

PROBING FUNCTIONAL DYNAMICS IN ENZYMES USING SIMULATIONS.

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The importance of enzyme conformational dynamics in catalysis is now generally accepted. However, the precise nature of this dynamical contribution remains unresolved. Using molecular simulations, we present a rationale of how enzyme dynamics affects the reaction dynamics and the catalytic rate in Cyclophilin A, a well-studied peptidyl-prolyl cis-trans isomerase. Our results are in notable agreement with experimental estimates. Furthermore, we isolate the contribution from transition state stabilization and provide a unified view of the role of enzyme dynamics in catalysis and recognition from an atomistic perspective.