

Figure 1. CryoEM maps of substrate-bound transcription elongation complex.
A close-up view of the active site reveals substrate ATP electron density depicted in yellow mesh.

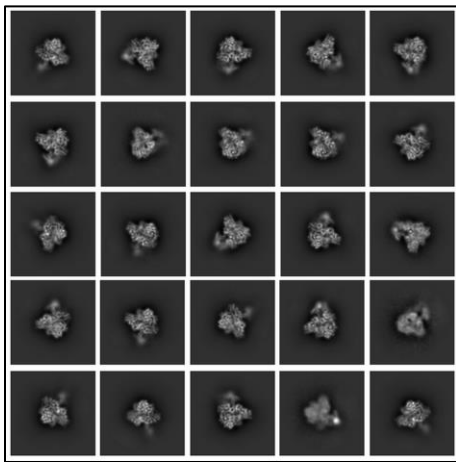


Figure 2. 2D Classes of the transcription Initiation Complex
2D classification of IC particles used for 3D reconstruction.

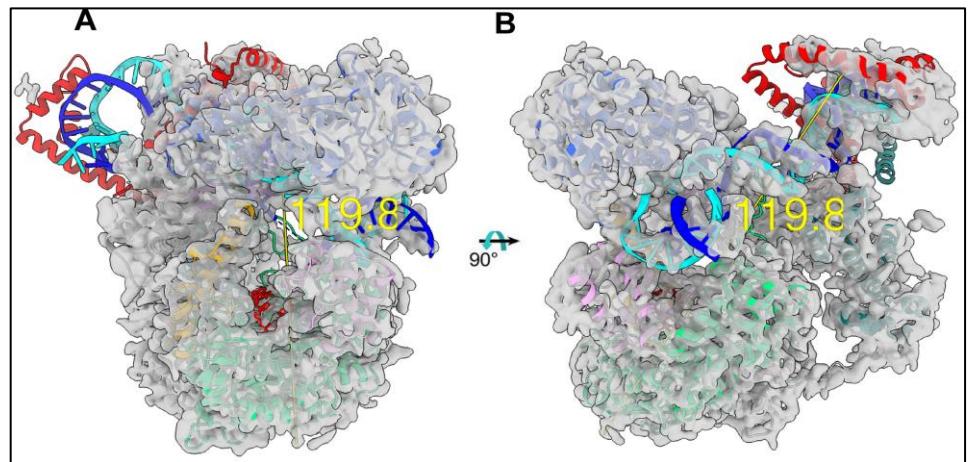


Figure 3. A high-resolution structure of the complete initiation complex.
Non-uniform 3D-refinement in CryoSPARC reported a 2.76 Å resolution map (A) which shows partial cryoEM density for the highly flexible TFAM (B). MtRNAP (grey), TFB2M (blue), TFAM (red), and promoter DNA (blue, cyan).

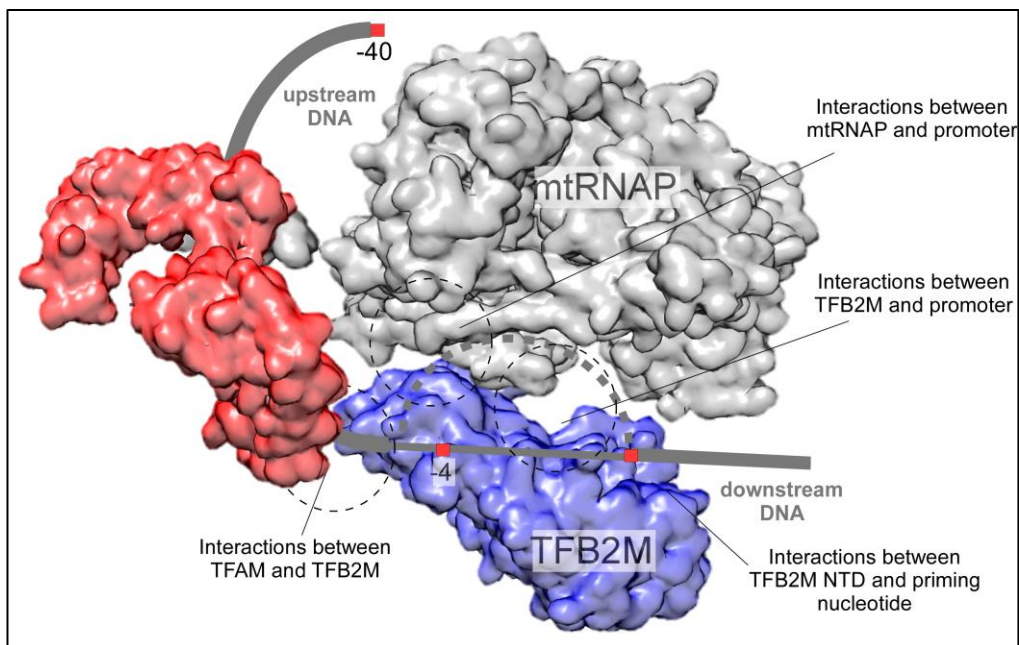


Figure 4. Schematic of the initiation complex annotated with potential interactions.

A combination of structural data from cryo-EM and functional data from biochemical assays will help reveal these interactions.