



Fig. 1. Cryo-EM structures of INTS11 complexes. (A) Cryo-EM structure of the *Drosophila* IntS11-CG7044 complex at 3.5 Å resolution (unpublished). (B) Cryo-EM structure of the human INTS9-INTS11-BRAT1 complex at 3.2 Å resolution (unpublished). (C) Cryo-EM structure of the *Drosophila* IntS4-IntS9-IntS11 complex (ICM) at 2.74 Å resolution (*Nature Commun.* 13, 5742, 2022). IP₆ (inositol hexakisphosphate, shown as sticks) is bound at an allosteric site, 55 Å from the active site of IntS11. (D) Cryo-EM density for IP₆. After we identified IP₆ binding to *Drosophila* ICM, we also observed EM density for IP₆ in reported structure of human ICM.