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Abstract: We carry out systematic Monte Carlo simulations of Go lattice proteins to investigate and compare the folding processes of two model proteins whose native structures differ from each other due to the presence of a trefoil knot located near the terminus of one of the protein chains. We show that the folding time of the knotted fold is larger than that of the unknotted protein and that this difference in folding time is particularly striking in the temperature region below the optimal folding temperature. Both proteins display similar folding transition temperatures, which is indicative of similar thermal stabilities. By using the folding probability reaction coordinate as an estimator of folding progression we have found out that the formation of the knot is mainly a late folding event in our shallow knot system.

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