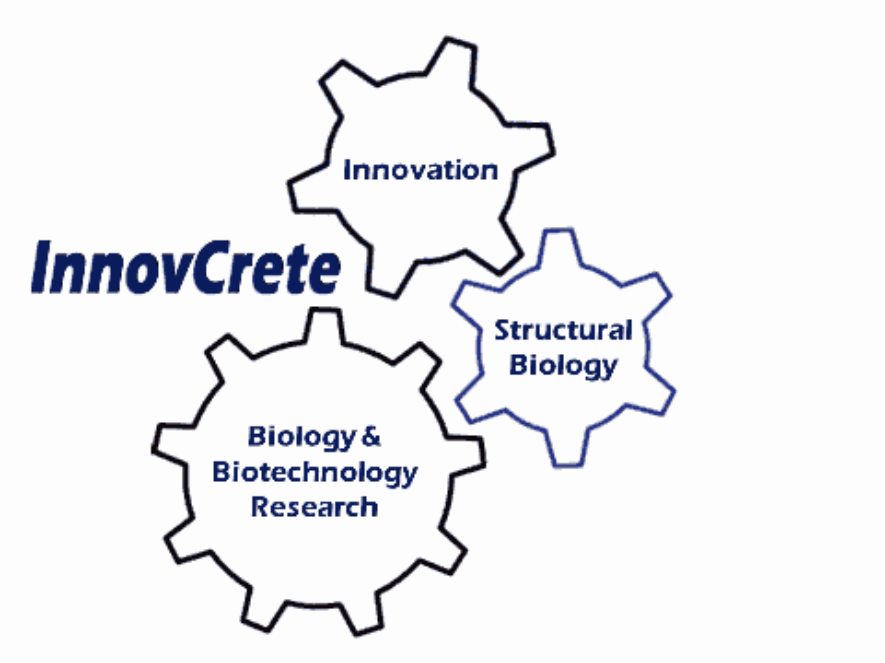

InnovCrete scientists explore mechanisms of protein folding

Protein folding is the physical process by which a protein structure assumes its functional shape or conformation.

When translated from a sequence of mRNA to a linear chain of amino acids, the polypeptide lacks any 3D-structure and exists as a so-called random coil. During the protein folding process, the amino acids interact with each other to produce a well-defined three-dimensional structure, known as the native state which is essential to function, although some parts of functional proteins may remain unfolded. Interestingly, overall similarities in tertiary folding are frequently observed in the absence of detailed amino acid sequence homology. These recurrences in functionally different proteins (recurrent tertiary motifs) presumably reflect convergent evolutionary solutions to requirements for protein stability and provide convenient systems for the study of protein folding.

The ColE1 Rop protein is a paradigm of the 4-α-helical bundle motif and has been repeatedly used in protein folding studies. In the framework of InnovCrete, Dr. M. Amprazi and her colleagues have studied Rop and several of its loop mutants, focusing on their extreme structural plasticity which produces a large variety of folding states. Apart from the so-called native state, the InnovCrete scientists have identified native-like and molten-globule states that depend on the formation of transient, non-native disulfide bridges and on the

extreme malleability of hydrophobic cores. This plasticity classifies Rop among the limited number of proteins that are suitable for the engineering of bio-inspired, responsive nanomaterials, with a wide range of technological applications. These results have been accepted for publication by the Proceedings of the National Academy of Sciences (USA).

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