PPI's can be predicted computationally by calculating the energy of a partial model of an outer membrane protein, incorporating only the transmembrane strands **(ref)**. Using only the transmembrane strands enables predictions to be made for proteins whose structures have not been solved. This is the most regular and ubiquitous feature of outer membrane proteins, and its structure can be computationally predicted from sequence data **(ref)**. **(protein next to Hayat Cα trace)**

After constructing the partial model, the energy of each strand is calculated. An energy function that has been successfully applied for these kinds of predictions is a knowledge-based potential, TmSIP. TmSIP is well suited to making energy calculations from rough predictions of structure from sequence. TmSIP is a function of little more than the Cα trace of the strand regions, and is insensitive to many of the geometrical details that are difficult to predict from sequence.

Central to this method of prediction is the finding that high energy strands in the partial model often have contacts with non-strand elements **(ref)**. The partial model differs from the native structure in that these contacts are missing; thus, it is intuitive that an accurate energy function will recognize these incomplete contacts as non-native. Furthermore, contacts with other barrels have also been found to correlate with weakly stable strands in the partial model.