

SEMINAIRE

*Auditorium Fernand Gallais (bât. LCC)
Campus CNRS, 205 route de Narbonne TOULOUSE*

Mardi 6 mai 2008 à 14 h.

Dr Salvator VENTURA (Institut de Biotechnologie et de
Biomédecine, Université autonome de Barcelone)

***" Protein models to study protein folding,
aggregation and interaction "***

Protein folding and aggregation are two closely related phenomena. This way, many times, the inability of a protein to fold and adopt its native functional conformation results in protein aggregation. In this regard, an increasing body of evidence points out at the anomalous misassembly of proteins into insoluble amyloid deposits as the fundamental cause behind some debilitating human disorders of growing incidence such as Alzheimer's disease (AD), Parkinson's disease (PD), type II diabetes, and many others. A common trait of these disorders is that the aggregated protein deposits in internal organs and interferes with normal function, sometimes lethally. On the other hand, protein aggregation in cell factories represents a major bottleneck in recombinant protein production, narrowing the spectrum of polypeptides obtained by recombinant techniques and hampering the development of priority research areas such as structural genomics and proteomics. Finally, when a protein reaches its native state almost never acts in an isolated manner: it interacts with other proteins in order to perform essential roles in many important cellular processes. Apart from their ability to form stable multiprotein complexes, proteins associate transiently with their targets to modify, regulate by steric effects, or translocate them to different cellular compartments. All these mechanisms are intimately linked to its function in such a way that identification of the molecules that bind to a given protein is one of the most useful approaches to understand its functional properties.

Our lab uses both theoretical and experimental approaches on top of different protein models to understand the sequential and structural determinants of protein folding, aggregation and interaction.

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