

*UBDB databank for protein-RNA interactions through magnesium ions*Urszula A. Budniak¹, Paulina M. Dominiak¹¹CNBCh, Department Of Chemistry, University Of Warsaw, Warszawa, Poland

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Electrostatic energy usually has the most significant contribution to interaction energy (especially in the biological systems) and at the same time it can be calculated for large complexes, thus it is a perfect tool for estimating interaction energy in biomacromolecules. However, most of the methods applied for macromolecular simulations base on simplified methods taken from classical mechanic (force fields), where electrostatics is usually approximated by Coulomb interactions of point charges. One of the more advanced methods to calculate electrostatic interaction energy is University at Buffalo Pseudoatom DataBank (UBDB) used together with Exact Potential Multipole Method (EPMM). UBDB enables reconstruction of charge density for macromolecules in quantitative manner. By UBDB+EPMM approach, which takes also charge penetration effects into account, it is possible to compute electrostatic energies with similar accuracy as with quantum chemistry methods, for wide range of types of interactions (hydrogen bonds, π - π stacking) and distances (not only at equilibrium geometry but also below or above).

Calculations of energy are based on the structures deposited in Protein Data Bank (PDB). After proper structure preparation, UBDB is transferred using LSDb program to reconstruct electron density distribution. For accurate calculations all atom types occurring in investigated structure must be represented in UBDB. Despite the fact that UBDB already contains many atom types including those present in amino acids and nucleotides residues, it does not yet cover all atoms necessary for calculations of proteins complexes with RNA containing cations. My aim was to add atom types of phosphorus in phosphate groups and magnesium cation often located in active site of enzymes. Afterward, electrostatic interaction energy of protein-ligand complexes will be calculated with EPMM method. Next, thorough calculations of interactions between ligand and particular amino acids in active site will be conducted.

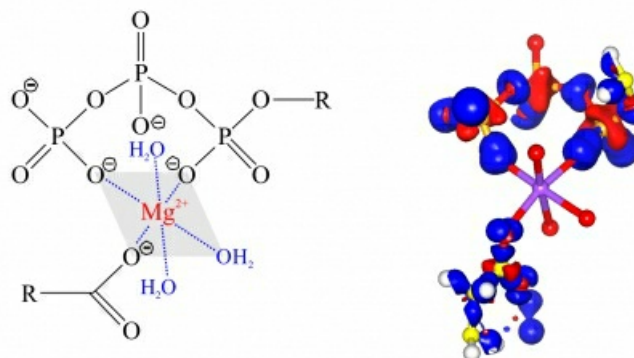
In this presentation I will introduce the idea of UBDB and show how generally the procedure of adding new atom types to the bank looks like. Next, I will give details how the procedure was adapted to achieve my aim and how the quality of parametrization of new atom types was benchmarked against referential electrostatic interaction energies. Finally, I will explain how UBDB can facilitate the accurate estimation of electrostatic interaction energy between proteins with RNA comparing to quantum mechanics methods.

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Active site of IFIT5 protein interacting with RNA through Mg^{2+} ion (PDB ID 4HOR): schematic picture (left) and aspherical part of protein and RNA charge density reconstructed with UBDB (right).



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