

Revisiting the paper on “Prediction of Tight Turns and their Types in Proteins”

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Abstract

In this short report, the works on predicting the tight turns in proteins and their types are recalled.

Keywords: δ -Turn; γ -Turn; β -Turn; α -Turn; π -Turn; Proteins

Short Communication

About 20 years ago a very important paper on prediction of tight turns and their types in proteins [1] was published. According to the definition given in that paper, a tight turn in protein structure is a site where [1] a polypeptide chain reverses its overall direction, i.e., leads the chain to fold back on itself by nearly 180°, and [2] the amino acid residues directly involved in forming the turn are no more than six. In the same paper, various types of tight turns and how to predict them have been systematically reviewed. Ever since then, this paper has played very important role for building protein three dimensional (3D) models for drug development [2-14].

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