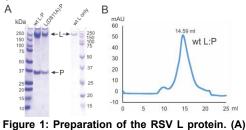
## Structural Basis of the Respiratory Syncytial Virus Polymerase Complexes

## 1. Preparation and characterization of the RSV polymerase.

Preparing high-quality and large-quantity of RSV L is challenging and the critical first step to understanding RSV catalytic core and has been proven challenging<sup>1</sup>. We have successfully co-expressed and co-purified full-length wild-type (wt) RSV RdRP (L:P) and catalytically inactive L(D811A):P using sf21 insect cells (Fig. 1).



A 3' UGCUCUUUUUUUQACAGUUUUUUGAU TrC template ACGAGAAAAAAGUGUCAAAAACUA

Figure 2: In vitro reconstitution of RSV RNA polymerization. (A) the template (TrC) and product (Tr). (B) Transcription assay using wt and mutant RdRP (L:P) on various RNAs. (C) Test RNA templates from different viruses for specificity. (<u>Cao</u> transcription et al. JVI 2020, Viruses 2022)

[a-32P]GTP + NTPs

2. In vitro transcription assay. We successfully adapted 1-3 and developed a novel RNA elongation assay to map insect cells. (B) The size exclusion chromatography key promoter features of RSV<sup>4</sup> (Fig. 2).

SDS-PAGE gel shows the expression of full-length wild-type (wt) and mutant RSV L:P, and L only in shows homogeneity. (Cao et al. Nat Comm 2020)

Our assay uses a short RNA template to incorporate [32P]-NTP into the reaction. We will optimize the parameters (i.e., the length and sequence of the template and primers) to identify suitable constructs for in-depth structural analysis.

## 3. Capture the initiation and elongation of RSV polymerase. We successfully

determined multiple highresolution structures of the polymerases from RNA viruses using cryo-EM<sup>5-7</sup> (**Fig. 3**). Using the template the assav and selected NTPs or analogs; we will trap the

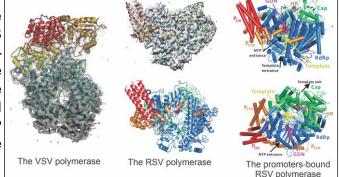


Figure 3: Cryo-EM structures of the NNS RdRPs by the Pl. (A) 3.8 Å cryo-EM structure of the VSV RdRP (Liang et al. Cell, 2015). (B) 3.67 Å cryo-EM structure of the apo RSV RdRP (Cao et al. Nat Comm 2020). (C) 3.40 Å and 3.41 Å cryo-EM structures of the promoters bound RSV RdRP (Cao et al. Nature 2024).

initiation and elongation stages of the RSV RdRP (Fig. 4).

[a-32P]GTP + NTPs

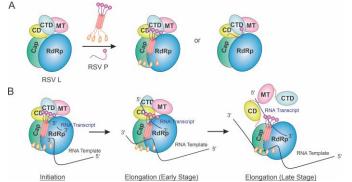
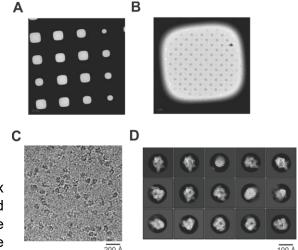


Figure 4: The overview of the proposed work. (A) The RSV RdRP (L:P). The domains of both monomeric L and tetrameric P are shown. Pfrag is the minimal P fragment used to stabilize the L protein domains in this proposal. (B) Initiation and elongation complexes. The RNA template and RNA transcript are shown as black or blue lines, respectively.

Preliminary data suggested that the RSV L:P:RNA complex showed reasonable homogeneity. The initial cryo-screen revealed good ice thickness and gradient in the cryo grids (Fig. 5A, B). The preliminary screen showed the particles are readily visible in the grid holes (Fig. 5C). A small cryo-EM dataset and the 2D class Figure 5: Preliminary cryo-EM analysis of RSV averages show both similar and different views compared to that of apo RSV L:P complex (Fig. 5D). In summary, we demonstrated the feasibility of preparing the high-quality RSV L:P:RNA complex. Besides the apo RSV RdRP (Cao et al., Nat Comm, 2020)6, we



polymerase complex with its RNA (L:P:RNA). (A) The low magnification view of the grid. (B) The medium magnification view of a representative grid square. (C) The raw image of L:P:RNA complex. (D) The class averages show both similar and different views to that of apo RSV L.P complex.

determined multiple 2.5-3.5 Å cryo-EM structures of the RSV RdRP in complexes of RNA templates (Cao et al., Nature, 2024)7 and more recently the intermediates involved in the nucleotide addition cycle of the RNA synthesis catalysis (Cao et al., in preparation).

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