This paper describes the conformational features of $6^{-1}$ hydrogen-bonded turns (ψ-turns) observed in proteins and peptides. The polypeptide conformations under the constraint of $6^{-1}$ hydrogen bond were selected from Brookhaven Protein Data Bank (PDB) using a FORTRAN program developed in our laboratory. The data set consisted of the co-ordinates of 228 non-homologous protein chains, determined by X-ray crystallography to better than 2.5 Å resolution. Totally 486 ψ-turns were located. 367 ψ-Turns were found to have 5th residue in left handed α-helical($\alpha_{L}$) region of Ramachandran map and were classified as $\pi_{\alpha L}$-turns. These turns are generally observed at the C-terminal end of helices, a result in harmony with previous observations. 286 $\pi_{\alpha L}$-Turns define ‘Schellman motif’ ($6^{-1} & 5^{-2}$ hydrogen bond), 111 $\pi$-Turns had 5th residue in $\alpha_{R}$ region, a novel finding and were referred by the name $\pi_{\alpha R}$-turns. $\pi_{\alpha R}$-Turns generally occur in α-helices as a distortion. Four $\pi$-turns were seen to be mirror images of $\pi_{\alpha L}$-turns and hence were termed as $\pi_{\alpha L}$-turns. The 5th residue in rest of the four $\pi$-turns were seen to adopt $\pi$-conformation, hence these four were named as $\pi_{\alpha R}$-turns. The former two classes of $\pi$-Turns ($\pi_{\alpha L}$ & $\pi_{\alpha R}$) form major classes. Nine $\pi$-turns observed so far in oligopeptides share the features of $\pi_{\alpha L}$-turns. Sequence analysis shows that hydrophobic residues are preferred at position 2,3 and 4 of $\pi_{\alpha L}$-turns while position 1 and 6 prefer hydrophilic residues. Residue 5 ($\alpha_{L}$) is mainly Gly and less often Asn. A high preference for Pro after the C-termini is observed in both the major classes. Poor α-helix formers like His, Tyr and Asn were found to be $\pi_{\alpha L}$-turns. Hence these are termed as $\pi_{\alpha L}$-turns. The AutoDep procedure is based on CIF and was built using CIF-based data dictionaries. Any changes to the deposition procedures or information content of PDB entries are easily accommodated by editing the dictionary files. The PDB is supported by a combination of Federal Government Agency funds and user fees. Support is provided by the U.S. National Science Foundation, the U.S. Public Health Service, National Institutes of Health, National Center for Research Resources, National Institutes of General Medical Sciences, National Library of Medicine, and the U.S. Department of Energy under contract DE-AC02-76CH00016.