- Deutscher, M. P. (1967). *J. biol. Chem.* **242**, 1132.
 Fromm, H. J. (1967). *Biochim. biophys. Acta*, **139**, 221.
 Hoagland, M. B. (1955). *Biochim. biophys. Acta*, **16**, 288.
 Hoagland, M. B., Zamecnik, P. C. & Stephenson, M. L. (1957). *Biochim. biophys. Acta*, **24**, 215.
 Loftfield, R. B. & Eigner, E. A. (1969). *J. biol. Chem.* **244**, 1746.
 Wong, K. K. & Moldave, K. (1960). *J. biol. Chem.* **235**, 694.

Comprehensible Models for Myoglobin and Haemoglobin

By IVOR SMITH and MARGARET J. SMITH. (*Courtauld Institute of Biochemistry, The Middlesex Hospital, London W1P 5PR, U.K.*)

The complexity of models of macromolecules built from Watson-Kendrew components is such that they are of limited value to those unused to viewing or building such models, particularly when viewing time is restricted. Conversely, Biobits molecular models are immediately comprehensible to both senior and junior workers and models of both myoglobin and haemoglobin will be shown.

Both models are suspended by practically invisible wire supports from frames such that the complete models are entirely visible; total weights and sizes of models are such that the complete units are readily picked up and orientated in any direction.

Myoglobin, based on the Kendrew co-ordinates, shows all helices and interhelical portions, the haem cleft or 'pocket', and the outer polar shell and every R group is immediately obvious. The haemoglobin model is built on two frames, each supporting an identical $\alpha\beta$ half-molecule so that the inner as well as the outer surfaces are readily available for study. Inter-subunit contacts are apparent, some being shown on the model whereas others are not. The myoglobin model may be built by two workers in about 2 days whereas the $\alpha\beta$ subunit requires about twice the time. Each individual R group or amino acid residue can be rapidly pinpointed and the lethal or benign effect of a mutational change can be readily understood or deduced.

The models, while being extremely stable, are flexible and mobile. Hence changes due to oxygenation, the Bohr effect etc. can be demonstrated by simply pushing parts of the model, which spring back on being released, in an allosteric manner. We have built a range of models of other proteins based on X-ray data, as well as of DNA and tRNA species etc.

- Smith, I. (1969). *J. biol. Educ.* **3**, 193.
 Smith, I., Smith, M. J. & Dore, C. F. (1969). In *Chromatographic and Electrophoretic Techniques*, 3rd ed., ch. 40. Ed. by Smith, I. London: Heinemann Medical Books; New York: John Wiley-Interscience.
 Smith, I., Smith, M. J. & Roberts, L. (1970). *J. chem. Educ.* **47**, 302.