Bacteriophages (viruses that multiply in bacterial cells) are the most numerous group of organisms found on Earth. They live in salt and fresh waters, both flowing and stagnant, soil and extreme environments such as hot springs, deserts and glaciers, as well as the organisms of animals and humans, which are part of the microbiome. The rapid development of molecular biology techniques in the 20th century, including high-throughput nucleic acid sequencing, provided in-depth understanding of the genomes of many organisms. In one of the largest databases depositing sequences at the US Institute of Public Health, out of more than 400,000 publicly available microbial genomes, only over 4,000 are bacteriophage genomes. Most of the published studies on the structure and function of phage capsid-building proteins and functional proteins concern only a dozen or so representatives of this large group, and these works were created over half a century ago, when the technical capabilities of scientists were relatively modest compared to the present day. During the work of our team on the morphological, genetic and functional biodiversity of bacteriophages isolated from the natural environment, it was found that they encode enzymes that duplicate genetic material (called DNA polymerases) of an unprecedented structure. The aim of this project will be to carry out a detailed physico-biochemical characterization of the above-mentioned DNA polymerases and answer the question of how enzymes with an unprecedented conformation function in a living organism. The overarching project will be to present the molecular diversity of phage enzymes as a reflection of their morphological diversity. The data obtained in this project will allow to verify the initial assumptions that the newly discovered DNA polymerases can be used in biotechnology.