## **Supporting information:**

1. Definition of the reduced chi-square:

reduced 
$$\chi^2 = \frac{1}{\text{degree of freedom}} \sum \frac{(\text{calculated scattering - measured scattering})^2}{\text{Experimental error}^2}$$

degree of freedom = number of data points - number of variables. Since the number of data points is  $10^5$ , much more than the number of variables in the simulation, degree of freedom  $\approx$  number of data points =  $10^5$ .

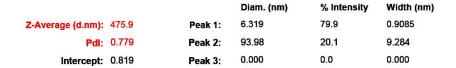
The rms value for the high-frequency electronic noise was used for the experimental error in the equation.

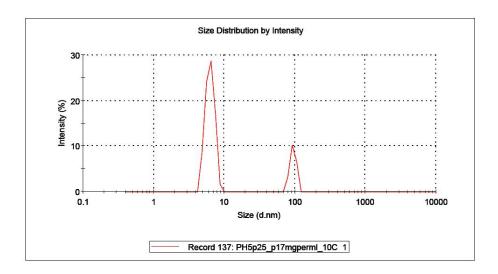
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## 2. Variable iteration procedure:

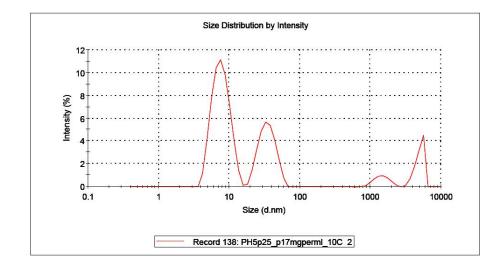
The set of variables considered for a simulation was: k0, k0-, k1, k1-, k2, k3 ... scattering cross-section

For a simulation, a random set of variable values was chosen in the beginning. Then parameter values were changed in the above order for many runs. In each run, the value of each specific variable was changed in the direction to decrease the reduced chi-square until a minimum of reduced chi-square value was achieved (1% change of the variable in either direction would result in the increase of reduced chi-square value). When every variable has been changed in a run, a new run will start. Iterations stopped when there were no changes of the variable values in a simulation run. This set of variables was reported as the final result.





			Diam. (iiii)	/6 IIICHSILY	width (min)
Z-Average (d.nm):	26.20	Peak 1:	7.810	57.1	2.180
Pdl:	0.243	Peak 2:	34.96	28.2	9.258
Intercept:	0.722	Peak 3:	4914	10.3	671.3



**Supplemental figure 1**: DLS spectra captured for BMV capsid assembly at 12second (top one) and 30 second (bottom) with the coat protein concentration of 4.19  $\mu$ M dimers at 10 °C. The ~7 nm peak represents the protein dimers while the ~30 nm one is for capsids. Other peaks are due to impurities or analysis errors. The picture shows capsid rose up between 12 and 30 second and no indication of distinguishable intermediates.