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The molecular weight of proteins from a single SAXS measurement on a relative scale

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An important step in the characterization of proteins is the determination of their molecular weights and their multimeric state in solution. Accuracies of classical methodologies for the determination of the molecular weight of proteins in dilute solution were recently evaluated by Mylonas & Svergun [1]. These authors demonstrate that the molecular weight of a protein can be obtained by comparing the experimental SAXS curve produced by the protein in dilute solution (i) to another experimental SAXS curve corresponding to a standard protein with known molecular weight, or (ii) to a SAXS curve corresponding to pure water leading in this case to the determination of SAXS intensity of the studied protein in an absolute scale. Both of these procedures require the determination of at least two SAXS curves. In addition, the first procedure requires the precise knowledge of the protein concentration, which is frequently not known with high accuracy, and the second method needs the determination of the SAXS intensity by water with a considerable precision, which implies in rather long counting times. Both methodologies yield the molecular weight of proteins with an error of about 10% provided the solute concentration is measured with an accuracy of 5 – 10%, which might not always be straightforward. A novel procedure for the determination of the molecular weight of proteins in dilute solution from a single SAXS curve measured on a relative scale is available, which uses experimental data of a single small angle X-ray scattering (SAXS) curve measured on a relative scale [2]. This procedure does not require the measurement of SAXS intensity on an absolute scale and does not involve a comparison with another SAXS curve determined from a known standard protein. The proposed procedure can be applied to monodisperse systems of proteins in dilute solution, either in monomeric or multimeric state, and it was successfully tested by applying it to SAXS data measured for 22 proteins with known molecular weights. The molecular weights determined by using this novel method of all the measured set deviate from their known values by less than 10% and the average discrepancy was 5.6%. Importantly, this method allows for a simple and unambiguous determination of the multimeric state of proteins with known monomeric molecular weight.

Keywords: SAXS, protein, molecular weight