Å resolution with R-merge 5.7, mosaicity 0.295 and completeness 86.9%[4]. On the other hand, L-PGDS crystals were previously obtained with citrate as a precipitant and diffracted to 2.0 Å (PDB ID: 2CZT). In microgravity, we obtained L-PGDS crystal which diffracted up to 1.0 Å resolution with R-merge 0.064, mosaicity 0.16 and completeness 98.8%.

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Keywords: atomic resolution crystallography, inhibitor and drug design, microgravity crystallization

P04.23.442

Protein helix-dipole calculations based on experimental electron densities

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Since the 1970's, it has been assumed that the alpha helix represents a macro dipole. This is due to the dipole moment of the individual peptide units, which are aligned parallel to the helix-axis and thus form a macro-dipole. The helix-dipole is guessed to have effects upon the functioning and structure of proteins [1]. However, the exact dipole strength is still unclear. Estimations include only the atomic charges of the main chain and not of the side chains. Dielectric measurements of the dipole strength using helical oligopeptides in solution have been made [2], but lack of precision as the percentage of the peptides with helical conformation is unknown. Here, we propose an estimation of the alpha-helix-dipole referring to experimental electron density distributions. The electron density of isolated amino acid compounds has been refined with the program MoPro (Molecular Properties, [3]) using the Hansen and Coppens multipole formalism [4] to create an experimental electron density distribution database (ELMAM, [5]). The atomic charges described in the ELMAM database are then transferred to the protein. The dipole moment of the alpha-helix is calculated either by using the transferred charges or, if the protein diffracts at subatomic resolution below 0.8 Å, by using charges that are refined against X-ray diffraction data.

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Keywords: helix-dipole, subatomic resolution, electron deformation density

P04.23.443

Charge density analysis of human aldose reductase active site

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Human aldose reductase (hAR) is a NADPH dependent enzyme involved in diabetes complications. Crystals of hAR in complex with NADPH and the Idd594 inhibitor diffract up to 0.66Å resolution [1]. Such subatomic resolution X-ray data allows, after a restrained IAM refinement, the observation of significant residual deformation electron density on covalent bonds. This residual electron density peaks are the deviation from the spherical approximation of the atomic electron clouds, due to chemical bonding. The Hansen & Coppens [2] multipolar model, implemented in the MoPro [3] software, allows taking into account the deformation electron density. Hence a constrained multipolar refinement of hAR has been performed, leading to decreased atomic thermal motion amplitudes and better stereochemistry [4]. Here we present the continuation of this work: a precise, unconstrained, charge density analysis focusing on hAR active site. Deformation electron densities of the NADPH cofactor, the Idd594 inhibitor and the catalytic amino acids have been modelled using the multipolar formalism. Then a topological analysis of hAR active site electron density has been performed in order to derive informations related to the inhibitor binding and the catalytic mechanism.

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Keywords: charge density, high-resolution crystallography, protein ligands

P04.23.444

Ultra-high resolution structure of endopolygalacturonase determined by X-ray and neutron diffraction

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Endopolygalacturonases (endoPGs) are inverting glycosidases that