

New relation between glycine and secondary structure

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The diversity of amino acids is crucial to explain the patterns of structure-function relationships in proteins. In this study, we observed the influence of glycine on the average secondary structure propensity of all amino acid in a large set of protein structures.

Glycine is the smallest residue and the most frequent amino acid in random coiled structure. It can be seen that as neighbour glycine has significant effects on any residue secondary structure. For example the average helix propensity of lysine is 23%. When a glycine is at position +2 in the sequence, the helix propensity of lysine falls down to 6%. The beta propensity of valine is 55% and increases to 68% when a glycine is at the position -3.

We concluded that generally and as supported in previous work, glycine next to any residue decreases its helix propensity, it is an helix breaker but we also highlighted that glycine has little effects on strand propensity of its neighbour when it is down stream the sequence (CO side) and favours that structure when it is up stream (N-H side) for some amino acids.

Glycine is an helix breaker it is not a beta breaker.