***OASIS-2004* and Difficult SAD Phasing**

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OASIS [1] is a direct-method program for resolving the phase ambiguity in single-wavelength anomalous diffraction (SAD) and in single isomorphous replacement (SIR) of proteins. The new version, OASIS-2004 includes algorithms for automatically tuning the scaling factor associated to the lack-of-closure error and for dynamically incorporating known structure fragment(s) in the iterative direct-method phasing. Details of the phasing strategy will be described. Application to SAD data from a series of known as well as originally unknown proteins will be given. The data sets were collected either with synchrotron radiation or with in-house sources (Cr-Ká and Cu-Ká) X-rays. Among the applications, an originally unknown protein with more than a thousand amino acids in the asymmetric unit has been solved with Cr-Ká sulfur-SAD data. Good quality phases have been successfully derived from sulfur-SAD data at the Bijvoet ratio $<|\Delta F|>/<F>$ lower than 0.6%. In all cases the combination of programs OASIS-2004, DM, RESOLVE-BUILD and ARP/wARP enabled automatic structure analysis from *ab initio* SAD phasing to model building. All resulted in a model containing more than 90% of the content of the asymmetric unit.

[1] Hao Q., Gu Y. X., Zheng C. D., Fan H. F., *J. Appl. Cryst.* , 2000, **33**, 980-981.

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