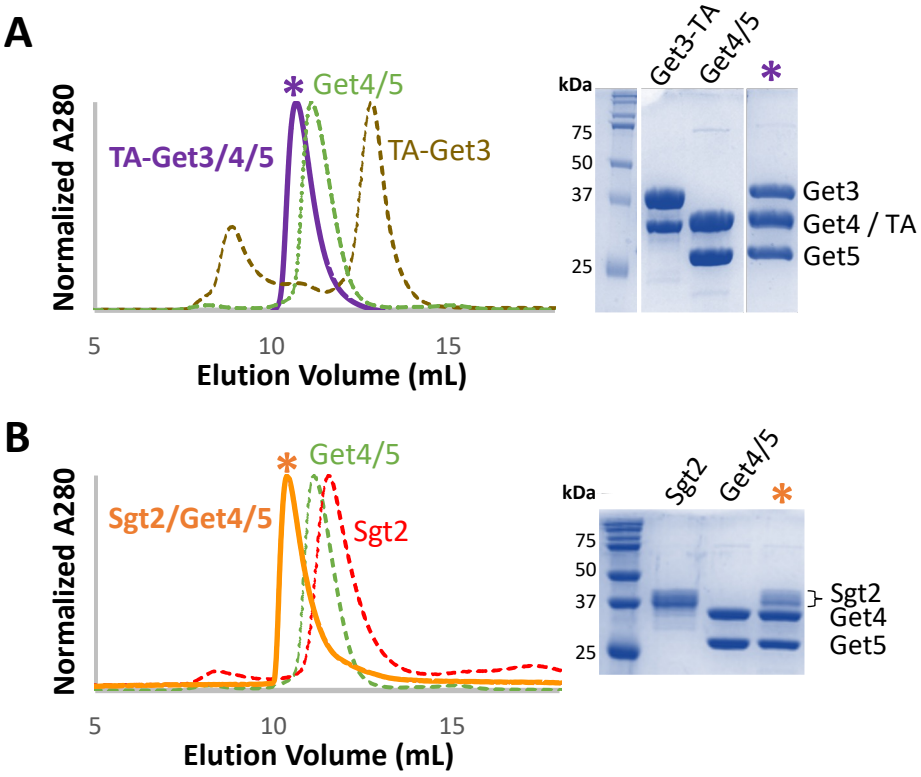

Figure 1. Purification of TA-Get3/4/5 and Sgt2/Get4/5 subcomplexes.

(A) A size-exclusion chromatogram of the TA-Get3/4/5 complex (purple) and the SDS-PAGE gel for the peak fraction (*). The chromatograms for TA-Get3 (brown) and Get4/5 (green) alone are also shown for reference.

(B) A size-exclusion chromatogram of the Sgt2/Get4/5 complex (orange) and the SDS-PAGE gel for the peak fraction (*). The chromatograms for Sgt2 (red) and Get4/5 (green) alone are also shown for reference. The purified Sgt2 shows signs of degradation, as judged by the presence of several bands of similar size on the SDS-PAGE gel. However, Sgt2 is still observed to form a stable complex with Get4/5 that co-elute from a size-exclusion column.

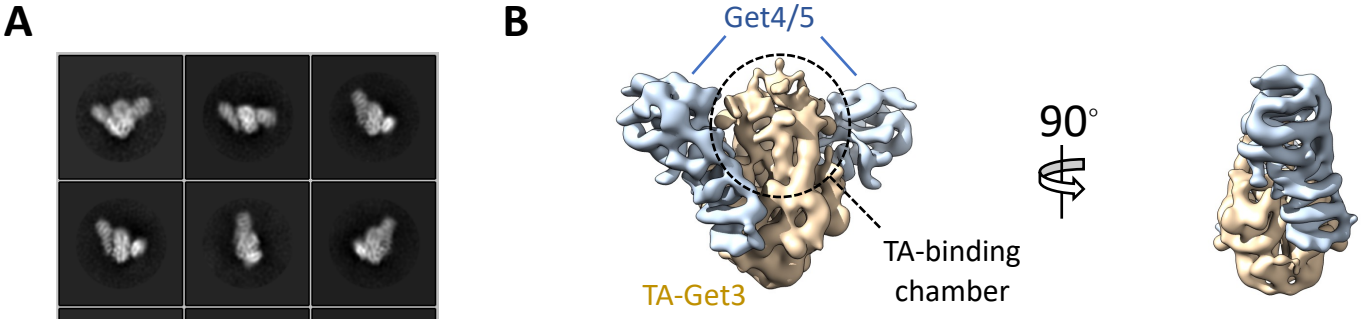

Figure 2. Cryo-EM Map of the TA-Get3/4/5 Complex.

(A) 2D class averages of TA-Get3/4/5 complex.

(B) 3D reconstruction of TA-Get3/4/5 complex is shown with the individual protein components of the complex labeled. The density of the TA-binding chamber is not resolved well enough to distinguish the TA substrate from Get3.

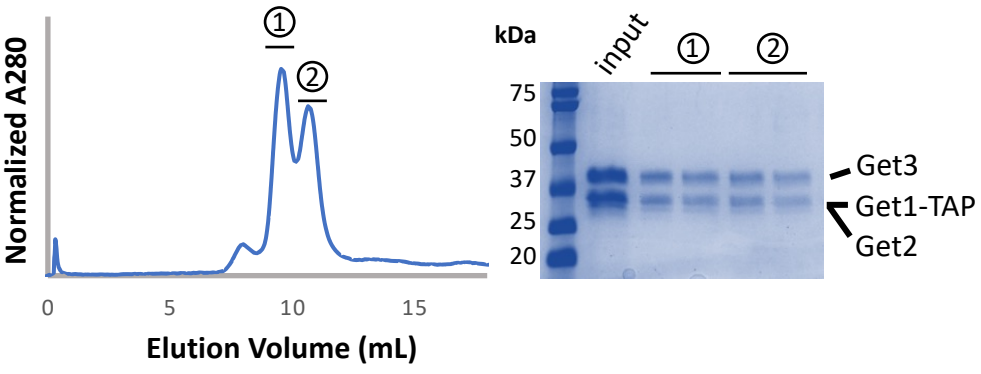

Figure 3. Purification of the Get1/2/3 complex.

A size-exclusion chromatogram of the Get1/2/3 complex purified by the TAP-tag purification method. The SDS-PAGE gel of fractions corresponding to the two peaks show two bands. Analysis by mass spectroscopy confirmed that the top band corresponds to Get3 and the bottom band to Get1-TAP and Get2 that have similar molecular weights.