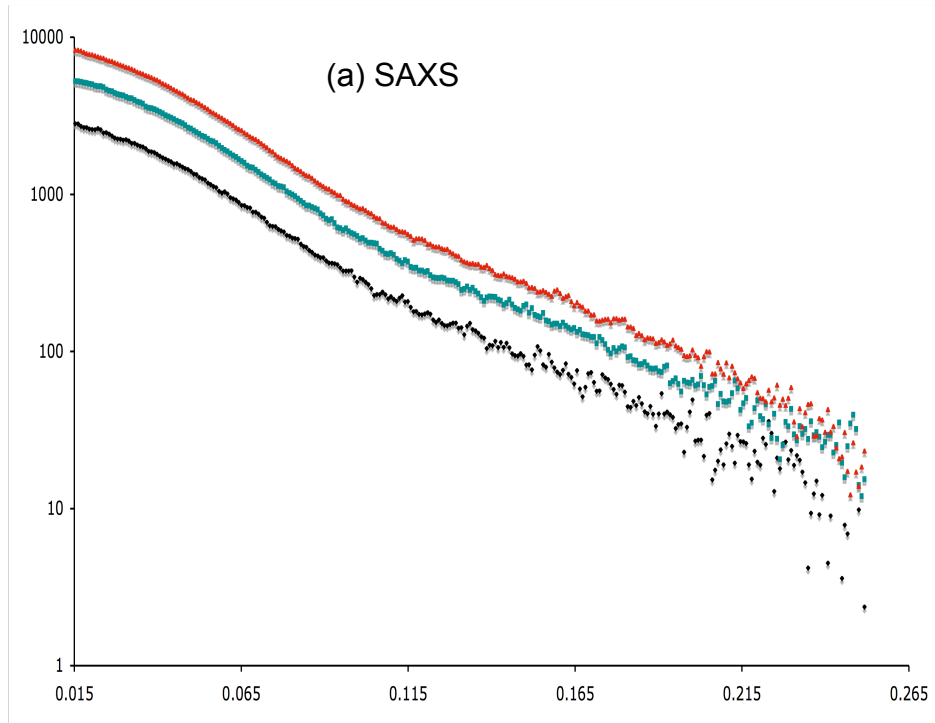


Supporting material I (Chaudhuri *et al.*)

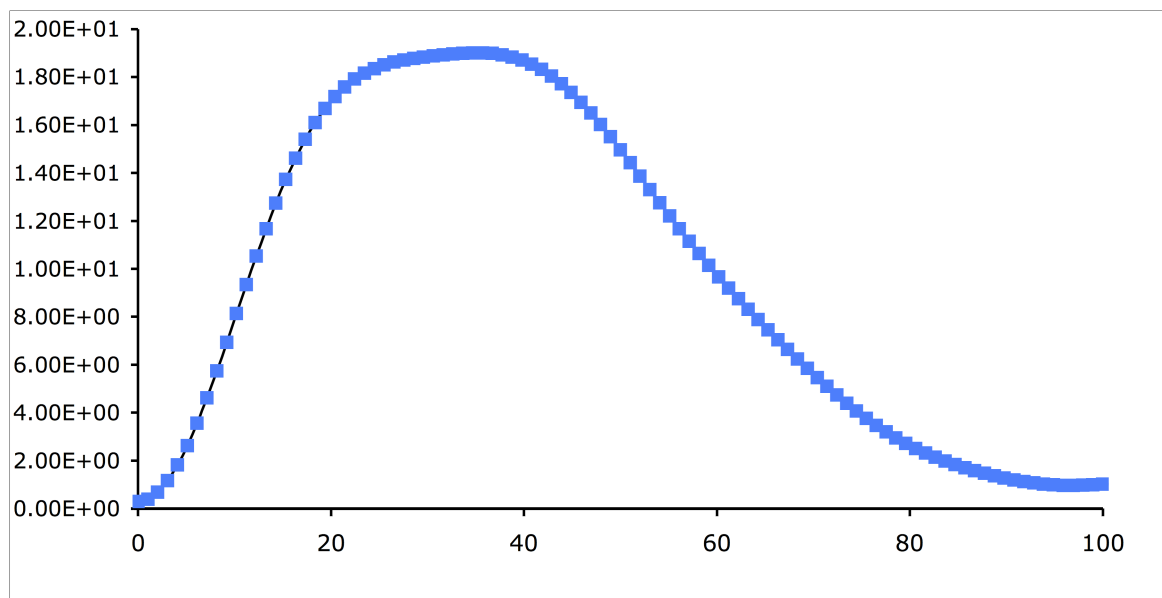
Figure S1. (a) SAXS and SANS H/D contrast variation data series ($\log I$ versus q in \AA^{-1}).

Scattering profile of the tbParB-parS22 assembly is shown at 3 different concentrations. Intensity is shown in arbitrary unit.



Supporting material I (Chaudhuri *et al.*)

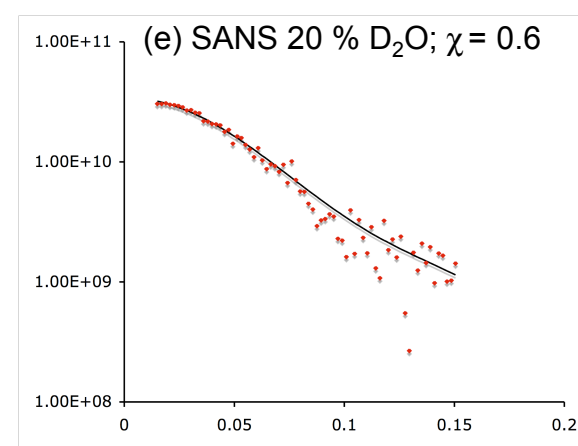
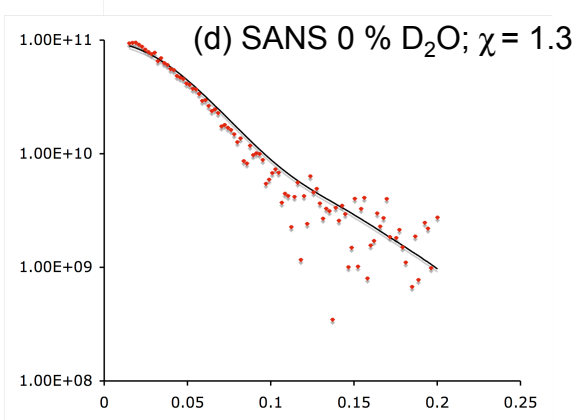
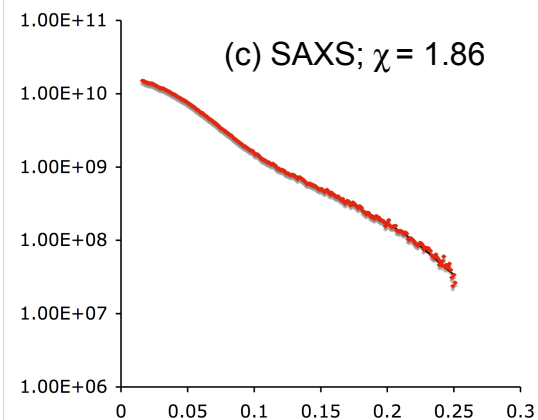
Figure S1. (b) The pair distribution function $P(r)$ plotted against the pair-wise distance (r in Å) is shown for the tbParB-*parS22* SAXS dataset (computed in GNOM (43), $P(0) = 0$ and $P(r \geq D_{\max}) = 0$ conditions were not imposed).



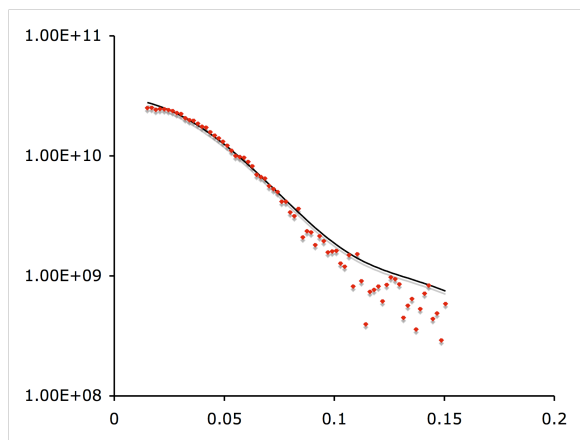
Supporting material I (Chaudhuri *et al.*)

Figure S1. (c-h) SAXS and SANS H/D contrast variation data series ($\log I$ versus q in \AA^{-1}).

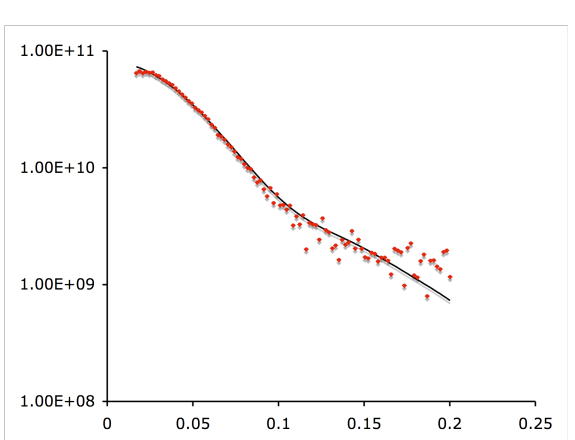
Fitting of the scattering profiles (black line) computed from the shape of the tbParB-parS22 to the solution scattering data sets are shown (red dots; overall $\chi = 1.3$, fit and the χ -values are reported by MONSA). The dataset with 34.5 % D_2O was not included in the shape reconstruction.



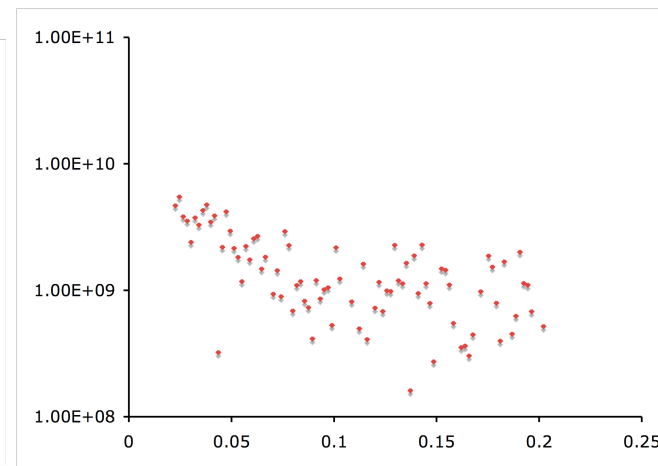
(f) SANS 78.5 % D_2O ; $\chi = 1.6$



(g) SANS 86 % D_2O ; $\chi = 1.6$



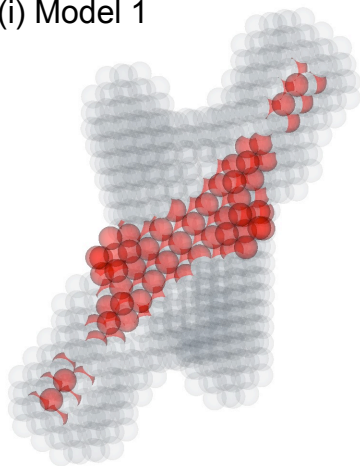
(h) SANS 34.5 % D_2O ;



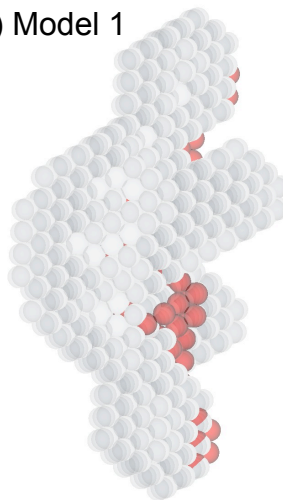
Supporting material I (Chaudhuri *et al.*)

Figure S1. (i-l) Two examples of individual MONSA shape reconstructions in two orientations are shown (protein: grey beads, DNA: red beads).

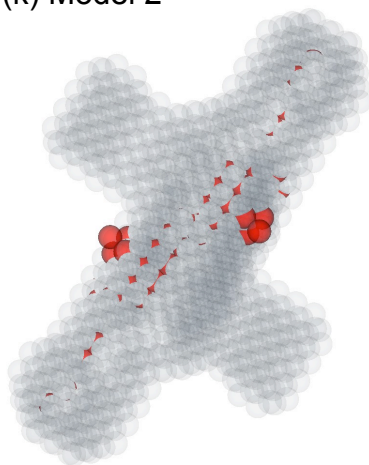
(i) Model 1



(j) Model 1



(k) Model 2



(l) Model 2

