When there is a covalent alteration to protein backbones and side chains that increase proteome complexities. The secondary structure features reveal intrinsic information regarding the characteristics of a protein sequence. IN this study, we considered three attributes that formulate the local structure of protein namely, the secondary structure, local backbone torsion angles, and accessible surface area.

We selected the peptide segment by sliding a window of size amino acids on the primary sequence taking the flanking upstream and downstream sequence of amino acids on each side of lysine residue K.FN denotes the number of incorrectly classified glycated sites. The effectiveness of any classifier is measured using cross-validation methods. The three most widely used cross-validation schemes across the literature are independent dataset, k-fold and jackknife .The dataset for our study comprised 235 glycated and1518 non-glycated lysine residues obtained from 55 protein sequences, which results in a highly imbalanced data between positive and negative sets with a ratio of over 1:6.

Therefore, pairwise comparison of performance with these state of the art methods was not possible.