Project 4.4. Computational studies of disulfide bonds (theoretical)

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Institute: IF PAN

Unit: ON5

www: http://www.ifpan.edu.pl/sdvs/pl/on5.html

Background:

Proteins are one of the most important biologically active molecules. They play many functions in living organisms, such as scaffold, storage, enzymatic and regulation. However, proteins to play effectively their functions need to obtain a correct structure, which knowledge of is often needed in scientific investigations. In addition to experimental methods, scientific research can be performed also using computational methods, which often are significantly cheaper and allows to study phenomena not possible to study by experimental methods. For that reason, the main goal of this project is to extend and improve existing force fields and use them to study role of disulfide bonds in proteins. Disulfide bonds are common and are present in over 23% of proteins stored in Protein Data Bank, but their function in most of them is not fully understood. For a long time, it was believed that disulfide bonds are only stabilizing the protein structure, however, with advances in science it was found that they often can play much different roles, and sometimes their presence can even be lowering the stability of proteins, instead of increasing it. For example, many toxins have at least one disulfide bond, which main function is to prevent digestion by the organisms in which they are acting. In case of many peptides, which are ligands of the receptors, disulfide bonds are necessary to stiffen the polypeptide chain and allow it to form a particular shape. Only such molecules can bind to the receptor and be active. It was also found that in some cases disulfide bonds are necessary for proteins to form correct oligomeric structures, and that forming and disrupting disulfide bonds can be used to regulate biochemical cycles.

Aim:

The main aim of the project is to develop and use potentials for static and dynamic (breakable) disulfide bonds in all-atom and coarse-grained force fields, which will allow to study thermodynamical properties and structure of biologically important proteins, such as RNase A and LTPs. Project will be done with collaboration with authors of UNRES coarse-grained force field: group of prof. Adam Liwo from University of Gdańsk.

Requirements:

Candidates are expected to possess at least basic skills and knowledge of:
- computational methods in biophysics (especially molecular dynamics simulations)
- biomacromolecules, especially proteins
- very good English in writing, reading and speaking
- ability to write scientific publications in English
- ability to write simple scripts and computer programs

Funding:

The PhD candidate will be funded from the NCN Sonata 2019/35/D/ST4/03156 grant for 33 months – 4250 PLN per month, minus obligatory employer and employee social security contributions. Afterwards, the standard PhD school scholarship will be paid.