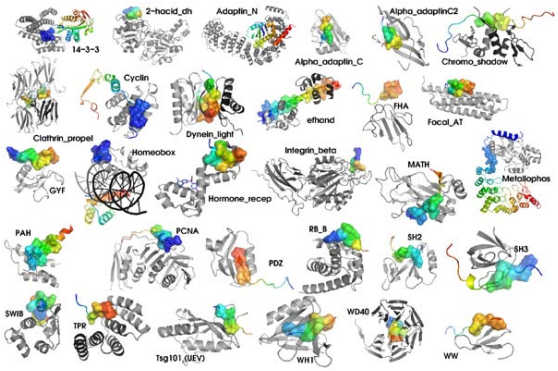
Scientists reveal the key mechanisms for affinity between transient binding proteins

The results have been published in the scientific journal PLoS One

Barcelona, 2nd July 2008.- Most of the functions performed by a cell are the result of interactions between proteins, which recognise their binding partner by affinity features localized on the protein surface. There are many kinds of interactions; however, the most complicated to study from the perspective of structural biology are those which are transient. This type of interaction is brief and occurs through a large section of the protein surface- the globular domain -, and a very small section of the surface of another proteins, the so-called lineal motif or peptide. The difficulty lies in the fact that these relations are of short duration and there are few crystallized peptide structures. Researchers at the Institute for Research in Biomedicine (IRB Barcelona) have performed the first computational analysis of transient interactions between proteins in order to reveal what determines their recognition as ideal partners and have unveiled part of the molecular mechanisms involved in the specificity of this binding. The results of this study have been published in the scientific journal PLoS One.



"Knowing what determines protein-protein binding may have implications, for example, in the design of new drugs", explains Patrick Aloy, ICREA research professor at IRB Barcelona and member of the joint IRB Barcelona -BSC research programme, "however, we currently know very little about this type of binding". These kinds of interactions occur mainly between proteins involved in signalling pathways and regulatory networks, and they serve to translate and transmit extracellular signals to the cell nucleus.

Representative structures for the different types of peptide-mediated protein interactions

The context is relevant

In Patrick Aloy's Structural Biology Laboratory they have detected all interactions possible between the globular domain and peptide by exploring the 45,000 3D protein structures currently available on the international database PDB (Protein Data Bank), and establishing rules from them. "One of the conclusions from the study is that what determines that two proteins recognise each other as binding partners falls outside the lineal contact motif, in what is called the context", explains Aloy. The contextual residues are amino acids that are found in nearby regions of the lineal motif but do not form part of it. "The binding strength between two proteins is determined by contacts found in the lineal motif but it is the contextual residues that hold information about the most suitable proteins, thereby preventing undesirable binding between similar proteins", explains Amelie Stein, a pre-doctoral student with Aloy's lab and first author of the article.

The analysis performed by the researchers has also revealed that in certain conditions non native interactions may occur, that is to say, interactions with other proteins that are not optimum. "This is what we refer to as complementary partners, other interaction proteins that can compensate for the lack of the ideal protein",

explains Stein. According to the researchers, these non-optimum interactions allow the establishment of emergency circuits that increase the strength of cellular networks. Specifically, one line of research derived from the study by Aloy and Stein focuses on the identification of proteins unable to establish safety circuits and therefore with a good chance of becoming future therapeutic targets.

Reference article
Contextual specificity in peptide-mediated protein interaction
Amelie Stein and Patrick Aloy PLoS One, e-pub ahead of print (2008). http://www.plosone.org/doi/pone.0002524