Overview of Human Protein Disorder

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Abstract:

Disorder predictions have become of increasing interest when determining protein structure and function. 'Disordered' is a term used to describe those regions or whole proteins that do not form a stable 3-D structure in their native state. The over-riding paradigm that protein structure directly infers protein function is challenged by the introduction of non-ordered regions. Subsequent studies of disordered regions have indicated that they are important areas, involved in many functions, such as DNA and protein binding, transcription and translational regulation (Iakoucheva, L. M. et al., 2004; Wright, P. E. et al., 1999). Disordered regions / whole proteins have been found within all organisms, but are more common within Eukaryotes. Previous studies on disorder have estimated that 33% of Eukaryotic proteins contain at least one region of > 30 contiguous disordered residues within their protein structure (Ward, J. J. et al., 2004b). Since the first-draft release of the human genome in 2001 (Lander, E. S. et al., 2001), functional analyses of the human proteome have been of increasing interest.