EPN BAG report
TiLV polymerase + ANP32
01-03 May 2023

(20,000 images)

Host ANP32 proteins are composed of a structured N-terminal leucine-rich repeat (LRR) domain and a disordered C-terminal low complexity acidic region (LCAR). These proteins are essential for the replication of the influenza virus genome. Differences in avian and mammalian ANP32 proteins represent a major driver of FluPol adaptation upon zoonotic infections of mammalian species with avian influenza viruses.

Recent research has provided new insights into the interaction between FluPol and ANP32A. A co-structure of a type C virus FluPol with ANP32A revealed that the ANP32A LRR domain binds to an asymmetrical influenza polymerase dimer, which is believed to represent the FluPol replication complex.

Given our previous findings on TiLV polymerase, we aimed to investigate whether critical host cofactors, such as ANP32, are conserved in the replication mechanism of distantly related orthomyxo-like viruses.

Through the use of CM01, we were able to obtain multiple high-resolution structures of TiLV polymerase bound to ANP32A, shedding light on the interaction between the viral polymerase and this essential host factor.