Supplementary Material

The effect of glycosylation on interparticle interactions and dimensions of native and denatured phytase

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Supporting material

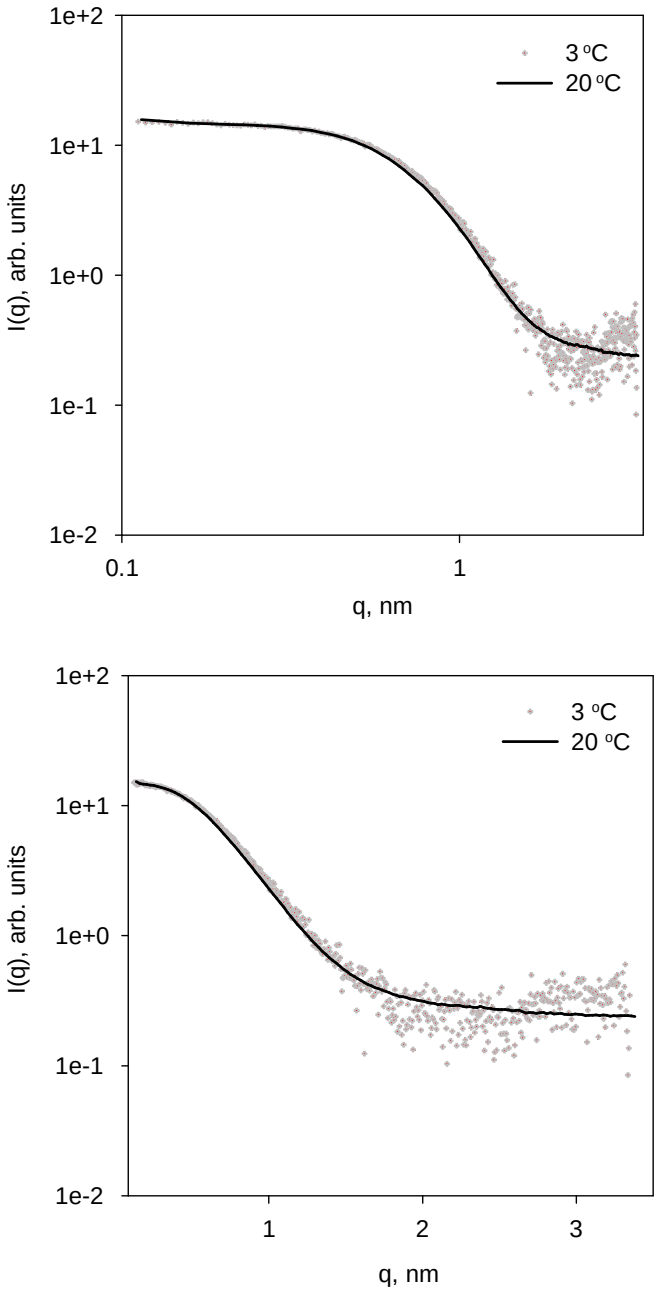

Fig 1: Comparison of the SAXS profile of dgPhy recorded at 3°C (gray dots) and 20°C (black line) plotted in a log *I(q)* vs. log *q* representation (left) and a log *I(q)* vs. *q* presentation (right). The 20°C data-set originates from a merge of 3 different concentrations (~4 mg/ml, ~8 mg/ml, ~12 mg/ml) whereas the 3°C data-set is recorded at one concentration only (5 mg/ml). For this reason the 3°C data-set appears somewhat noisier, however, despite this it is clearly seen that the two data-sets have a very high degree of resemblance. This finding shows that the conformation of the protein do not changed to any significant extent when temperature is increased from 3°C to 20°C. The SAXS-

data were collected at MAXlab, Lund, Sweden on the beamline I711 operating at 0.105 nm. The scattered beam was registered on a MAR165 CCD detector in the q-range 0.1-3.3 nm^{-1}.

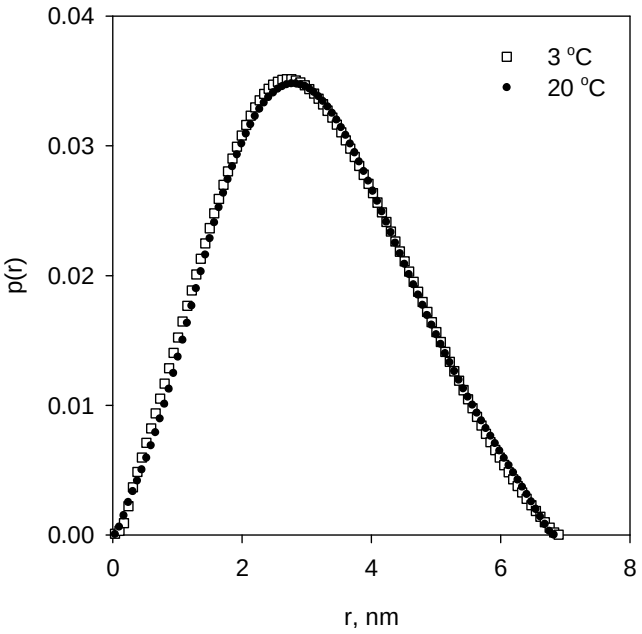

Fig 2: Indirect Fourier transformation of the dgPhy SAXS data recorded at 3°C (white squares) and 20°C (black dots). The *p(r)*-functions of the SAXS data-sets are very similar and both data-sets have a D_{max} of 7.0 nm which additionally suggest that the protein has not started to denature at 20°C to any significantly extent. At lower inter atomic distances (0-2.5 nm) small differences between the two curves can be noticed. Subtle differences like these, however, can easily be explained by the differences in the counting statistics between the two data-sets. The 20°C data-set consist of a merge of 3 different curves for which reason it has a much improved counting statistics at high-q, equivalent to better precision at low inter atomic distances, relative to that of the 3°C data-set.