The aim of the study was to contribute to the understanding of regulatory functions of nuclear hormone receptors by studies focused on a group of multiplied nuclear receptors present in the genome of Caenorhabditis elegans, specifically nhr-40 and nhr-60. The work presented in this thesis was a part of an effort to characterize the selected nuclear receptors systematically by means of Caenorhabditis elegans functional genetics and genomics. Studies constituting this thesis were meant as an application of proteomics in the functional analysis of the selected nuclear receptors in the frame of the complex biology of Caenorhabditis elegans.

The proteomic scope of this thesis was aimed at understanding of the selected receptors at the level of the protein, the protein nature, localization and dynamics as well as the proteomic characterization of the consequences of the protein loss of function.