Determination of protein structure in space is a crucial part of protein function analysis. But structure determination is an expensive and time consuming process, therefore structure prediction model raised on popularity. The most notable subproblem of protein structure prediction is prediction of local conformation of the adjacent amino acids, ie. secondary structure. This thesis studies usage of deep neural networks for protein secondary structure prediction. We implemented prediction model and different modifications are evaluated. Especially compassion of LSTM and GRU memory cells was done. Furthermore, two new preprocessing methods are evaluated. Fast PSSM calculation method was proposed and prediction of tertiary structure was used as input for prediction model. Last part of this thesis examine application of filtering methods for models predicting secondary structure with eight classes.