

Determination of the overall motion correlation time for some globular proteins in dilute solutions on the basis of Maxwell effect

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The behaviour of globular proteins in a streamline flow of a solution is determined by two effects: (1) the flow induced orientation of their principal axis parallel to the flow direction and (2) the rotational Brownian motion acting against this orientation. As a result, the orientation of the protein principal axes is anisotropic in space and can be described by the distribution function which fulfils a diffusion-type equation. When the external stress field disappears, the anisotropy in the principal axes space distribution vanishes because of the rotational Brownian motion of proteins. The time in which the initial orientation decreases by the factor of e^{-1} is called the overall motion correlation time. For dilute solutions, it can be determined if the intrinsic viscosity, molecular mass and axial ratio of the proteins in solution is known. The intrinsic viscosity has been measured using an Ubbelohde-type capillary microviscometer immersed in a water-bath controlled thermostatically for four globular proteins. The obtained numerical values of the overall motion correlation time are in the following range: from 622 ns (10C) up to 111 ns (550C) for human IgG immunoglobulin, from 121 ns (10C) up to 33.6 ns (450C) for human serum albumin, from 65.7 ns (10C) up to 14.3 ns (550C) for ovalbumin, and from 13.2 ns (10C) up to 2.43 ns (550C) for hen egg-white lysozyme.