁₋₁₇₇ homodimeric configurations and overview of the crystal packing. (A) The largest interface between monomers buries 1831Å² of the surface area of each monomer. (B) The extensive β sheet interface buries 1075Å². (C) Homodimeric associations give rise to an infinite spiral in the crystal with the pitch equal with the crystallographic c axis. (D) Crystal packing viewed along the 6₅ crystallographic axis.

The native data set was collected at the EMBL beamline X13 (DESY, Hamburg, Germany) and the selenomethionine derivative data sets were collected at the EMBL beamlines BW7A, X11 as well as at ESRF beamline BM14 (Grenoble, France).

Publication

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