Since the dawn of time, humanity encountered a great problem with agricultural pests – viruses, bacteria, undesirable fungi, plants, and animals. The largest group of pests are insects, affecting not only agriculture but also forest areas. Insects can be vectors of dangerous diseases and negatively affect the health of plants, animals, and humans. On the other hand, they are an extremely important part of the ecosystem. For example, approximately 75% of crop species in agricultural and horticultural cropping systems are pollinated by insects. Therefore, pesticides and insecticides has to be designed with extreme care.

Extensive research on insect physiology has provided a lot of information about their anatomy, organs, structures, and functioning. Great amount of work were devoted to analysing the insects development process. It was found, that the juvenile hormone (JH) is crucial in the insects' metamorphosis. Nowadays, it is thought, that the juvenile hormone epoxide hydrolase is a key enzyme in this process. The inhibition of JHEH could prevent the development of an adult form of insects and consequently lead to the degradation of particular species. It would be desirable in the case of insects that are agricultural and forest pests, but also in relation to insects, which can be vectors of dangerous diseases.

The proposed project brings together different fields of research: chemistry, biology, microbiology, biotechnology, entomology and ecology. In the proposed project, we would like to use *in silico* methods to identify differences in the structural properties and dynamics of JHEH among different insect of closely related species. By carrying out a comprehensive structural analysis focused mainly on the definition and description of intramolecular voids that are available for the binding of small molecules, it will be possible to identify regions in JHEH that are unique to individual insect species and potentially able to distinguish selective inhibitors dedicated to specific pests and safe to