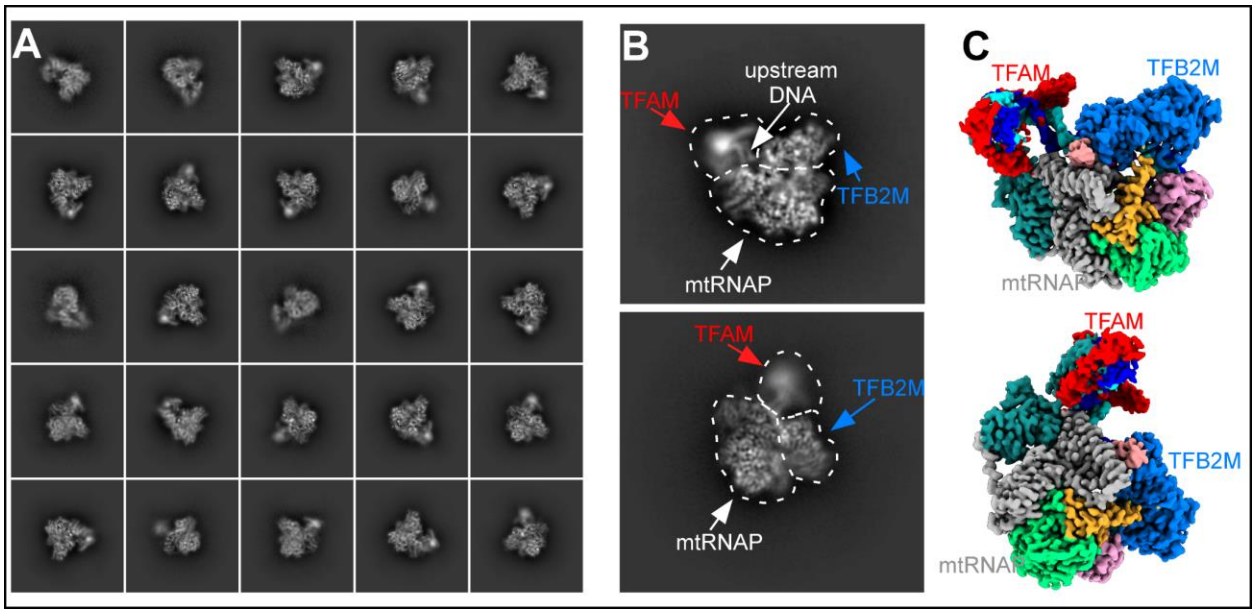

Figure 1. High-resolution single-particle analysis data of the transcription initiation complex.
(A) Final selection of 2D classes of particles representing transcription initiation complex intermediates. **(B)** Close-up view of representative 2D classes with individual components labeled corresponding to their density (white outlines) **(C)** Final cryo-EM density maps. Views are shown in the same orientation as the particles in **(B)**.

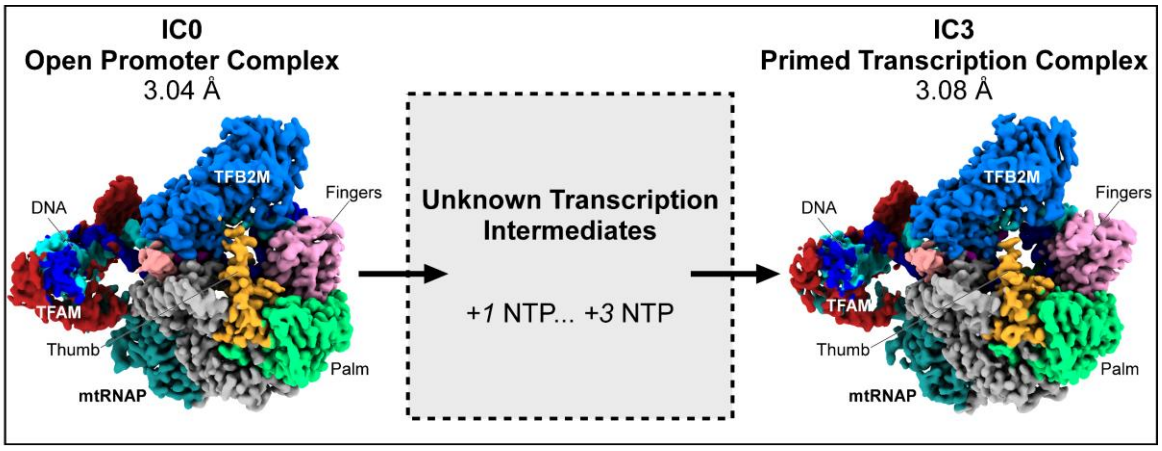

Figure 2. Cryo-EM maps of transcription initiation complex intermediates.
Left, cryo-EM density for the open promoter complex (IC0). *Center*, Undetermined transcription intermediates bridging the structural space between the open promoter complex and the primed transcription complex. *Right*, cryo-EM density for the primed transcription initiation complex (IC3). TFAM and TFB2M are colored in brick red and marine blue, respectively.

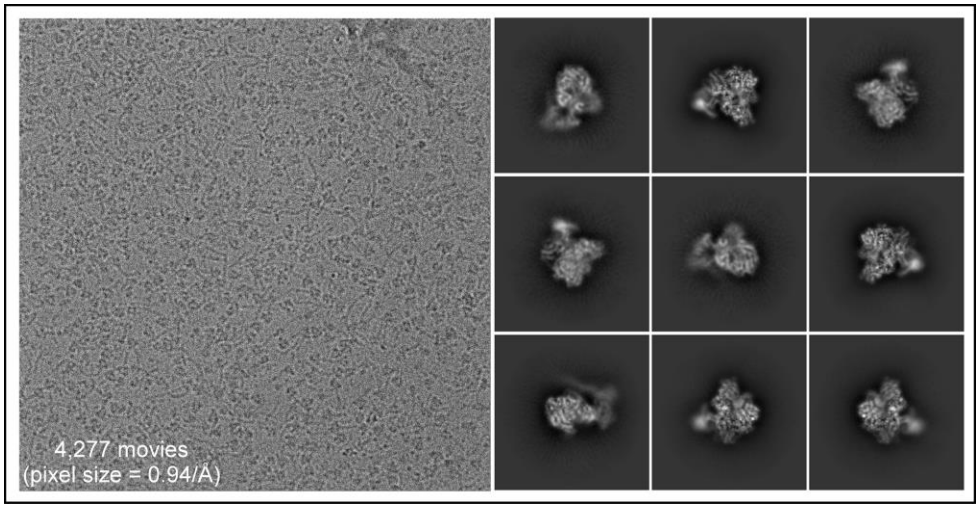

Figure 3. Cryo-EM screening of h-mtIC.
Representative micrographs (*left*) and populated 2D classes (*right*) of h-mtIC assembled on a fully complementary promoter template during a screening session.