Protein Nkr-p1b is a surface receptor of cytotoxic NK cells, that mediates inhibitory signal toward the body's own cells. In this study, the ligand binding domain of the mouse protein receptor Nkr-p1b (mNkr-p1b LBD) was prepared by recombinant expression in *E. coli* cells. Isolated protein was subsequently used for NMR structural analysis. Prediction of protein secondary structures ratio was carried out using three different methods (CD, PSIPRED and TALOS). Results correlate well with the structure of CTLD domain, that plays a key role in ligand binding and thus to function of Nkr-p1b receptor. We managed to prepare this protein in a form suitable for NMR experiments. Based on the data obtained by NMR spectra analysis, a preliminary model of the mNkr-p1b LBD protein structure was created. However, for more precise learning of the 3D structure accurate positions of individual atoms need to be determined by other NMR spectra evaluation in the next phase. Explaining the structure of the ligand binding domain of mNkr-p1b protein could help to better understand the complex mechanism of activation of NK cell cytotoxic activity, thereby contributing to its controlled use as a therapeutic against some viral and tumor diseases.