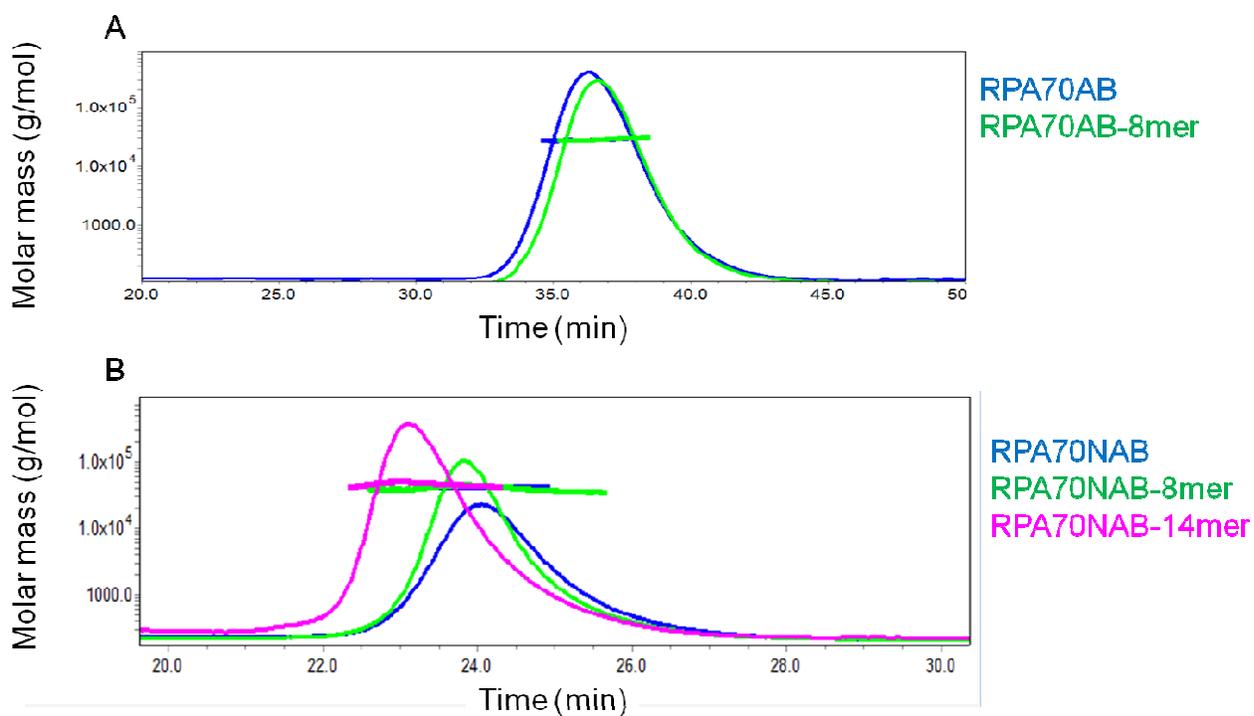


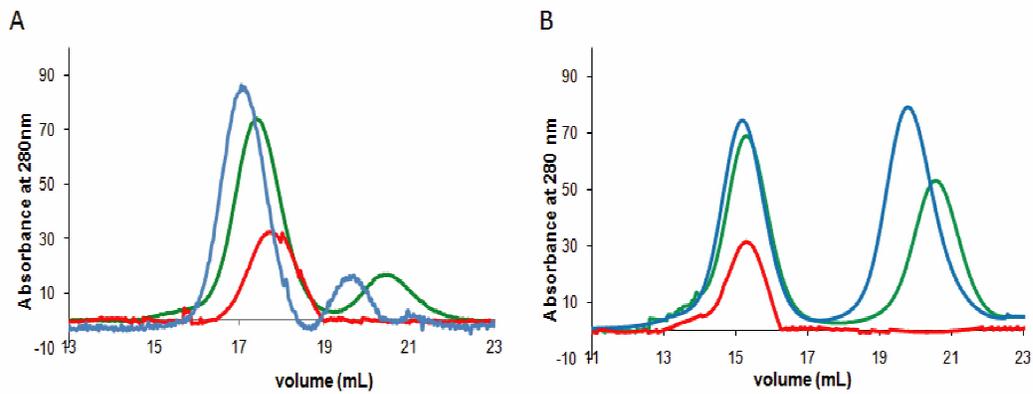
Supplementary Figure 1. TSK-gel G200sw elution profiles of (A) RPA70AB SEC-MALS experiments prior to SAXS data collection and (B) RPA70NAB SEC-MALS experiments prior to SAXS data collection, and (C) the corresponding calculated and experimentally determined molecular weights. The colored horizontal lines in A and B are the output from the MALS system indicating the molar mass at a given retention time, which relate to the axis at left.



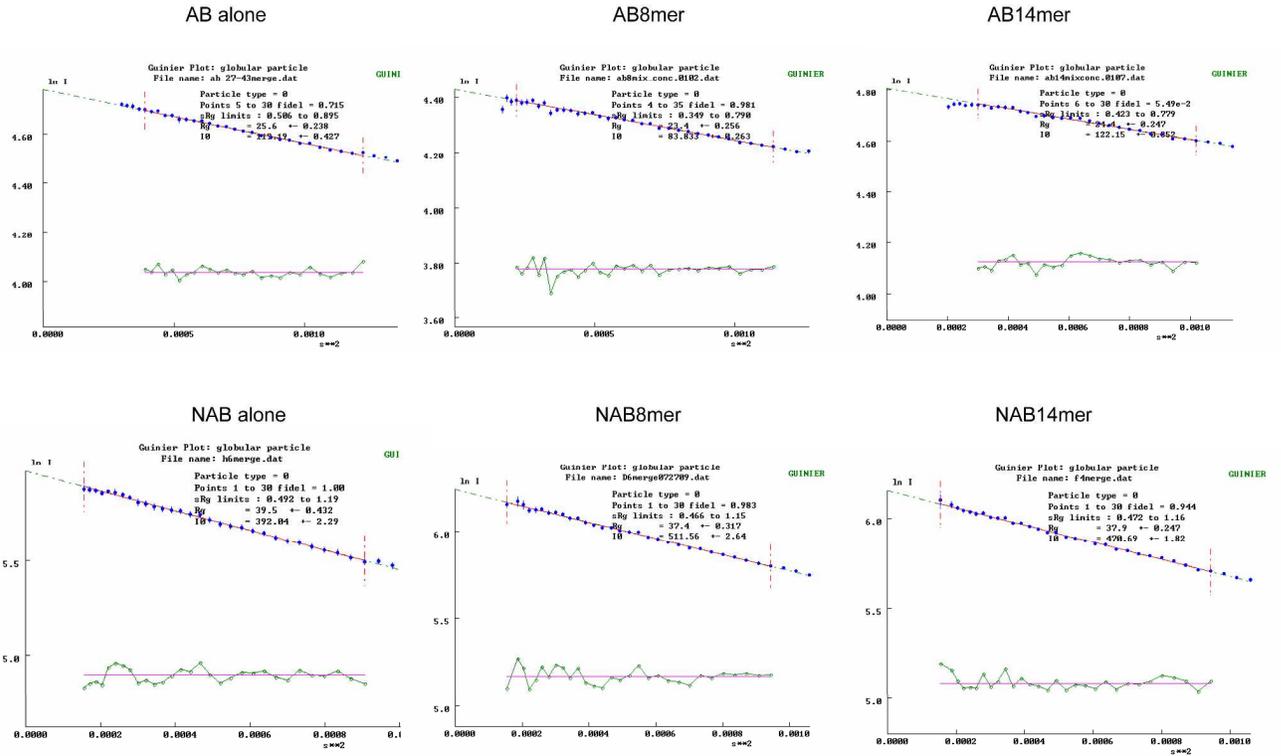
C

Molecular Weight (KDa)	AB	AB-8mer	NAB	NAB-8mer	NAB-14mer
Expected	27.2	29.6	46.1	48.5	50.3
Calculated	27.9	27.5	40.9	41.3	45.6

Supplementary Figure 2. Superdex 200 SEC elution profiles for (A) RPA70AB and (B) RPA70NAB prior to SAXS data collection. All protein samples are monomers and the protein:ssDNA complexes are 1:1 ratios. Red= NAB or AB alone; Green = NAB or AB with 8-mer; Blue = NAB or AB with 14-mer. Excess ssDNA peaks are observed centered around 20 mL.



Supplementary Figure 3. Guinier plots for RPA70AB, RPA70NAB and their ssDNA complexes.



Supplementary Figure 4. Models of RPA70NAB in the presence of the ssDNA 14-mer. The complex with with  $R_g = 29$  was generated by manually positioning the RPA70N domain in a position that mimics ssDNA binding. All other conformers were generated using BILBO-MD as indicated in the Methods section.

