

X-ray powder diffraction on proteins

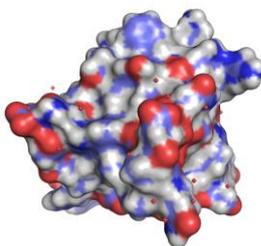
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Macromolecular structures are traditionally determined by means of single crystal X ray diffraction from protein crystals of micrometer dimensions. Nevertheless, the growth of good quality single crystals can be very difficult or even impossible, especially in cases of large proteins, membrane proteins or protein complexes.

The structure of the SH3 domain of Ponsin determined using powder diffraction [2].



Modern developments of X-ray powder diffraction have allowed the structural investigation of a range of proteins establishing the method as a useful complementary tool to traditional approaches [1]. Protein powder specimens consist of a large number of randomly oriented

diffracting micro-crystals which are usually formed rapidly by batch crystallization under a variety of conditions. An overview of the most recent developments in this field will be presented including: (a) application of the molecular replacement technique and structure refinements of selected proteins (b) methods for successful cryocooling (c) experimental phasing and extraction of molecular envelopes (d) high throughput automated data collection allowing systematic investigations such as screening and phase diagram mapping and (e) application of the method on biologically interesting proteins such as non-structural viral replication proteins coming from emerging viruses [3].

References

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