Gene expression regulation is critically important for bacterial survival. Changes in environmental conditions force bacteria to adjust their physiology so that cellular homeostasis is maintained. Since gene expression must be controlled and precisely coordinated, special mechanisms responsible for its fine-tuning evolved. In bacteria, one of such mechanisms involves small regulatory RNAs (sRNAs). sRNAs associate with their target mRNA, which alters mRNA molecular fate. However, to achieve their full functionality, sRNAs usually interact with special proteins, called RNA chaperones. FinO-domain protein family, thanks to recent global profiling experiments, has emerged as a new class of RNA chaperones widely distributed in Gram-negative bacterial species. They might be either plasmid-encoded (*Escherichia coli* FinO, *Salmonella. enterica* FopA) or chromosome-encoded (*Escherichia coli* ProQ, *Neisseria meningitidis* ProQ) and constitute a relatively diverse group.

The FinO domains, which are characteristic for proteins from this family, have a conserved structure, which consists of five α-helices. The RNA motif that is often recognized by the FinO domains in their RNA ligands is the 3′-terminal Rho-independent transcription termination structure followed by several uridine residues. However, different studies showed that FinO-domains vary greatly in ligand specificities. While some of them recognize few RNA ligands, others are global RNA-binding regulators. This suggests that either the FinO domains contain features explaining the differences in ligand preferences or other protein regions are also involved in RNA binding.

To elucidate what drives these RNA specificities I plan to compare the binding of the *E. coli* ProQ, *E. coli* FinO, *N. meningitidis* ProQ and *S. enterica* FopA along with their isolated FinO domains to the same set of RNA ligands. This will allow evaluating the contribution of the FinO domains from these four proteins to the RNA binding. To compare how these FinO domains interact with RNA molecules, I will analyze the effects of mutations in homologous positions of amino acid sequence on RNA binding by these four proteins. Finally, I plan to identify the RNA regions engaged in interactions with the FinO domains. To achieve this, I will apply a method based on site-specific hydroxyl radical probing of RNAs in contact with the individual FinO domains.

I expect that the results of the planned studies will help to better understand the roles of the FinO domains from different proteins in RNA recognition, and explore the differences in the molecular details of their interactions. In summary, these results will help to better understand the molecular basis of the biological functions of this important and interesting group of RNA-binding proteins.