Poster Presentation

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Reconstruction of charge density of vitamin D analogues

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Commonly, the Independent Atom Model (IAM) of electron density is used in the case of routine X-ray data analysis. However, this model does not give a quantitative description of electron density distribution because atoms are assumed to be neutral and spherical. A far better model that allows for modelling of deformation of spherical charge density was introduced by Hansen and Coppens and is called a pseudoatom model of electron density. However, application of this kind of model requires an excellent quality of crystals and high resolution XRD data – which quite often is difficult to fulfil. Therefore, new methods have been developed that enable reconstruction of electron density. These are: Hirshfeld Atom Refinement (HAR) [1] or Transferable Aspherical Atom Model (TAAM). The HAR model is based on calculated theoretical wavefunction deformed by multipoles simulating influence of crystal lattice, whereas TAAM is based on multipole model derived from the pseudoatom databanks, for example, from UBDB [2].
One of the most interesting area of research is chemistry of vitamin D. Vitamin D regulates calcium-phosphate metabolism, antiproliferation action decreasing the possibility of developing a tumor. Vitamin D action is mediated by Vitamin D Receptor which occurs in many tissues, where it plays various roles [3]. Until now, several structures of vitamin D analogues were deposited in Cambridge Structural Database (CSD). However, none of them was analyzed with the subatomic resolution due to limited crystal quality and in consequence poor quality of diffraction data. Therefore, in our work electron density of model vitamin D was reconstructed by means of HAR and TAAM approaches and used in refinement against collected single crystal XRD data of new, biologically active analogues of vitamin D. Both, HAR and TAAM enable to obtain more accurate geometry parameters, better R-factors and GooF than IAM. Additionally, all these parameters suggest that the HAR method as a better way of refinement of data than TAAM and far better than IAM. However, HAR is much more restrictive with reference to the quality of original data and time-consuming in comparison with TAAM.

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[1] Capelli, S. C., et al., (2014). IUCrJ, 1(5), 361-379.
[2] Jarzembska, K. N., et al. (2012). Acta Crystallogr. Sect. A. 68(1), 139-147.
[3] Cheskis, B., et al. (1994), Mol. Cell. Biol., 14(5), 3329-3338.
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