

Summary

The theoretical part of this bachelor thesis deals with the group of processing peptidase of the M16B family. The main focus is on the structure and the evolution of mitochondrial and hydrogenosomal processing peptidase and also the hypothetical peptidase from the bacterium *Rickettsia prowazekii*.

In the practical part of this work, the constructs coding the α -subunit of hydrogenosomal processing peptidase (α -HPP) with the substituted tryptophan residue in the position 236 for phenylalanine and tyrosine were prepared using the site-directed mutagenesis. Subsequently, the new reporter tryptophan residue was introduced in α -HPP in positions 256, 260, 267 or 271 in the so-called glycine-rich loop.