For this task we used a one-hot encoding scheme in order to encode the position of the different amino acids. For this we used the OneHotEncoder from the sklearn library. The classification was solved with the MLPclassifier from the sklearn library. In order to achieve a balanced data set we applied a self-written method which up and down samples the training data. The up and down sampling is simply done by copying positive values and not using negative ones. The optimal hyperparameters used in the sampling and for the classifier were found through cross validation. The found hyperparameters are a downsampling factor of 30 and upsampling factor of 15 and the alpha of the classifier as 0.00001. We also tried different classifiers, such as RandomForest, SVC, etc. but the MLPclassifier performed the best.