Ovarian cancer is one of the leading causes of cancer deaths women. Part of the reason is that ovarian cancer detection methods are unreliable until the later stages of the disease. The most common method of detection tests for elevated levels of cancer antigen 125 (CA-125) in the blood. However, CA-125 levels consistent with the disease may not be present until the disease is terminal. The sensitivity and specificity of this test is low enough to merit investigation of alternative detection methods.

A peptide (J18) derived from phage display selections has been shown to have a high binding affinity to ovarian cancer cells, and was found to successfully image and detect ovarian tumors in mice. To be able to use this peptide to detect ovarian cancer in humans, the exact binding partner of the peptide on the cell surface must be determined. For a protein or peptide, structure and chemical properties often dictates the function and interaction with other molecules.

In this study, the known amino acid sequence of peptide J18 will be used to determine the potential binding partner using bioinformatics. This will allow a gained understanding of what the peptide binds and how this interaction proceeds. This information will be used to help further the development of J18 as a potential cancer imaging agent.