SUPPLEMENTARY DATA

Supplementary Table 1. Scattering conditions of the SEC2 complexes and contrasts used in the MONSA calculation. The contrast values were obtained from the ATSAS on line server at www.embl-hamburg.de/biosaxs/atsas-online/.

Sample	% D_2O in buffer	% deuteration of protein	Contrast (10^{10} cm^{-2})	
			Protein	DNA
SAXS				
H-SEC2	0	0	1.00	2.00
SANS				
H-SEC2	0	0	2.50	4.50
H-SEC2	100	0	-3.00	-1.5
D-SEC2	65	72.5	1.83	0.60
D-SEC2	100	72.5	-0.1	-1.50

The fraction (x) of the total scattering of H-SEC2 contributed by Mos1 is given by:

$$x = \frac{Vf_{Mos1} \text{ x } Constrast_{Mos1}}{(Vf_{Mos1} \text{ x } Constrast_{Mos1}) + (Vf_{DNA} \text{ x } Constrast_{DNA})}$$

The excluded volumes of the Mos1 dimer and the DNA duplex are 99.2 nm^3 and 25.9 nm^3 respectively. Thus, the fraction of the total volume of H-SEC2 contributed by the Mos1 dimer (Vf_{mos1}) is ~0.8 and the fractional volume of the DNA duplex (Vf_{DNA}) is ~0.2.

Therefore, for H-SEC2 in 100% H_2O,

$$x = \frac{(0.8 \text{ x } 2.5)}{(0.8 \text{ x } 2.5) + (0.2 \text{ x } 4.5)}$$

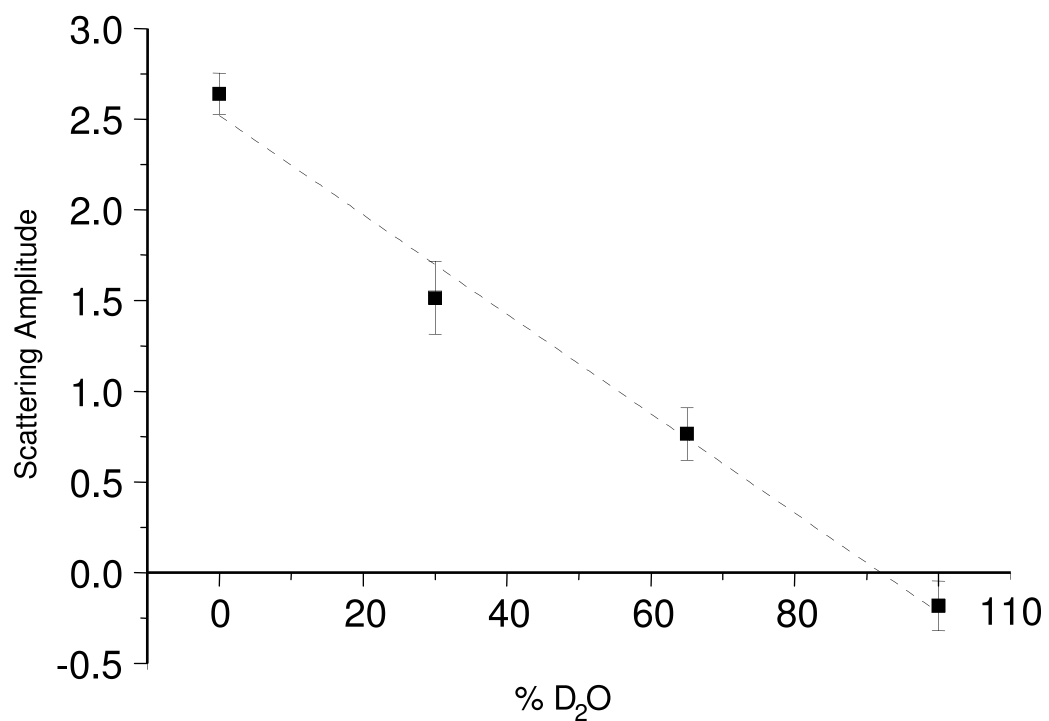
$$x = 0.69$$

Supplementary Table 2. Predicted extinction coefficients at 260 nm and 280 nm for the DNA duplex, Mos1 transposase and transposase-DNA complexes.

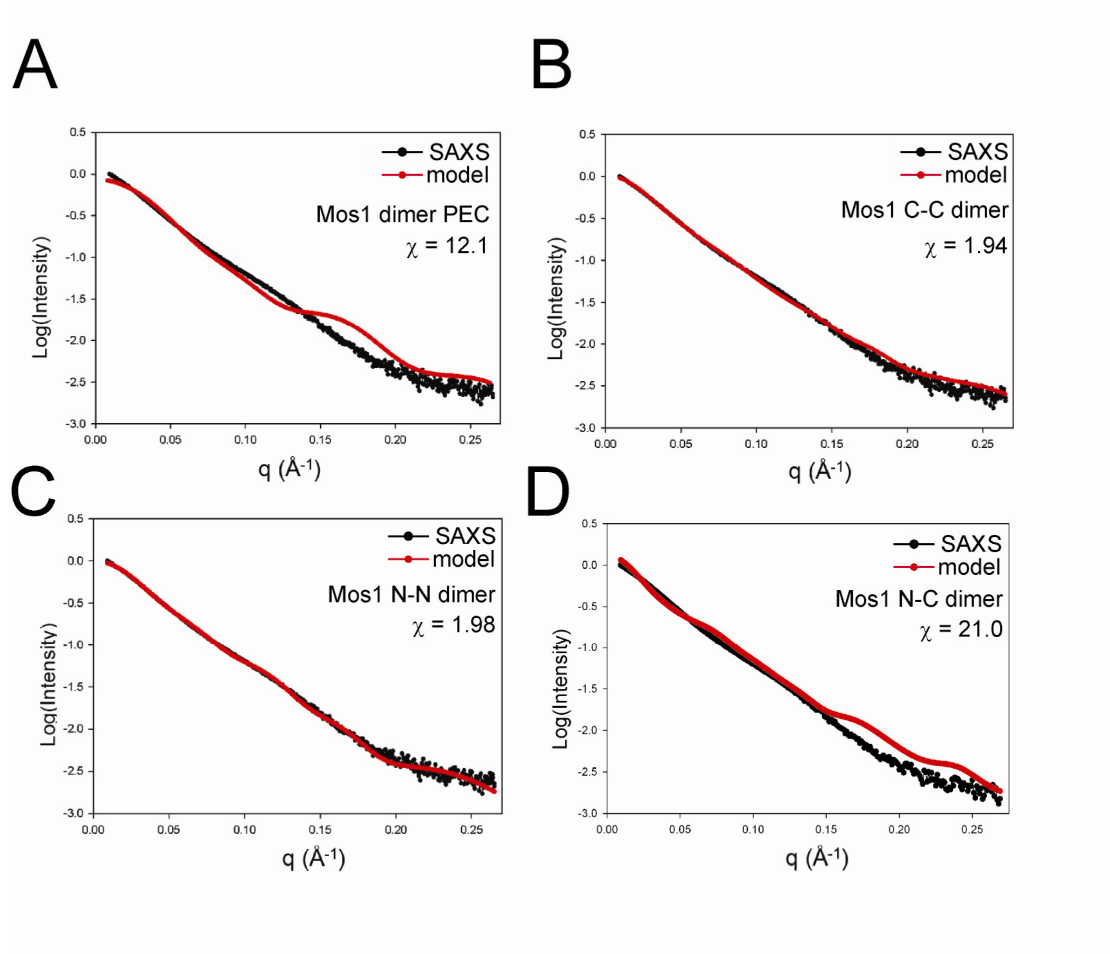
	Extinction coefficient at 260 nm ($M^{-1}cm^{-1}$)	Extinction coefficient at 280 nm ($M^{-1}cm^{-1}$)	Ratio of extinction coefficients (260/280)
50 mer DNA duplex	777,531*	428,431 *	1.81
Mos1 transposase (monomer)	40,521	72,880 ‡	0.56
SEC1	818,052	501,311	1.63
SEC2	858,573	574,191	1.49
PEC	1,636,104	1,002,622	1.63

*Obtained from IDT biophysics (http://biophysics.idtdna.com/UVSpectrum.html)
‡ From protparam (http://web.expasy.org/protparam/)

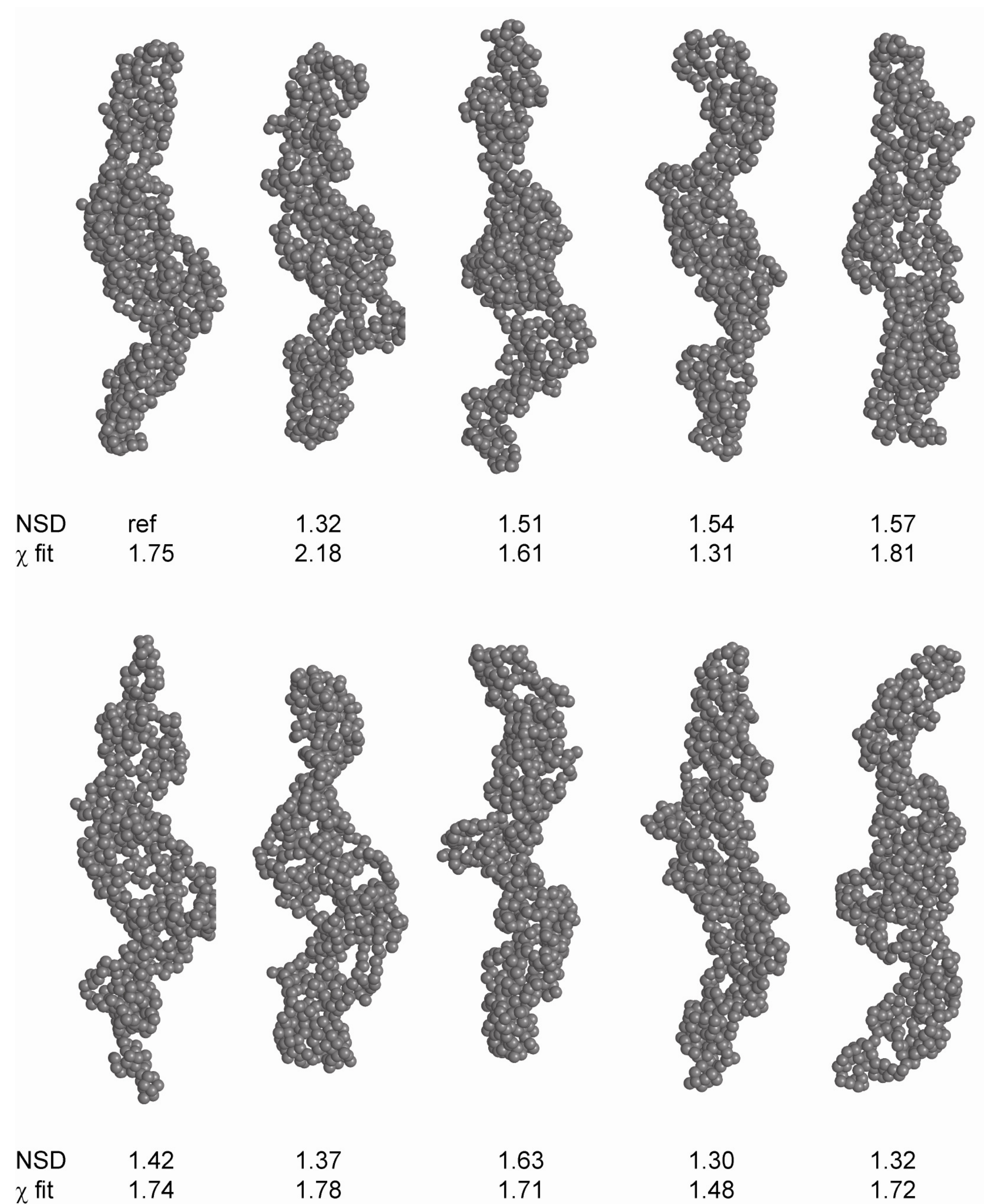
Supplementary Figure 1. The contrast match point of D-Mos1 Transposase. Plot of the scattering amplitude at zero angle against the percentage of D_2O in the buffer. The scattering amplitude at zero angle is defined as √(I(0)/tcl) - where I(0) is intensity at zero angle; t is transmission of sample; c is concentration (mg/ml) and l is the path length (mm). The linear fit to the data points (dashed line) intercepts the x-axis at 92 % D_2O, the contrast match point of D-Mos1.



Supplementary Figure 2. Comparison of the experimental SAXS data and calculated scattering curves for models of Mos1 homodimers. The experimental SAXS data is shown as a black line and for each model the calculated scattering curve is shown as a red line. Fits of (A) the transposase dimer from the PEC crystal structure (Figure 3B), (B) Mos1 homodimer with the catalytic domains at the dimerisation interface (Figure 3C), (C) N-terminal Mos1 dimer model (Figure 3D) or, (D) The head-to-tail (or N-C) dimer model (Figure 3E).



Supplementary Figure 3. Gallery of ten spherical bead models of the H-Mos1 dimer calculated from the SAXS data in GASBOR, with P2 symmetry imposed. The χ of the fit to the experimental SAXS data and the NSD between models is indicated below each model.



Supplementary Figure 4. (A) Gel filtration of N130 Mos1 with peak fractions labelled 1 to 8. (B) SDS-PAGE of the gel filtration fractions (labelled), starting sample (input) and molecular weight markers. Fractions 1 to 4 (500 µL each) were precipitated with TCA and resuspended in 40 µL before loading. The gel was visualised with silver stain for maximum sensitivity. A faint band at ~15 kDa is visible in lane 3 confirming that the minor peak contains a tetramer of N130 Mos1.