

Supplementary Information

The impact of hydrophobic sequence patterning on the coil to globule transition of protein-like polymers

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Density calculation from an R_g value

Due to the lack of a measured density of polypeptoids, the density of a polypeptide¹ was used to determine the volume of polymer present in each globule.

$$\rho_{globule} = \frac{mass_{globule}}{volume_{globule}}$$

$$mass_{globule} = mass_{polymer} + mass_{water}$$

$$volume_{globule} = \frac{4}{3}\pi R_g^3$$

$$mass_{water} = volume_{water}\rho_{water}$$

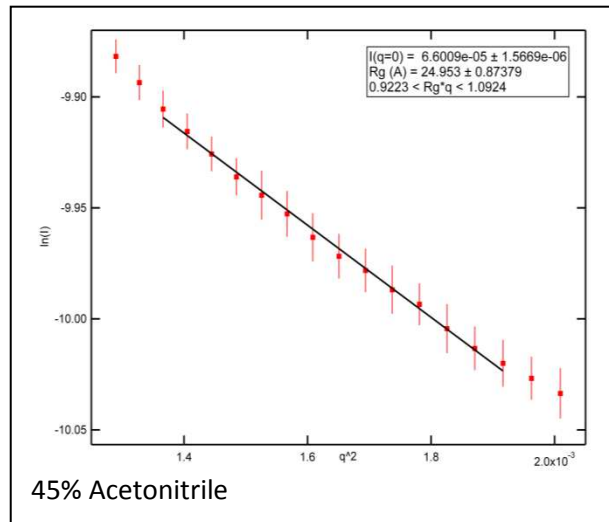
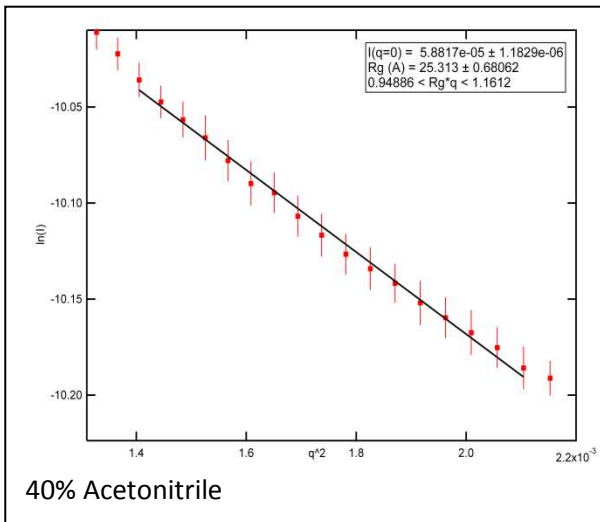
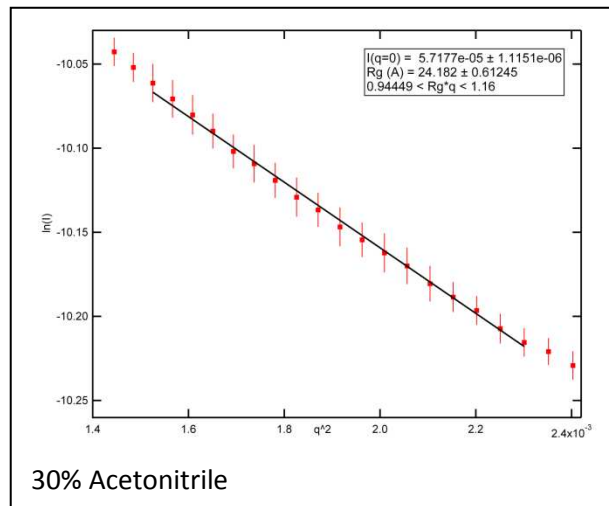
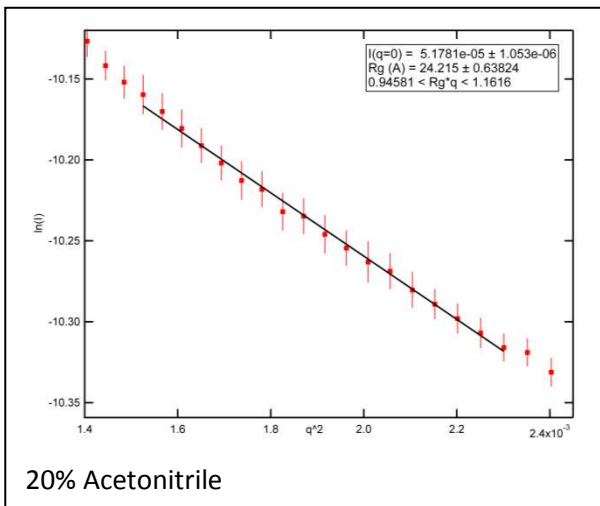
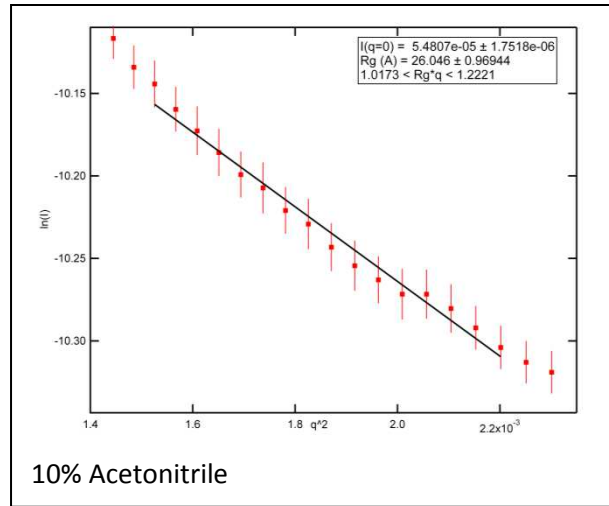
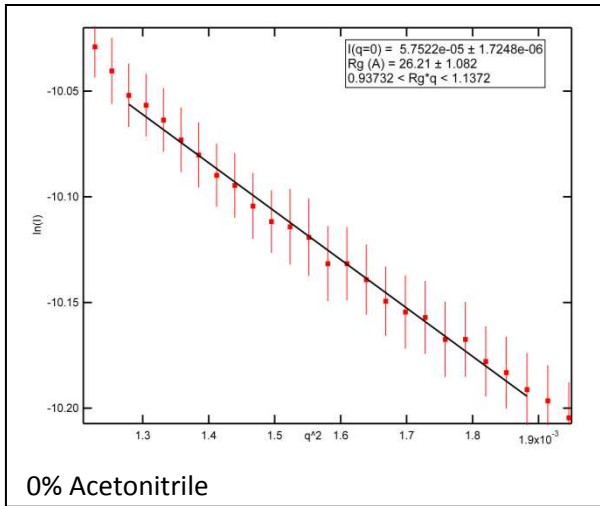
$$volume_{water} = volume_{globule} - volume_{polymer}$$

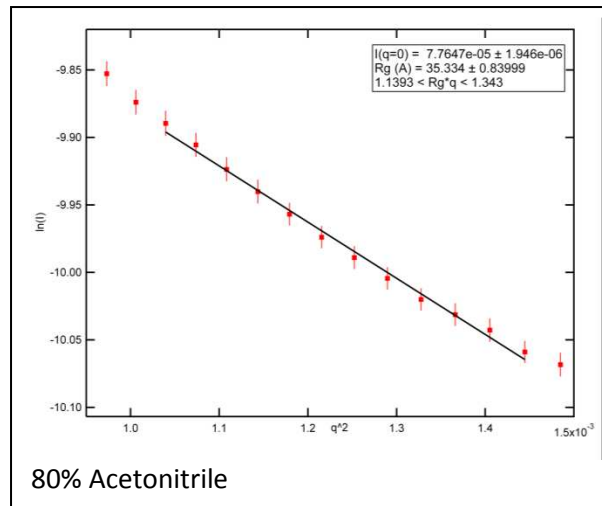
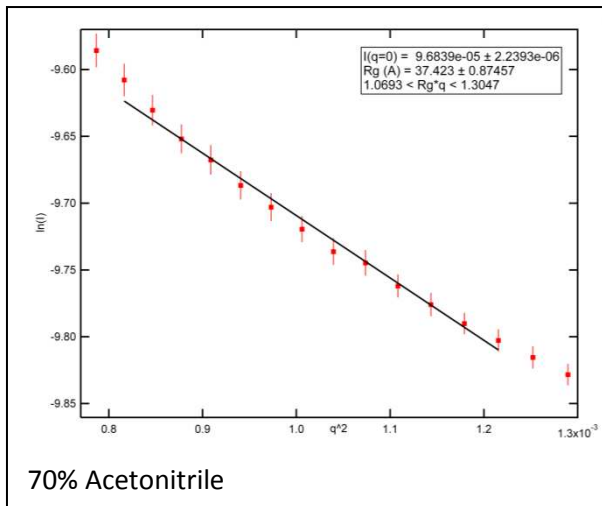
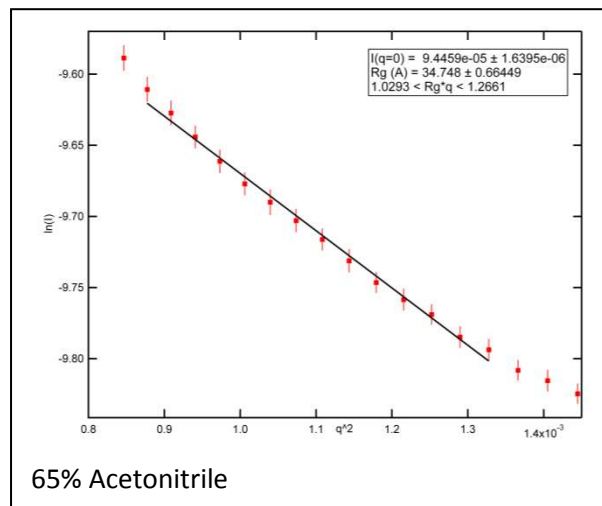
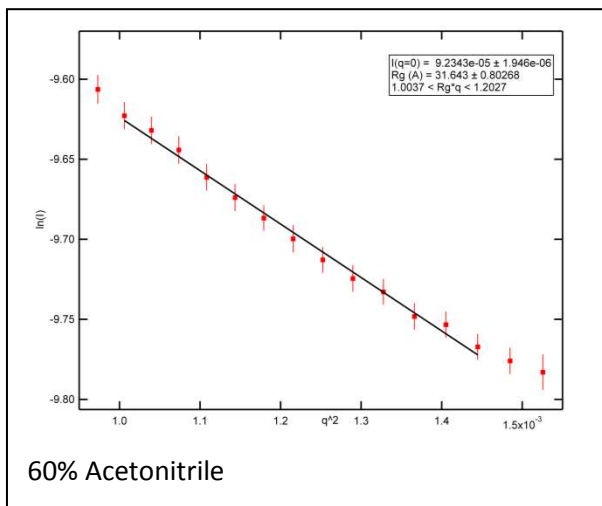
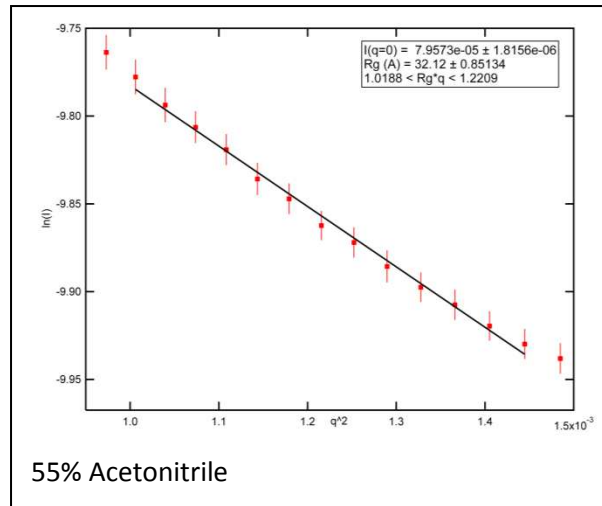
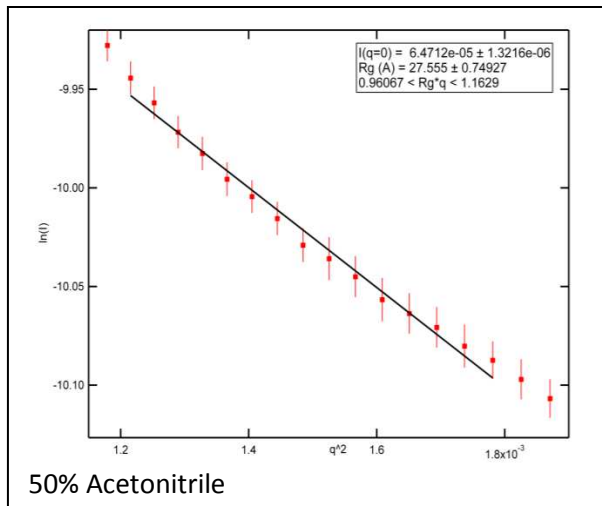
$$volume_{polymer} = \frac{mass_{polymer}}{\rho_{peptide}} = \frac{8517g/mol}{Na * 1.22g/cm^3} = 1.159 * 10^{-20} cm^3 = 11.59nm^3$$

¹ Andersson, K.M. and Hovmöller, S. The average atomic volume and density of proteins. *Z. Kristallogr.* 213 369–373 (1998).

Guinier fits for SAXS analysis of peptoid 100mers: Pages S2 – S5

Repeating Sequence Guinier Fits:





Protein-like Guinier Plots:

