[MS4-04] AMPLE - Using de novo protein structure modelling techniques to create and enhance search models for use in Molecular Replacement. Ronan Keegan,[a] Jaclyn Bibby,[b] Jens Thomas,b Daniel Rigden,[b] Martyn Winn,[c]

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The prediction of protein folds through *de novo/ ab initio* modelling is a rapidly developing field. Recent years have seen advances in the techniques used to the point where the conformations of smaller proteins or protein domains (120 residues or less) can now be reliably predicted in a significant fraction of test cases. It has been shown that these models can be good enough for use as search models in the molecular replacement technique of protein structure solution by X-ray diffraction methods. [1,2] This can be particularly useful in cases where no homologous structure is available. It has also been shown to be effective in preparing low sequence identity homologues for molecular replacement where these homologues have proven insufficient as search models when prepared using more traditional methods. Here we present AMPLE [3], a new software tool jointly developed by the University of Liverpool and CCP4 which is designed to make this technique available to users in an automated way and requiring only limited computational hardware resources. It calls upon Rosetta [4-6] for the generation of de novo template models, these are then put through an intricate processing procedure to optimize their suitability for molecular replacement. Our initial tests on a set of 296 cases drawn from the PDB have shown that the techniques employed in AMPLE can result in solutions in approximately 40% of the trials. AMPLE has already proven its worth in novel protein structure solution and a beta release version is included in the latest release of the CCP4 software suite [7].

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