Plastids and mitochondria are organelles that evolved in a process of endosymbiosis, in which a bacterium was transformed first into an endosymbiont and then a true cell organelle. During this transformation, most of the endosymbiont genes were transferred to the host nuclear genome and consequently their genomes became significantly reduced. In order to compensate for the endosymbiotic gene transfer, an efficient way of importing of nuclear-encoded proteins had to evolve in endosymbiont membranes along with appropriate targeting signals.

The appropriate localization of a protein is essential for its proper function and this information is contained in the protein as a short amino acid sequence called a targeting or sorting signal. As experimental methods for identification of targeting signals are time-consuming and laborious, we have decided to develop a software to recognize different sorting signals that are responsible for protein targeting to mitochondria, plastids and endomembrane system. We are interested in finding motifs and/or physicochemical features responsible for their function. Our goal is to identify characteristics that are shared among all the sorting signals, but also those that differentiate them. The functional significance of targeting sequences makes their prediction an important step in drug development but also could provide a new insight into the mechanisms of endosymbiosis, which is one of the most important evolutionary processes on our planet.

In the project, we will also test the hypothesis that sorting signals of plastids and mitochondria evolved directly from antimicrobial peptides, which target and kill, among other organisms, bacteria. This proposal is based on structural similarities between antimicrobial peptides and mitochondrial/plastidial sorting signals, and their capacity to interact with bacterial membranes.