

Charge Density Studies of Ultra High Resolution Protein Structures

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The recent advances in synchrotron radiation and crystallogensis methods have brought bio-crystallography in a context favorable to subatomic resolution protein structures. At this resolution, electron density reveals fine details related to the deformation of the valence electron density due to chemical bonding and intermolecular interactions. A spherical atom model of electron density does not allow to take into account these features in the refinement. However, in small molecules charge density studies, the Hansen & Coppens [1] multipolar model is commonly used, and allows the asphericity of the atomic electron density to be parameterized and quantified against experimental data.

Here we will show how charge density studies principles can be applied with the software MoPro [2] on protein structures obtained at subatomic and atomic resolution, using specific methods like the multipolar parameter transferability from our experimental database [3]. We will also present derived electrostatic properties based on the multipolar formalism and computed on high resolution Human Aldose Reductase – inhibitors complexes [4] of pharmacological interest.

[1] Hansen N.K., Coppens P., *Acta. Cryst.*, 1978, **A34**, 909-921. [2] Jelsch C., Guillot B., Lagoutte A., Lecomte C., *J. Appl. Cryst.*, 2005, **38**, 38-54. [3] Jelsch C., Pichon-Pesme V., Lecomte C., Aubry A., *Acta. Cryst.*, 1998, **D54**, 1306-1318. [4] Howard E. et. al., *Prot. Struct. Funct. & Gen.*, 2004, **55**, 792-804.

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