



**Fig. 1. Cryo-EM structure of a reconstituted human U7 snRNP in an active conformation.** (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 pre-mRNA (in orange) is bound in the active site of the CPSF73 endonuclease, poised for the cleavage reaction. (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).