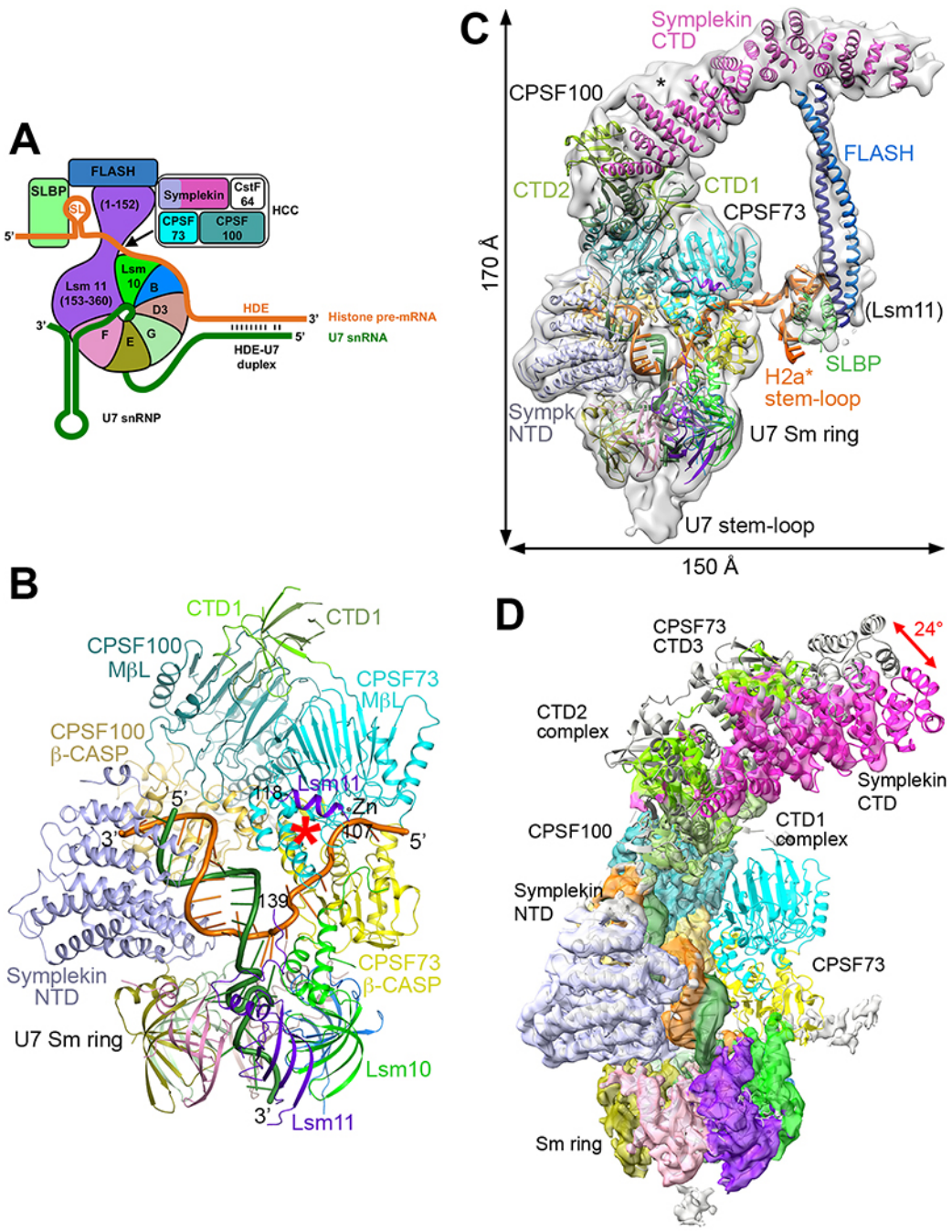

Fig. 1. Cryo-EM structures of a reconstituted human U7 snRNP. (**A**) Schematic drawing of the human histone pre-mRNA 3'-end processing machinery, U7 snRNP. (**B**) Cryo-EM structure of the stable core of the human histone pre-mRNA processing machinery. The Lsm11 helix that interacts with CPSF73 is highlighted with the red asterisk. (**C**) Cryo-EM structure of the entire human histone pre-mRNA processing machinery. Proteins at the periphery are more dynamic and their structures could only be determined at a lower resolution. (Y. Sun, Y. Zhang, W.S. Aik, X.-C. Yang, W.F. Marzluff, T. Walz, Z. Dominski, L. Tong. *Science*, 2020). (**D**) Cryo-EM structure of the U7 snRNP with mutations in the Lsm11 helix to block interactions with CPSF73. CPSF73 is disordered and has no EM density in 60% of the particles. (A. Desotell, W.F. Marzluff, Z. Dominski, L. Tong. Manuscript under review).