unicat
Unifying Concepts in Catalysis

Vortragsankündigung

- im Rahmen des UniCat-Kolloquiums -

(www.unicat.tu-berlin.de)

Es spricht: **Professor Dr. Gunter S. Fischer, Max-Planck-Forschungsstelle für Enzymologie der Proteinfaltung, Halle**

Zeit: **Mittwoch, 14. Januar 2009 17:15 Uhr**

Ort: **TU Berlin**
Institut für Chemie, Altes Chemiegebäude
Straße des 17. Juni 115, 10623 Berlin
Raum C 243

Thema: **Unscrambling the Puzzle of the Protein Backbone: the Peptide Bond as the Hot Spot**

Abstract: Polypeptide chains can undergo a reversible structural transition called protein folding involving ordered and disordered states. Beside the vectorial process of folding of newly synthesized polypeptide chains, native proteins constantly oscillate between a multitude of conformational states adjacent to the global Gibbs free energy minimum conformation of the polypeptide chain. This process can establish conformational polymorphism of native proteins that in many cases might also lead to a diversity of protein function. The role of side chains in folding reactions has been widely examined using site-directed mutagenesis. Less is known to which extend the conformation of the polypeptide backbone can control functional properties of a protein. The peptide bond itself forms the “hot spot” of the backbone. It is conformationally constrained and a multifaceted functional group. Consequently, peptide bond cis/trans isomerases have evolved that kinetically control the conformation of the protein backbone in the cell. At first glance, the limited structural impact of a one-bond conformational change in a large protein, as might be achieved by a peptide bond cis/trans isomerization suggests functional irrelevance. However, we showed by means of triggered conformational changes of photoresponsive thioxo peptide bonds that conformational effects are efficiently transmitted to distant parts of a protein subsequent to a one-bond triggering event, enabling the target molecule to respond functionally. Another attempt uses unfolding-refolding reaction sequences to explore whether a protein can lose or gain activity on the basis of a one-bond conformational change.
An attempt to interpret peptide bond *cis/trans* isomerase catalyzed reactions in tl cell on the basis of these results will be the final goal of this presentation.

Organisator: Prof. Dr. R. Suessmuth (TUB)

Gäste sind herzlich willkommen!

Prof. Dr. Matthias Drieß
Sprecher des Exzellenz-Clusters UniCat