Supporting Materials

Solution Model of the Intrinsically Disordered Polyglutamine Tract-Binding Protein-1

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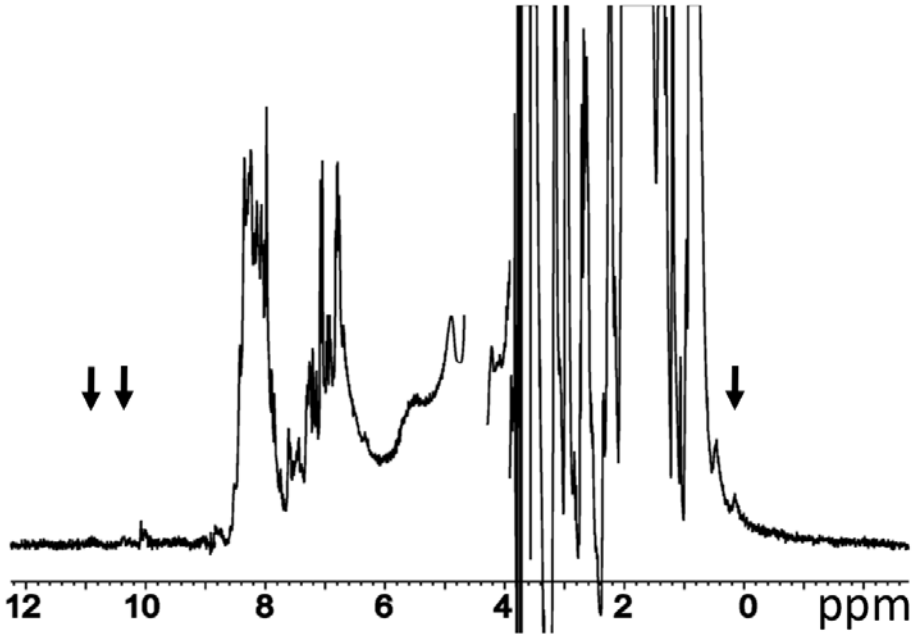

Figure S1. 1D 1H NMR spectrum of PQBP-1. The spectrum of full-length PQBP-1 recorded on a Varian 600MHz spectrometer at 25°C. Data was acquired at a sample concentration of 0.2 to 0.5 μM in Native buffer (20mM Tris-HCl pH7.0, 150mM NaCl, 1 mM DTT). The arrows indicate chemical shifts at 0.2, 10.4 and 10.9 ppm.

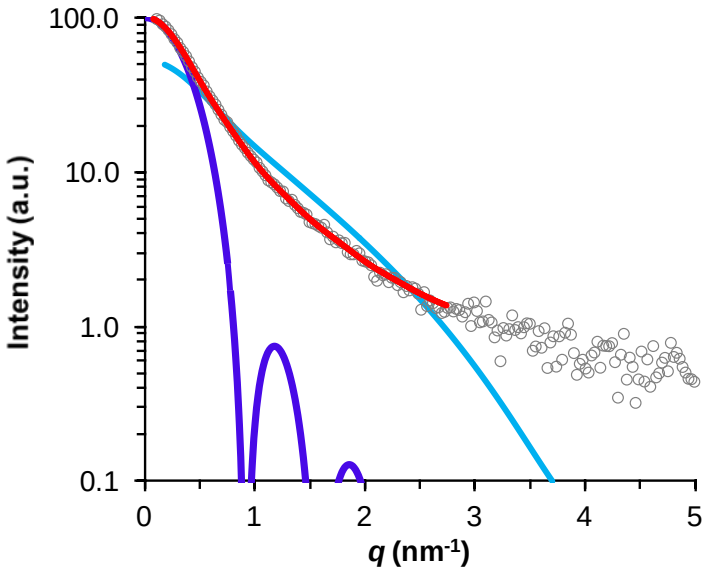

Figure S2. Alternative shape models for SAXS analysis of PQBP-1. The experimental X-ray scattering is shown as circles, along with the scattering calculated from the DAMMIF bead model of PQBP-1 (red, same as black curve in Figure 5b). The curve in cyan shows the scattering calculated from the best-fit ellipsoid-of-revolution model (half axes a=1.0 nm and c=5.4 nm). The scattering calculated from a spherical model having an R_g of 3.8 nm, the same as that of PQBP-1, is shown in blue. Intensity values smaller than 0.1 arbitrary units (a.u.) are truncated.