

**Figure 3- figure supplement 2**



**SIRT6**

**SIRT6 + DNA**

**Peak3**

**Peak2**

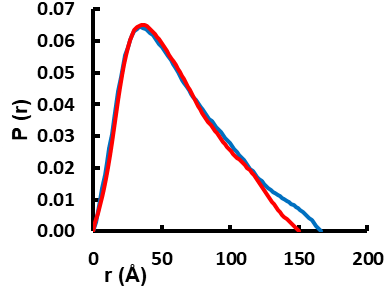
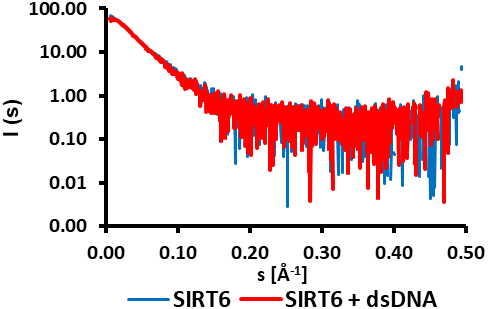
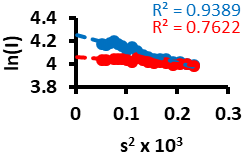
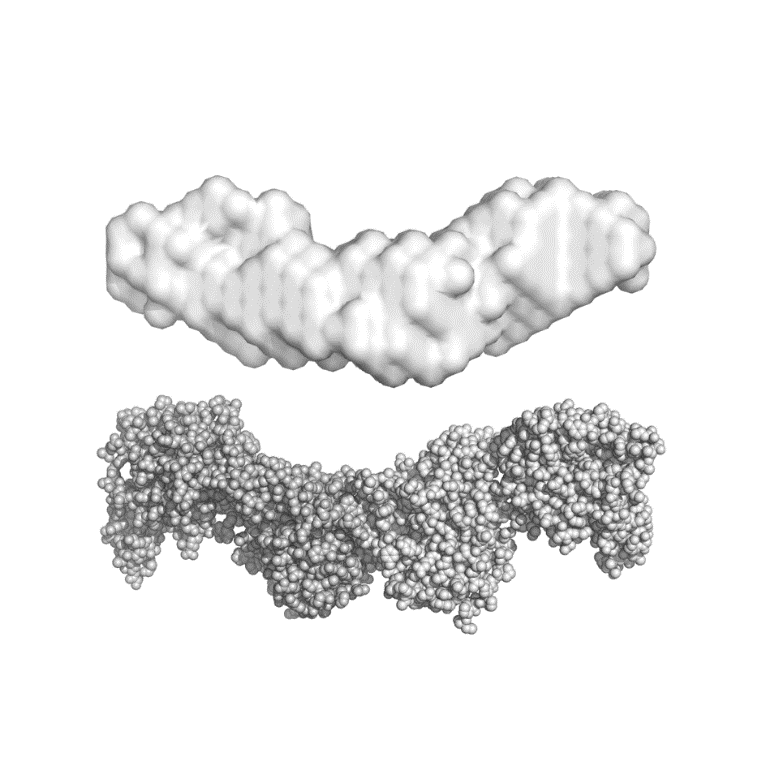
**Peak1**

**Peak3**

**Peak2**



**Peak1**



**Figure 3- figure supplement 2**

**(A)** SEC-MALS analysis of SIRT6 or SIRT6 with dsDNA  10bp oligo with 3 overhanging ends on both sides. **For SIRT6:** Peak 1: Protein mass (calculated by UV) = 66.7±3.3 kDa, Protein mass (calculated by RI) = 70.7±3.5 kDa. Peak2: Protein mass (calculated by UV) = 114.3±5.7 kDa, Protein mass (calculated by RI) = 103.8±4.9 kDa. Peak3: Protein mass (calculated by UV) = 609.7±14.6 kDa, Protein mass (calculated by RI) = 833.6±16.4 kDa. **For SIRT6 +DNA:** Peak 1: Protein mass (calculated by UV) = 52.5±3.1 kDa, Protein mass (calculated by RI) = 55.7±3.2 kDa. Peak2: Protein mass (calculated by UV) = 99.4±3.8 kDa, Protein mass (calculated by RI) = 94.6±3.5 kDa. Peak3: Protein mass (calculated by UV) = extremely high, Protein mass (calculated by RI) = 9224±258 kDa. **(B)** X-ray scattering profile (right) and the distance distribution function (left) of SIRT6 (blue) and SIRT6 bound to dsDNA (red). **(C)** Overall parameters for small angle X-ray scattering of SIRT6 alone and SIRT6 bound to dsDNA determined from the distance distribution function P(r). Rg is the radius of gyration and Dmax, maximum dimension of the particle **(D)** SAXS structure of SIRT6 (grey surface). Ab initio models were reconstructed from SAXS data using the computer program DAMMIN [D. I. Svergun (1999) Restoring low resolution structure of biological macromolecules from solution scattering using simulated annealing. Biophys J. 2879-2886] and were averaged by the computer program DAMAVER [V. V. Volkov and D. I. Svergun (2003). Uniqueness of ab-initio shape determination in small-angle scattering. J. Appl. Cryst. 36, 860-864]. The crystal structure of SIRT6 tetramer (grey spheres) was extracted from the crystal structure of SIRT6 (pdb id: 3PKI) and compared with the obtained SAXS model in PyMOL (http://www.pymol.org).

**A.**

**B.**

**C.**

**D.**