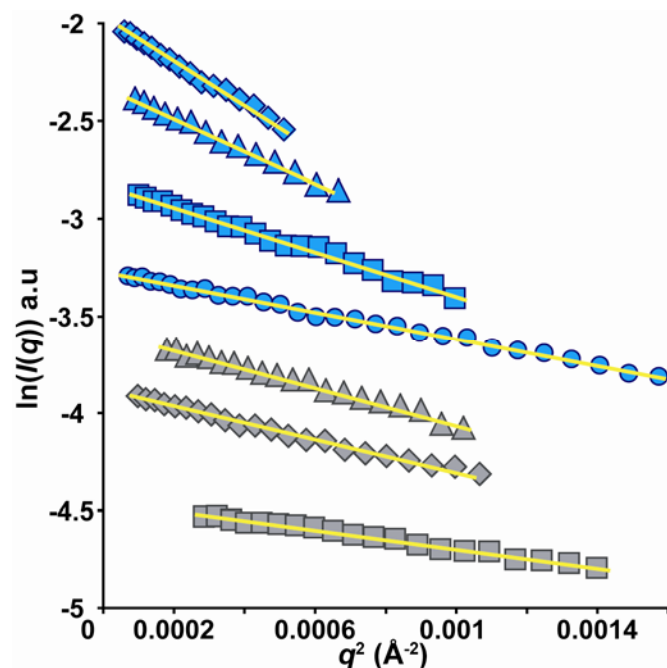


## Supplementary Figures.



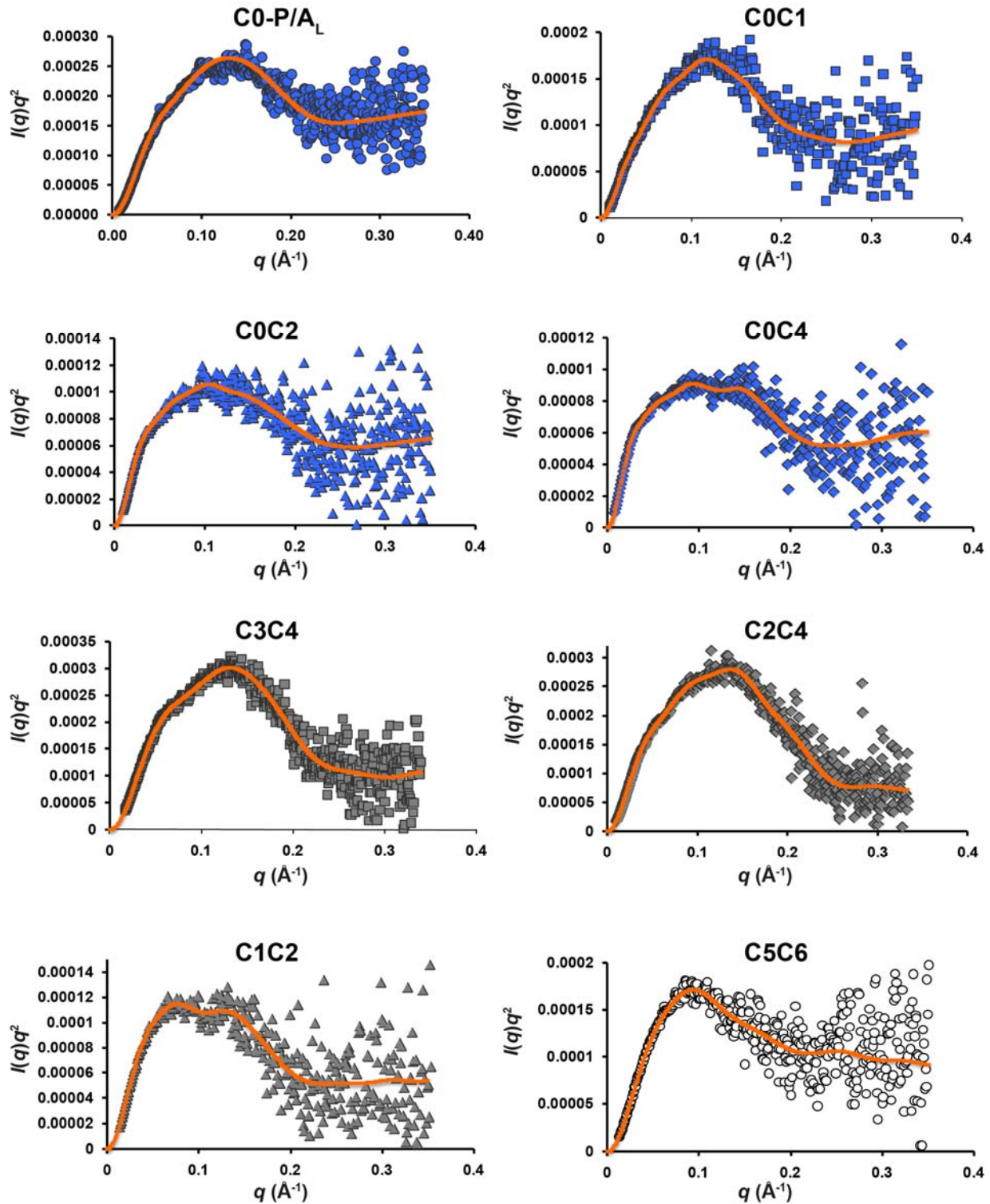
### Supplementary Figure 1. Guinier plots of various N-terminal cMyBP-C constructs.

Excellent linear correlations (yellow lines;  $R^2 = 0.99$ ) are observed at very low- $q^2$  in the Guinier region of the SAXS data for each N-terminal cMyBP-C fragment investigated in this study indicating that the data are not significantly affected by aggregation or interparticle interference. For clarity, data have been scaled via subtracting the following constants from  $\ln(I(q))$ : C0C4, 0.15 (blue diamonds); C0C2, 0.35 (blue triangles); C0C1, 0.7 (blue squares); C0-P/AL, 1.25 (blue circles); C1C2, 1.35 (grey triangles); C2C4, 2.2 (grey diamonds) and; C3C4, 2.45 (grey squares).

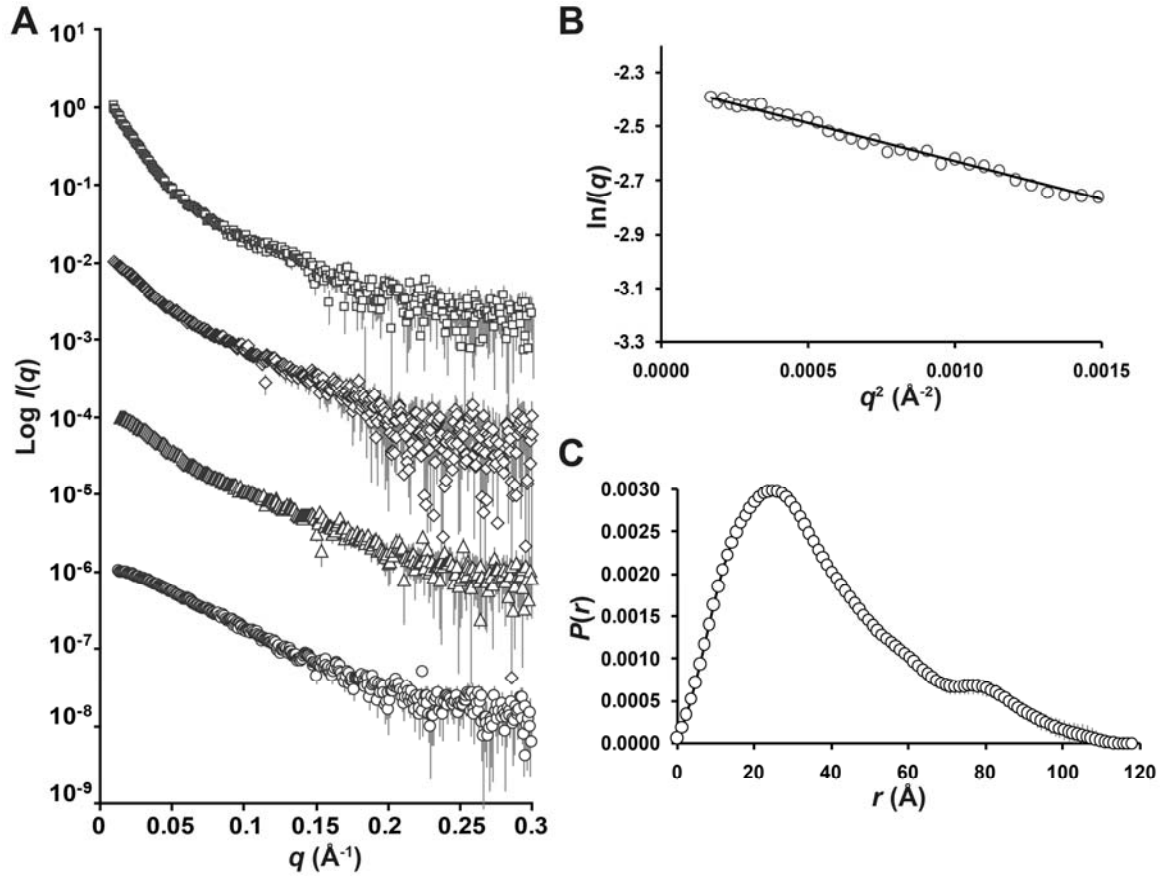
### Amino acid Sequence Human C0C1:

MPEPGKKPVSAFSSKKPRSV EAVAAGSPAVFEAETERAGVKVRWQRRGSDISASNKYGLATEGTRHRTLTVR  
 EVGPADQGSYAVIAGSSKVKFDLKVIEAEKAEPMLAPAPAPAEATGAPGEAPAPAAELGESAPSPKGSSSA  
 ALNGPTPGAPDDPIGLFVMRPQDGEVTVGGSSITFSARVAGASLLKPPVVKWFKGKWVDLSSKVGQHLQL  
 HDSYDRASKVYLFELHITDAQPAFTGSYRCEVSTKDKFECSNFNLTVE

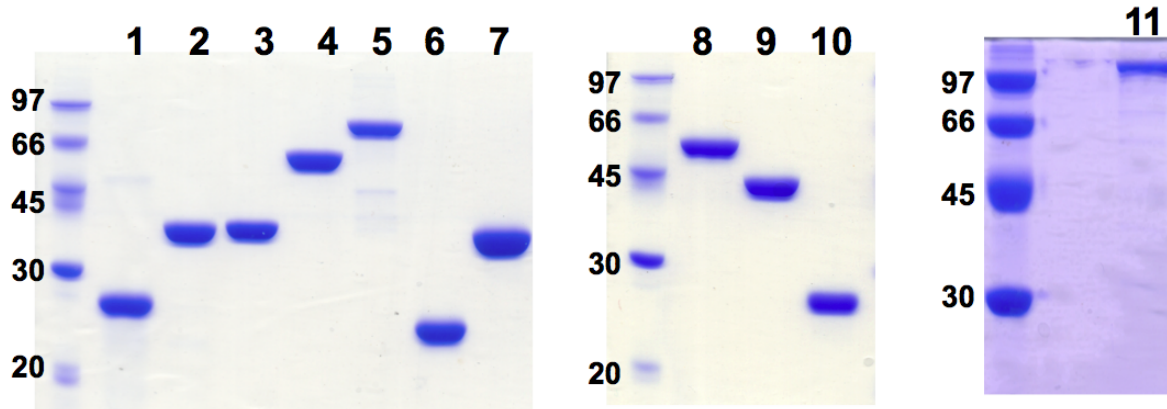
### Supplementary Figure 2. Amino acid sequence of C0C1. Amino acids encompassing C0, P/AL and C1 are colored black, blue and red, respectively.



**Supplementary Figure 3. Kratky plots of various human cMyBP-C fragments.** Orange lines are derived from the smoothed  $I(q)$  vs  $q$  profile fit to the data.



**Supplementary Figure 4. SAXS analysis of full-length cMyBP-C and C-terminal domain fragments.** **A.** SAXS data derived from full-length cMyBP-C ( $2.2 \text{ mg mL}^{-1}$ , squares), C5C8 ( $4.35 \text{ mg mL}^{-1}$ , diamonds), C5C7 ( $5.3 \text{ mg mL}^{-1}$ , triangles) and C5C6 ( $4.75 \text{ mg mL}^{-1}$ , circles). For clarity the data have been scaled on the  $I(q)$  axis by applying the following multipliers: Full-length cMyBP-C, 2.227; C5C8, 0.048; C5C7,  $5.69 \times 10^{-4}$  and; C5C6,  $1.09 \times 10^{-4}$ . **B.** Guinier plot of SAXS data (unscaled) for C5C6,  $R^2 = 0.99$ . **C.**  $P(r)$  vs  $r$  profile of C5C6 (scaled as in Fig. 4).



**Supplementary Figure 5. SDS-PAGE of human cMyBP-C fragments and full-length protein.** Lane 1 = C0-P/A<sub>L</sub>; Lane2 = C0C1 ; Lane3 = C1C2; Lane4 = C0C2; Lane5 = C0C4; Lane6 = C3C4, Lane7 = C2C4; Lane8 = C5C8, Lane9 = C5C7; Lane10 = C5C6 and; Lane11 = full-length human cMyBP-C. Some fragments containing C0, e.g., C0C1, consistently migrate at 'larger than expected' molecular weights.