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A new picture of hemoglobin allostery

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Since the crystal structures of hemoglobin (Hb) in both unliganded (T) and liganded (R) forms were determined in the 1970s by Perutz and co-workers, its cooperative oxygenation process has been used as a model for allosteric protein interactions, namely based on a two-structure concerted allosteric model. In spite of extensive studies of this protein molecule by numerous investigators during the past 48 years, the molecular basis for its physiological functions is not fully understood. An evolving picture of Hb allostery from the classical two-structure model is being developed through the results obtained from multinuclear nuclear magnetic resonance (NMR), wide-angle X-ray scattering (WAXS), and genetic engineering techniques of the Hb molecule. These new results show that the structures of hemoglobin in solution are different from those in crystals and are a dynamic ensemble of multiple structures. Protein dynamics plays an important role in regulating both the structure and function of a protein molecule. The implications of these new results to the structure-dynamic-function relationship of hemoglobin will be discussed.

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