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Molecular Envelope Determination and *ab initio* Phasing. Quan Hao, MacCHESS, Wilson Synchrotron Lab, Cornell Univ., Ithaca, NY 14853-8001, USA.

Small angle X-ray scattering (SAXS) or electron microscopy (EM) data have proven to be very useful in providing low resolution structural details of proteins and other macromolecules. To utilize the envelope information for crystallographic phasing, it is essential to develop a method for correctly positioning the known envelope in a crystallographic unit cell. The low resolution phases calculated from the correctly positioned molecular envelope can be used as a good starting point for phase extension. I will describe the development of the FSEARCH program for locating envelopes in the unit cell and plans to extend phases to crystallographic data resolution.

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