First Application of EXPO2007 to Proteins

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In EXPO2007 all the traditional steps necessary for the *ab-initio* crystal structure solution from powder data are automatically carried out: indexing, space group determination, decomposition of the experimental diffraction pattern for extracting the observed structure factor moduli, phasing step, model refinement by non-Rietveld and Rietveld techniques.
EXPO2007 has been modified to allow it to deal with protein data. In particular we have modified the indexing section and we have introduced a link with the program REMO, a package dedicated to molecular replacement.
We will show the first results obtained by application of EXPO2007 to a set of proteins.