The blueprint of every living organism is encoded in a very long molecule made of deoxyribonucleic acid (DNA). DNA has a helical structure with two strands, which are complementary to each other. This means, using an analogy, that each strand is a chemical mirror image of the other. This blueprint is called genetic information and it is present in each cell of an organism. DNA molecules are not indestructible, they constantly undergo damage either spontaneously or as an effect of external factors such as chemical substances or radiation. This distorts the genetic information and can lead to cell's death. If the cell survives, DNA damage can convert to mutations – typos in the genetic code. I higher organisms (humans) the mutations deregulate cellular processes leading to cancer. This is why all forms of life have sophisticated and efficient mechanisms of fixing the damage of the DNA. One way to achieve this by a process called nucleotide excision repair. The damage is first detected and then the damaged strand of the DNA is cut on both sides of the chemical modification. The modified fragment is removed and the gap is filled by fresh undamaged stretch of DNA made based on the other (mirror) strand. The first goal of this project is to understand how the cutting of the DNA occurs in bacteria at the level of single atoms. We plan to obtain a complete three-dimensional picture of the bacterial molecules (enzymes) that perform this task to understand how they work.

The other powerful way of fixing DNA is by using an identical or very similar undamaged region of the genetic information to guide the repair. This process is called homologous recombination. It can be used for example for fixing particularly dangerous DNA damage when both of its strands are broken and two parts of the genetic information separated from each other. A critical step of this process is the search for the undamaged copy of the DNA. It is guided by a special enzyme called RecA. This enzyme needs to be first loaded, with the aid of other specialized enzymes, on the DNA strand which will perform the search. The second aim of this project is to understand how this loading process occurs in bacteria. Similarly to the first part of the project, we plan to define the exact three-dimensional shape of the enzymes involved in this process at the level of single atoms. This will allow us to understand how they perform their tasks.

Once this project is completed we will be able to construct "molecular movies" that will provide complete description of the selected steps of bacterial repair of genetic information.