Recent developments in the field of X-ray crystallography, e.g. 3rd generation synchrotron radiation of increased intensity and improved detectors, facilitate macromolecular structure determination of biological samples at high resolution. Several protein and DNA structures are known with a resolution better than 1.0 Å. High-resolution diffraction data reveal electron density features more clearly and enable the use of non-spherical scattering factors. Such data also allow to resolve static disorder that remains undetected at lower resolution or when using data of low quality. In order illustrate the benefits of combining high-resolution crystallography and non-spherical scattering factors we studied the 16-residue thiopptide Thiostrepton and a DNA structure by invarion refinement [1]. For this purpose complete and redundant Bragg data from the thiopptide Thiostrepton were measured at the Swiss Light Source synchrotron at a temperature 100K to a resolution of 0.65 Å and compared to laboratory data to 0.81 Å. Furthermore Dauter et al. kindly provided a 0.55 Å resolution dataset from a Z-DNA structure [2]. These datasets were initially evaluated with the independent atom model (IAM) and afterwards re-refined using non-spherical scattering factors of the invarion database [1],[3] which is based on the Hansen-Coppens multipole model [4]. High resolution single-crystal diffraction data evaluated with invarions provide not only detailed and accurate molecular geometries, but also information on the electron-density distribution and on properties derived from it. With a view to biological, structural and medical functionality of Thiostrepton as well as DNA, an analysis of the electrostatic potential on the electron-density distribution and on properties derived from it will be reported.

Keywords: macromolecules, biocrystallography, charge density

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Automatic identification of alpha-helices in Patterson maps
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Protein crystal structure solution is often challenging due to limitations of current phasing methods, occurring at low data resolution and/or high structure complexity. Ab initio and SAD/MAD phasing methods are also hampered by the lacking of heavy atoms in the crystal, while molecular replacement is ineffective when low homology models are available. Recently brute force methods have been developed, which use minimal apriori structural information to drive the phasing process towards solution [1]. They find all possible positions of alpha-helices in the crystal cell by molecular replacement and explore systematically all of them. Knowing in advance the orientations of the alpha-helices would be a great advantage for this kind of approach. This is exactly the aim of the method we developed, which consists in a fully automatic procedure to find the orientations of alpha-helices within the Patterson map. The method is based on pattern recognition techniques, specifically addressed to the identification of helical shapes in low resolution Patterson maps. This approach has been first outlined in [2]. In our implementation, Fourier filtering techniques operating on Patterson maps described in polar coordinates supply a list of candidate orientations, which are then refined by using proper figure of merits based on the local comparison between the experimental Patterson map and that calculated from a template poly-alanine helix, calculated along each candidate direction. The first step has been optimized to work at 3Å resolution, while the second operates at 5Å resolution. The algorithm is complementary to the molecular replacement approach.