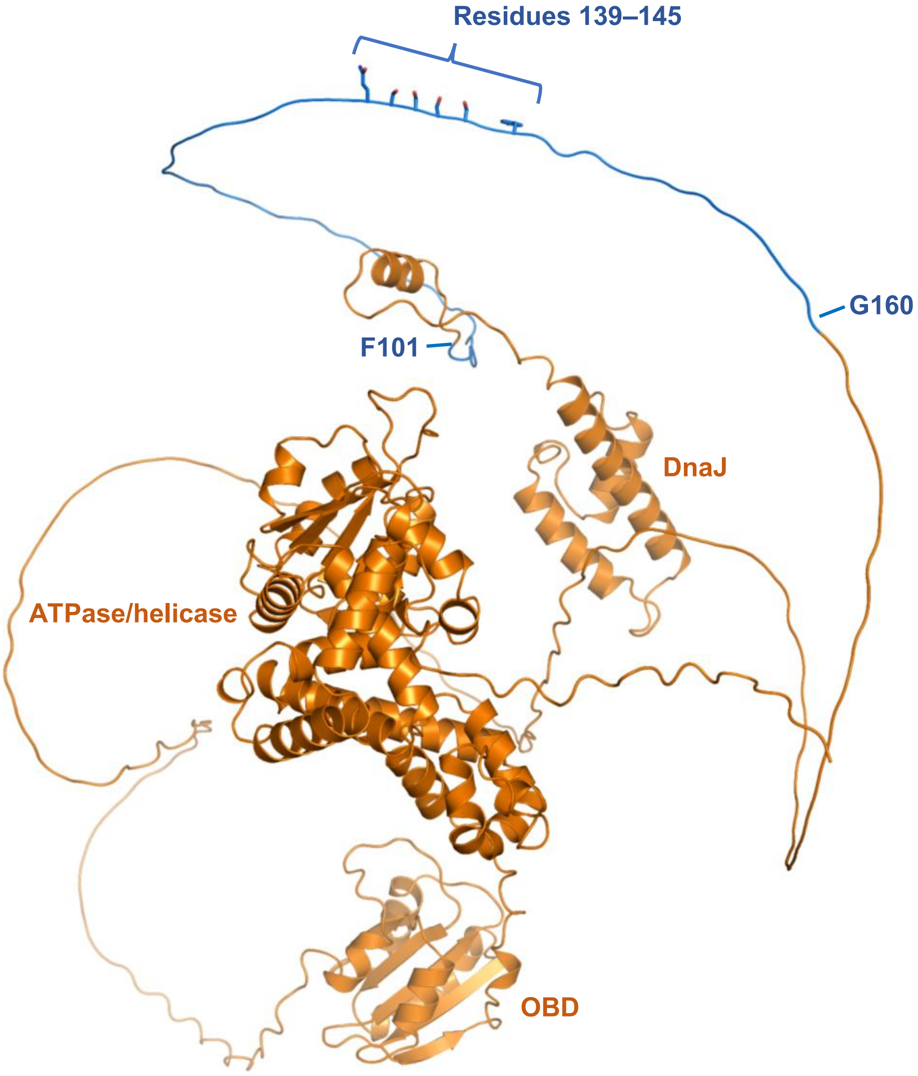

Fig. S1. AlphaFold 3-predicted full-length structural model of MCPyV LT. Residues 101–160 of MCPyV LT are shown in marine, while the remaining residues are shown in orange. The side chains of the USP7TRAF-bindinn motif of MCPyV LT, comprising residues 139–145, are represented as sticks and indicated. The three well-folded domains of MCPyV LT, DnaJ, OBD, and ATPase/helicase, are labeled.