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Title of presentation: Computational analysis of Post translational modifications in Human Proteins

Abstract

Proteins are large biomolecules, or macromolecules, consisting of one or several long chains of amino acids, i.e. polypeptides. Proteins have complex shapes that include various alpha helixes, beta sheets, loops, and disordered regions. Functions of Human proteins are determined by their structures and many of these structures are still unknown and difficult to derive experimentally. To solve this problem, computer-aided data modelling has been widely applied. Our project focuses on identifications of patterns between two specific post-translational modifications – sulfide pairs (i.e. disulfide bond) and N-glycosylation, in human proteins and examine how the positions of these post-translational modifications affect the structures thereof functions of proteins. Human protein data is download from UniProt, and python programming is used to compute the relative positions and relationships between disulfide bonds and N-glycosylation. Proteins with unique patterns of these modifications are identified, and their functions are further analyzed. Our study provides useful insights for structures and functions of proteins and particularly to proteins with unknown structures.