SUMMARY

Mitochondrial processing peptidase (MPP) is heterodimeric matalopeptidase (α-, β-MPP) that plays a key role in mitochondrial protein import, by recognizing and cleaving the targeting presequences of host nuclear-encoded mitochondrial matrix proteins. Here was characterized a novel processing peptidase from the hydrogenosomes of *Trichomonas vaginalis* – the hydrogenosomal processing peptidase (HPP). Hydrogenosomes are highly reduced versions of mitochondria that are found in diverse parasitic or microaerophilic microbial eukaryotes. It was demonstrated that, contrary to previous reports [100], the *Trichomonas* hydrogenosomal processing peptidase (HPP) functions efficiently as a αβ heterodimer, rather than as a β-homodimer.

Whereas β-MPP is catalytic subunit, α-MPP has regulatory function. Glycine-rich loop of α-MPP (GRL) is almost absolutely conserved among different organisms and is probably very important in substrate recognition. Molecular dynamics methods were used to confirm that the interaction between substrate and GRL is mediated by hydrophobic interactions. Futher was shown the importance of GRL flexibilty during translocation of the substrate to active center of MPP