Ovarian cancer (OC) remains one of the most lethal gynecologic malignancies worldwide. High-grade serous ovarian carcinoma (HGSOC) is the most aggressive and deadly subtype of OC. It is typically diagnosed at an advanced stage, and most patients experience disease relapse despite an initial good response to platinum-based chemotherapy. Furthermore, despite early optimism, immunotherapy which has revolutionized treatment for many other cancers shows very limited effectiveness in HGSOC. This suggests the presence of previously unknown mechanisms hindering effective treatment of this disease.

As a result, there is growing interest in identifying molecular factors that may play a key role in the development of HGSOC. Particular attention has turned to the TRIM (tripartite motif-containing) protein family. These proteins play crucial roles in regulating the cell cycle, apoptosis, immune response, and protein degradation. Interestingly, many TRIM proteins are active in cancer cells and may either promote or suppress tumor development depending on the cancer type.

Some TRIM proteins, such as TRIM24 and TRIM27, have already been studied in the context of ovarian cancer, but the roles of most TRIM family members including TRIM32 and TRIM34 remain largely unexplored. Our preliminary research shows that TRIM32 and TRIM34 are significantly more active in ovarian cancer cells than in healthy fallopian tube tissue the structure now believed to be the origin of HGSOC. This finding suggests that these proteins may be involved in driving the disease and potentially in therapy resistance.

The aim of this project is to investigate the role of TRIM32 and TRIM34 in HGSOC pathogenesis, focusing both on their biological function and potential clinical relevance. Using advanced molecular biology and bioinformatics tools, we seek to understand how TRIM32 and TRIM34 influence tumor development, immune interactions, and treatment response.

In summary, elucidating the functions of TRIM32 and TRIM34 in HGSOC may be groundbreaking. These studies could uncover new molecular pathways responsible for disease progression and treatment resistance, and ultimately enable the development of more effective and personalized therapeutic approaches. In the future, this knowledge may allow physicians to better predict disease course and tailor treatments to individual patients, improving outcomes and quality of life.