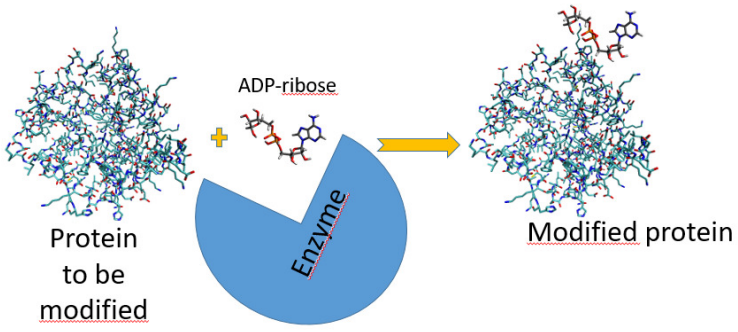
DESCRIPTION FOR THE GENERAL PUBLIC (IN ENGLISH)

The basic elements of living cells, proteins, are subjected to chemical modifications that involve addition of chemical groups, e.g. phosphates or sugars. Such modifications are important phenomena in physiological functioning of a cell and in disease. One of such important modifications is ADP-ribosylation, i.e. addition of an ADP-ribose. This modification regulates cell differentiation, among other processes. Moreover, ADP-ribosylation is used by pathogenic bacteria (e.g. cholera or diphteria), to rewire cellular signalling pathways to a mode convenient for the pathogen. The process of ADP-ribosylation is catalised by specialised protein catalysts, enzymes, named ADP-ribosylotransferases (ART). Approximately 15 families of ART enzymes are known.

Using bioinformatics methods for analysis of genomic sequences from databases, our group has discovered, as part of preliminary efforts, five novel ART enzyme families. They appear very interesting, one is foundin uncharacterised animal and plant proteins potentiall involved „monitoring devices" for infection threat in the cell. Another of the novel families is found in bacteria including the tetanus causing strain, an d may be linked to infection. These preliminary resuts, obtained to some extent „by accident", suggest that there are likely many undiscovered ART families. The main aim of this project is a systematic search, using bioinformatics methods, for novel ART enzyme families, and, consequently, search for novel signalling pathways important for healthy and infected cells. An additional aim is a careful bioinformatics analysis of known and novel ART families, cataloguing them and predicting their cellular roles. Also, we will perform initial experimental characterization of molecular functions of these fascinating enzymes.



Protein ADP-ribosylation (protein and ADP-ribose images acc. to Wikipedia)