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Abstract

The elucidation of the 3-dimensional structures of proteins needs crystals suitable for X-ray analysis. An absolute prerequisite for any crystallographic analysis is that well-ordered single crystals of the proteins are obtained. Unfortunately, the crystallisation of proteins and their complexes is still more of an art than a science and represents the major bottleneck in the determination of the 3d-structures by X-ray analysis.

The presented investigations provide an insight into molecular interactions, optimal crystallisation conditions and enhanced and novel crystallisation kits. For this photon-correlation-spectroscopy and laser-doppler-velocimetry were utilized. The former method provides essential information on the diffusion coefficient and hence on the radius and particle size distribution in the protein solutions. The latter method determines the zeta potential and the surface net charge of a protein via the measured electrophoretic mobility.

Both measuring systems, also used in hanging drops with volumes of $10\mu l$, provided a better understanding in aggregation phenomena, which could be partly correlated with optimal crystallisation conditions. The fundamental coincidence of the measured data with the aggregation state of the proteins in form of crystals or amorphous precipitate is confirmed, but a sure prediction between the outcome and the conditions of a protein crystallisation is only tendentiously possible.

Nevertheless it is feasible to reduce the expense for a successful crystallisation by achieving additional information by means of light scattering techniques. The usefulness lies in the ability of getting a rational protocal of protein crystallisation and in the facilitation of protein crystallisation diagnostics.