pl1 **Information transfer in proteins: combining crystallographic and genomic approaches**. L. Moulinet, O. Poch, J.C. Thierry, D. Moras, *UPR9004/CNRS, Laboratoire de Biologie et Génomique Structurales IGBMC, 1 rue Laurent Fries, 67400 Illkirch.*
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The transfer of information from a particular activation site to a remote catalytic site is a caracteristic of allosteric enzymes, that is multisubunits proteins which exhibit cooperativity. The search for the signal transfer path within the molecules gave rise to an impressive amount of studies. The availability of sequence and 3D structure databases, thanks to the genomic efforts, allows novel approaches to this problem.

We have analysed aspartyl-tRNA synthetase, a dimeric enzyme with a modular structure, to understand the molecular mechanisms of cooperativity. A comparative analysis performed over 55 primary sequences, using multialignements programs and the knowledge of the crystal structure of at least one member of each living kingdom (eubacteria, eucarya and archeous), lead to the identification of conserved residues that connect functional parts of the enzymes. These until now hidden communication paths correlate well with the atomic movements revealed by a comparison of the crystal structures of AspRS in different functional states.

Notes