Retroviral polyprotein precursor Gag is cleaved by viral protease during the course of virus particle maturation to yield individual structural components – matrix protein (MA), capsid protein (CA) and nucleocapsid protein (NC). CA consists of two domains: N-terminal (NTD) and C-terminal (CTD) and forms a hexameric lattice. Conformational switch upon proteolytic release of CA mediates disassembly of an immature and assembly of a mature capsid.
3D structure of M-PMV CANTD consists of six -helices and N-terminal -hairpin. The -hairpin is stabilized by a salt bridge between Pro1 and Asp57 and another, yet uncharacterized interface between Arg14 and helix 5. Proper -hairpin formation is critical for mature particle assembly.
This thesis analyses the impact of the helix 5 and -hairpin point mutations (D111N and R14K, respectively) on the CANTD structure by NMR spectroscopy. None of the mutations affect overall fold of the protein. Comparison of NOE contacts of WT and D111N indicates structural identity of these proteins. R14K mutation shows significant changes in the helix 5 and the -hairpin regions in comparison with WT. These results confirm presence of the interface stabilized by -hairpin and helix 5 interactions, with Arg14 being the critical part. Role of Asp111 in this interface was not confirmed and other possible interacting partners of Arg14 have been revealed.