

Figure 1. Overlay of apo- (white) and dsRNA-bound (light blue) dmDcr-2 and their fitted models. Note that “Core” and “Cap” densities were not resolved in the dsRNA-bound structure.

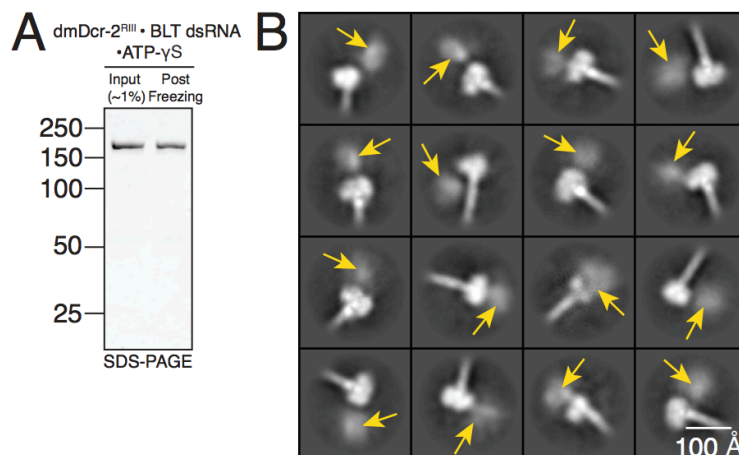


Figure 2. (A) Coomassie-stained SDS-PAGE sample of dmDcr-2 bound to dsRNA before and after plunge freezing. Note that absence of degradation/cleavage products in the right lane indicates that full-length protein remains intact post-vitrification. (B) 2D class averages of dmDcr-2:RNA complex showing poorly resolved densities (yellow arrows) connected to the Dicer helicase domain.

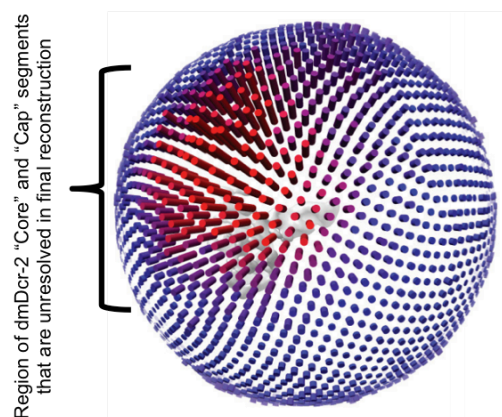


Figure 3. Orientation distribution of the dmDcr-2:RNA reconstruction. Note that the direction of over-represented views (red cylinders) coincide with the locations of unresolved portions of dmDcr-2, i.e. the “Core” and “Cap” regions.

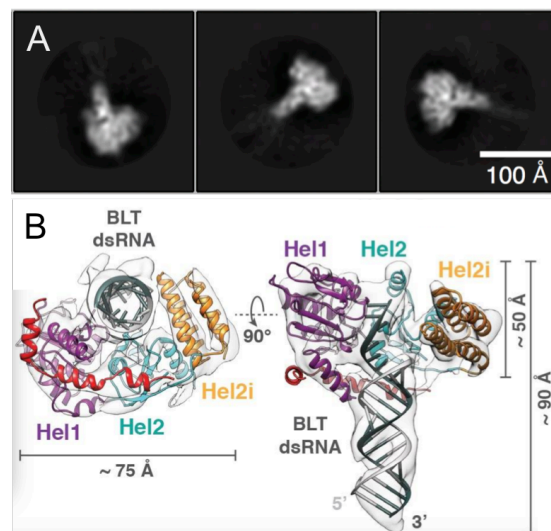


Figure 4. (A) 2D class averages of dmDcr-2:dsRNA complex after subtracting excess dsRNA. (B) 6.8 Å resolution reconstruction of signal-subtracted dmDcr2:dsRNA particles and its fitted model.