The unfolded ensemble in aqueous solution represents the starting point of protein folding. Characterisation of this species is often difficult since the native state is usually predominantly populated at equilibrium. Previous work has shown that the four-helix protein, Im7, folds via an on-pathway intermediate. To determine the conformational properties of the unfolded state of a globular protein in the absence of denaturant we have introduced destabilising amino acid substitutions into the sequence of the natively four helical protein, Im7, such that the unfolded state becomes predominantly populated at equilibrium in the absence of denaturant. In this lecture I will present our studies of this species using far and near UV CD, fluorescence, urea titration, and heteronuclear NMR. The results reveal an unfolded ensemble that is conformationally restricted in regions of the polypeptide chain in that ultimately form helices I, II and IV in the native state. The studies complete a full atomistic view of the entire folding landscape of this protein, and these results will be summarised and presented.