The objective of this study is to develop a unique data mining framework for the structural comparison and classification of proteins, by representing each of them in terms of a pair of secondary structure geometric descriptor distributions. In this thesis, we propose novel geometric parameters based on a comparison protocol that uses a previously unexplored pair of dihedral angles for the similarity search. The similarity analysis is performed based on the pairwise dihedral distribution representation of the protein structure. As a part of the similarity calibration procedure, a frequency transformation is employed on the two-dimensional distribution for feature extraction and selective feature filtering, which is then represented in an indexing schema later used for similarity calibration. The proposed similarity measure captures the structural similarity among proteins with less sequence identity, and its ability to classify the proteins is evaluated by conducting experiments across four datasets, of varied sizes, of protein structures belonging to different families randomly selected from Alpha, Beta, Alpha and Beta (alpha/beta), and Multi-domain proteins (alpha and beta) classes. The results demonstrate the success of this dimensionality reduction based similarity measure in performing a rapid and length-independent similarity analysis of the protein structures.