

INDIRECT EVIDENCES OF CONFORMATIONAL  
REGULATION IN PROTEIN REACTIONS:  
HOW MUCH CAN BE LEARNT?

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S u m m a r y

Almost all reactions of proteins manifest deviations from the simple behaviour prescribed by standard (bio)chemical kinetics. This is caused by the extraordinary structural lability of protein macromolecules which is often not less important for the reaction efficiency than the properties of the active center. Unveiling the mechanisms of structural regulation encounters serious difficulties because of their hidden character, as either modern experiments or computational methods still fall short of monitoring simultaneously the reaction events and concomitant conformational changes, so that one has to decipher the reaction kinetics only. Nevertheless, it is possible to come to reliable conclusions on the mode of operation of proteins and the character of their structural relaxation with the help of a convenient and computationally accessible approach expounded in the present paper.