One of the major challange in biology is to understand how expression of genetic information is regulated. That process, coordinated and regulated on many levels, is responsible for the diversity of cell types and for controlling their specific bahaviors in response to changing environmental conditions. It is generally accepted that in eukaryotic cell, apart from transcriptional regulation, there is additional level of gene expression regulation - translation of mRNA. That mechanism allow quick reaction of the cell to changes in environmental conditions and reprogramming of the whole matabolism by protein expression profile modification. Ribosome, ribonucleoprotein complex, is a crucial element of the translational machinery responsible for decoding of genetic information and protein synthesis. There are three centers on the ribosome responsible for its activity: the decoding center (DC) localized on small ribosomal subunits, where genetic information in mRNA is decoded, peptidyltransferase center (PTC), where peptide bonds between amino acids are formed and polipeptides are synthesized and GTPase associated center (GAC), considered as a major structure powering the ribosome with energy, released from GTP hydrolysis, conferring unidirectionality of translation. GAC, localized on large ribosomal subunit, is composed of rRNA and P-protein complex called ribosomal P-stalk that in eukaryotic organisms has pentameric stoichiometry. The main function of ribosome is the synthesis of proteins on the basis of mRNA, but nowadays ribosome can be regarded as a regulatory element itself, that according to "specialized ribosomes" hypothesis can undergo structural modifications leading to functional specialization. That modifications can affect rRNA and protein component and may modulate speed and specificity of ribosome performance depending on the metabolic needs of the cell. GAC play a key role in ribosome functioning and is considered as an interesting regulatory element that can "calibrate" ribosomal activity through structural alterations in pentameric protein complex. The research problem undertaken in this project is to cast more light on the function of ribosomal P-protein complex in adaptation of cell metabolism to changing environmental conditions. Our scientific hypothesis assume that P protein complex modification can be induced in response to some metabolic changes, that can lead to functional specialization of certain ribosome pool and as a consequence to changes on protein level.

The realisation of the project will be performed by using various broadly defined molecular biology techniques using mammalian cell lines as a research model. Analysis mainly performed *in vivo*, will be complemented with *in vitro* experiments. Physiological characteristics of P-proteins (localization, dynamics, interactions) on the single cell level, in normal and stress induced condtions mimicking specific metabolic states, will be performed with the use of genetic, biochemical, biophysical and cell biology techniques. These experiments will allow to verify if various metabolic conditions lead to P protein complex alterations and formation of "specialized ribosomes" pool. Realisation of the proposed project will allow to learn and characterize functions of P-proteins in gene expression regulation at the translational level. As a consequence, obtained information from one hand expand the knowledge about the role of P-proteins, from the other hand allow to understand molecular basics of diseases connected with P-proteins like cancer and depression. The results of the proposed project may therefore become the fundamentals for new diagnostic methods and efficient therapies and also can establish new direction in disease treatment, which unknown molecular basis are hidden in the web of interactions of ribosomal P-proteins.