The High Arctic regions, such as the Svalbard Archipelago, are considered the coldest and most extreme environments on Earth. A greater part (58%) of the Svalbard Archipelago is permanently covered in snow and ice, and this region also experiences low humidity, strong winds and cyclical, long periods of daylight and darkness. The mean annual air temperature (at the Spitsbergen) is -4.4°C, although due to the frequent winds, usually exceeding 30 m/s, the perceived temperature can be even lower. The annual amplitude of temperatures is 49.4°C, with a minimum of -35.9°C, and a maximum of 13.5°C.

At those regions bacteria tolerating low temperatures (i.e. cold-active) are the dominant life forms. The diversity and molecular basis underlying the adaptation of psychrotolerants to the permanent cold has been extensively studied in recent years, which is a consequence of their potential biotechnological application. However, polar bacterial microbiocenoses are also good candidates to study evolution and overall microbial ecology within primal (with limited anthropogenic influence) habitats, since e.g. High Arctic is considered as one of the most wild and endemic environment.

The main aim of this project is to perform complex metagenomic, genomic, metatranscriptomic and functional analyses of heavy metal and antibiotic resistance and metabolism in Arctic bacterial microbiocenoses, in course of recognizing the ecological role and adaptive features of bacteria inhabiting this extreme environment.

The detailed objectives of the presented research proposal are as follows:

- Evaluation of an adaptive potential of bacteria (focusing on heavy metal and antibiotic resistance and metabolism) inhabiting extreme Arctic region in the light of the systems modeling approach for microbial community study.
- Overall insight into the metabolic potential of cold-active bacterial microbiocenoses, combined with the metatranscriptomic analysis evaluating if the identified genes are active or remain silent.
- Identification and analysis of genes whose products are directly and indirectly involved in the biogeochemical processes occurring in Arctic – evaluating the ecological role of cold-active bacteria in shaping the abiotic environment and their potential for self-purification of polar environments.
- Identification of novel strains and genes relevant for biotechnology, including: novel antimicrobial agent (antibiotic) and siderophore producers, and microbial strains or consortia suitable in bioremediation processes.
- Identification of novel "primal" resistance mechanisms to antibiotics and heavy metals.
- Analysis of the distribution and dissemination of heavy metal and antibiotic resistance genes in the environment with a limited anthropogenic influence and testing the hypothesis that those genetic determinants are mainly an outcome of antibiotic/industrial era.
- Analysis of the co-selection, co-resistance/co-localization and cross-resistance phenomena in an extreme, not significantly changed by the humans, environment.
- Identification and analysis of novel mobile genetic elements (MGEs) of cold-active bacteria and evaluation of their link with the heavy metal and antibiotic resistance and metabolism genes.
- Construction of novel databases of heavy metal and antibiotic resistance and metabolism genes, as well as mobile genetic elements of cold-active bacteria.
- Designing the novel sets of primers for the environmental analyses of heavy metal and antibiotic resistance and metabolism genes.

In our opinion, the most significant advantage of the project is that it integrates the results of various "omics", chemical, functional and computational analyses to microbial ecology of extreme Arctic environment. This may shed a new light on the molecular mechanisms underlying bacterial resistance and metabolism of heavy metals and antibiotics.