

Laser-aligned molecular-beam diffraction for proteins. Serial Crystallography

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The possibility of obtaining electron and X-ray diffraction patterns from a beam of hydrated proteins which are aligned by a laser beam is discussed. This "serial crystallography" method uses the non-linear effect of the RMS electric field from a CW fiber laser on the nonresonant electronic polarizability for alignment. The laser beam crosses a steady beam of proteins within a jet of vitreous iceballs. The rotational recoil of the iceballs, dissipation mechanisms and the conditions of temperature and laser power needed for a given degree of alignment and resolution will be discussed. Exposure times and charge-density reconstruction methods are briefly outlined with the aim of seeing secondary structure in proteins which cannot be crystallized.

Experimental apparatus under construction will be discussed also. For more details, see Phys. Rev. Lett. 92,198102 (2004) and Spence et al. (Acta A , submitted, 04).