Fig. 1. Preliminary cryoEM data for human full-length monomeric α-catenin. **Left**, Representative 2D class averages of the particles used for structure determination. **Middle**, Cα trace of our preliminary monomeric human α-catenin cryoEM structure. The vinculin binding domain is shown in white, the remainder of the α-catenin middle domain is shown in black, and the carboxy-terminal F-actin binding domain is colored spectrally from shorter to longer wavelengths for residues 669 to 863. The linker residues (636-650) that form an unexpected α-helix. **Right**, The number of particles and resolution computed using two half-maps using a gold-standard Fourier shell correlation cut-off value of 0.143 are indicated. The 3D reconstruction of monomeric α-catenin resulted in a preliminary 6.9 Å resolution map.
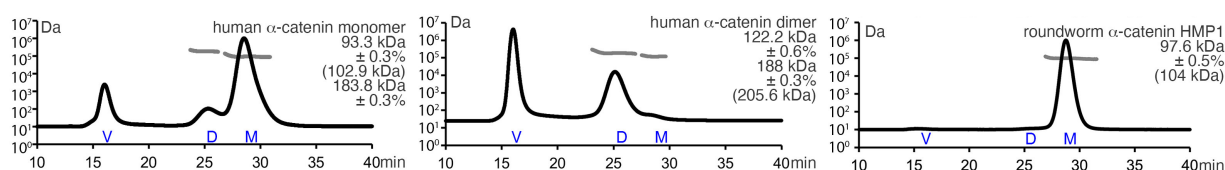

Fig. 2. Determination of absolute masses by size exclusion chromatography multi-angle light scattering. Full-length human α-catenin forms a dimer and monomer, while the roundworm α-catenin ortholog, HMP1, is strictly monomeric. Separate pooling of monomeric or dimeric peaks from a size exclusion chromatography run were subsequently analyzed by size exclusion chromatography multi-angle light scattering. The ordinate indicates the molar mass (light gray trace) expressed on a logarithmic scale, and the abscissa represents the time in minutes for the light scattering profile (black trace). For simplicity, the ordinate corresponding to the light scattering signal is not shown. The experimental absolute masses are shown. Values in brackets are the molecular weights as calculated from the respective polypeptide chains. **Left,** human monomeric α-catenin. **Middle**, human dimeric α-catenin. **Right**, roundworm α-catenin ortholog, HMP1. V, void; D, dimer; M, monomer.
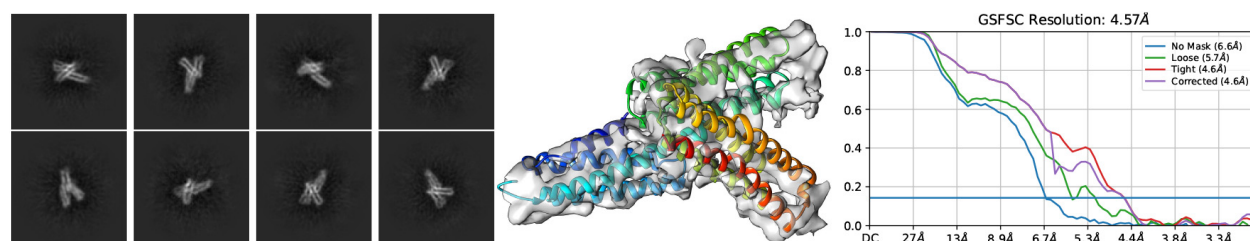

Fig. 3. Preliminary cryoEM data for roundworm full-length monomeric α-catenin. Left, Representative 2D class averages of the particles used for structure determination. **Middle**, Cα trace of our preliminary monomeric roundworm α-catenin cryoEM structure, colored spectrally from shorter to longer wavelengths. **Right**, The gold-standard Fourier shell correlation curve is shown for the 3D reconstruction of monomeric roundworm α-catenin that resulted in a preliminary 4.6 Å resolution map.