**Supplementary data**

**Material :**

**Primers :**

5’biot-temp-30 : biotin-CCGAATCAGGAAGATAACAGCGGTTTAGCC

temp-25 : TCAGGAAGATAACAGCGGTTTAGCC

prim-20 : GGCTAAACCGCTGTTATCTT

Primer combinations:

for SAXS : temp-25 + prim-20

for SPR : 5’biot-temp-30 + prim-20

**Methods:**

**Annealing:**

The primers 5’biot-temp-30 and prim-20 or temp-25 and prim-20 were mixed at a final concentration of 100 µM each in 20 mM Tris pH 7.0, 75 mM NaCl, 2 mM Mg Ac and annealed using a linear temperature gradient from 98°C to 23°C at 0.5°C temperature decrease per minute using an Eppendorf Mastercycler pro.

**SPR experiment:**

Data were collected on a BIAcore 3000 on a streptavidin coated chip. All experiments were performed in 20 mM Tris pH 7.0, 100 mM NaCl with a flow rate of 15 µl/min.

Sensor preparation : 75 µL of a 1 µM solution of 5’biot-temp-30 + prim-20 annealed primers were loaded at 5µL/min on one flow cell, a second flow cell was used for background subtraction. Unbound DNA was eliminated by a 2 min wash with 0.05% SDS.

SPR run: A dilution series from 0.625 to 320 nM of E9 exominus (2-fold step) was injected each during 3 min followed by a 5 min dissociation. The protein was washed between injections with a 2 min 0.05% SDS wash before being re-equilibrated in running buffer for 5 minutes.

Data analysis: Background subtracted signals were imported to LibreOffice Calc for curve fitting using the Solver non-linear function. Single exponential fit gives a KD of 12 ± 6 nM. Figure was generated using MS Excel.

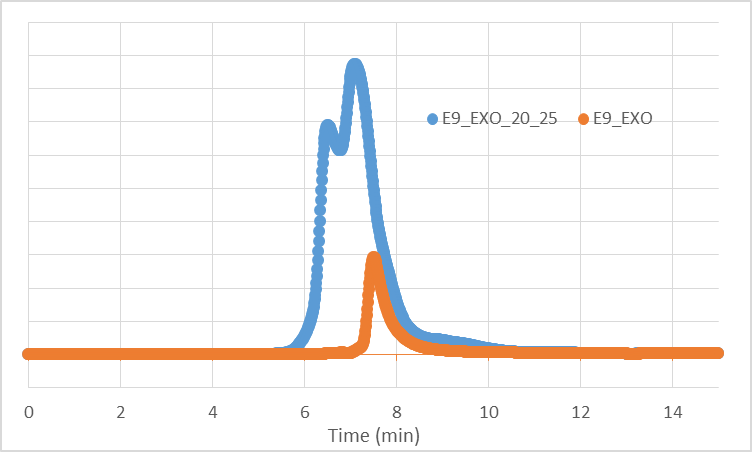
**Supplementary Figure 1:** SPR signal curves for binding of E9 exominus to DNA.

**Sample preparation for SAXS:**

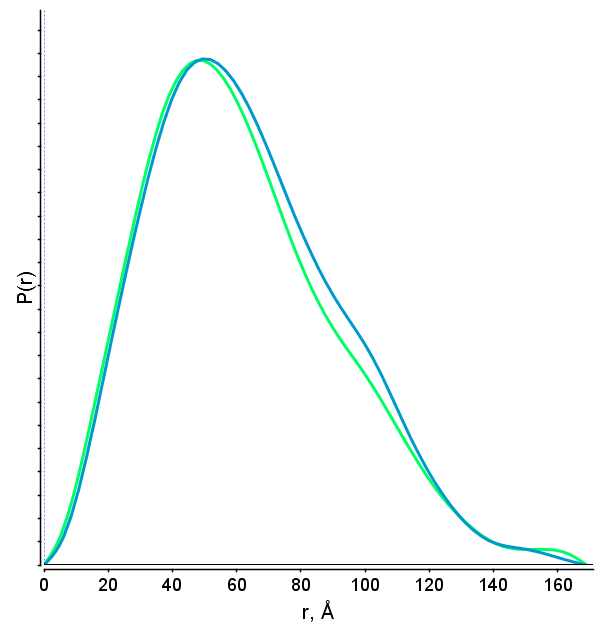
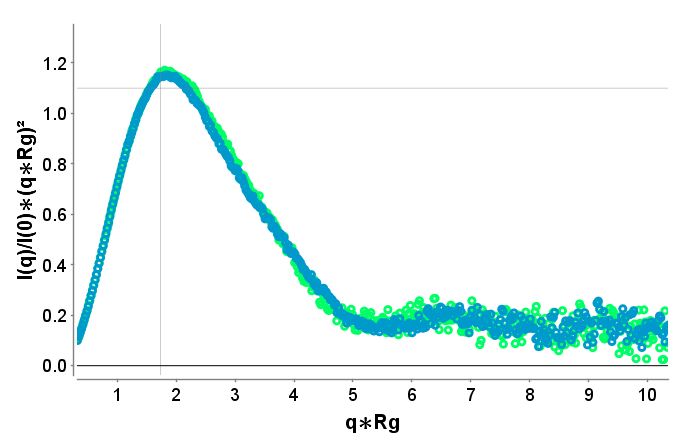
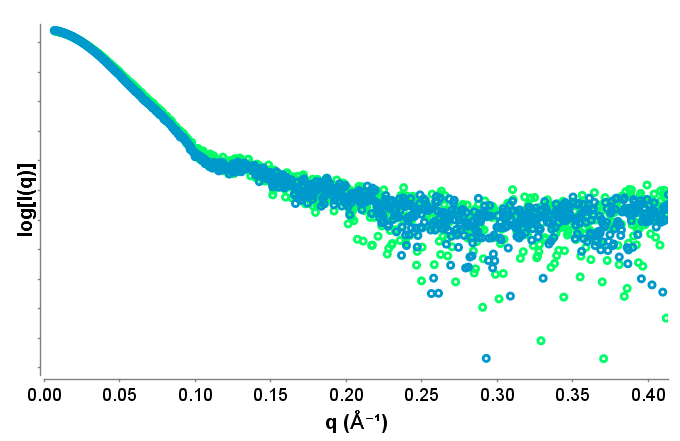
800 µl of E9exominus (7.8 µM) were mixed with 80 µl annealed primers at 100 µM. The salt was diluted to 75 mM and the sample then concentrated to 60 µl (~ 8-10 mg/ml protein, DNA 1.2 x).

**Concurrent SAXS analysis of the first peak:**

The analysis of the first peak representing the E9 exominus +DNA complex using classical frame selection and EFA analysis shows that in this case there is no significant improvement of the scattering signal using deconvolution.



**Supplementary Figure 2:** UV spectra from SEC-SAXS of the E9 exominus with (blue) versus without (orange) DNA (data not shown) showing that the second peak corresponds to E9 exominus unbound form.



a)

b)

c)

**Supplementary Figure 3:** a) I versus q curve, b) Kratky plot, c) P(r) of E9 exominus +DNA. The blue curve represents the analysis using EFA and the green curve represents the analysis without EFA. The Rgs differ slightly (49.1Å versus 48.4 Å in real space).