DYNAMICS AND ELECTRON TRANSFER BETWEEN HEMOGLOBIN AND CYTOCHROME b_5

Korin E. Wheeler, Judith M. Nocek, and Brian M. Hoffman.
Northwestern University, Department of Chemistry

The weakly interacting complex of hemoglobin (Hb) with cytochrome b_5 (b_5) has been used to extend our understanding of the 'dynamic docking' paradigm (DD), in which a large ensemble of weakly binding protein-protein configurations contribute to binding, while only a few configurations are reactive.[1] The affinity of b_5 for the α-chain of Hb is greater than that for the β-chain of Hb or for myoglobin.[2] As a result, studies of the α-chain/ b_5 complex provide an improved opportunity to study enhanced decoupling of binding and reactivity that is characteristic of the DD regime. In order to modulate the decoupled binding and reactivity, we have neutralized the charge of the electron transfer reactive site separately and severally by neutralizing the heme propionates of the two proteins with a heme dimethyl ester. The impact of neutralized propionates on the dynamics associated with the binding and the kinetics of electron transfer within these protein complexes has been studied as a function of ionic strength, pH, and viscosity.

1. Liang, Z.-X.; Jiang, M.; Ning, Q.; Hoffman, B. M. (2002) J Bio Inorg Chem: 7, 580-588.
2. Naito, N.; Huang, H.; Sturgess, W.; Nocek, J. M.; Hoffman, B. M. (1998) J Am Chem Soc: 120, 11256-11262.