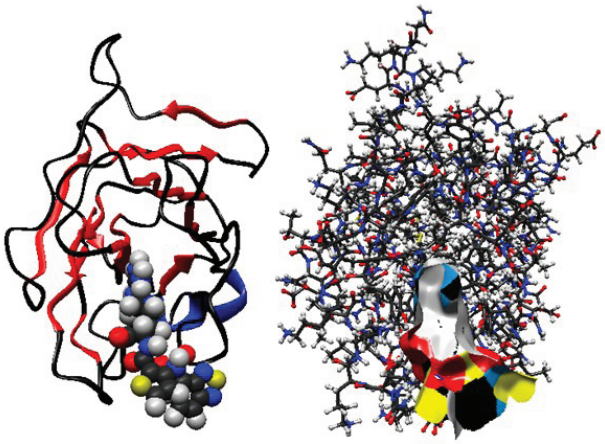

Figure 1. Left: Ribbon view of neuropilin 1, fragment b1 3D structure with bound inhibitor EG00229. Right. Hirshfeld surface of the protein/ligand interface coloured according to protein atom species.

Keywords: Charge density refinement, Restraints, Constraints, Molecular Properties, Molecular Viewer, Hirshfeld surface.

MS44-O3 Likelihood based molecular replacement model pruning in Phaser

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The use of likelihood as a target for molecular replacement (MR) calculations in *Phaser* [1] has increased sensitivity over traditional Patterson-based methods, allowing structures to be solved with smaller fragments or models derived from more distant homologues. Both the likelihood score and the probability of success are enhanced if the MR model is pruned *a priori* using tools such as Sculptor [2] or Chainsaw [3] to remove domains, loops or side chains that are predicted from the sequence alignment to be poorly conserved. However, the optimal sequence alignment and optimal pruning become more ambiguous as the sequence relationship becomes more distant, and there can be unexpected domain motions even in close relatives. In these circumstances, potential solutions can be lost because of poor signal or failure in packing tests.

A new likelihood-based *a posteriori* MR model pruning feature has been added to Phaser to deal with such problems, thereby improving clear MR solutions as well as rescuing potential solutions with poor signal-to-noise. Smoothly varying occupancies are refined along the protein chain, and then a threshold occupancy is chosen to decide which parts of the starting model should be retained. The residues discarded are typically from poorly-conserved surface loops or domains that have undergone a rigid-body motion. Removing these parts of the structure can rescue MR solutions that would otherwise be discarded by the packing test. In addition, the likelihood-based model pruning also clarifies which domains still need to be placed in multi-component structure solutions.

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Keywords: Phaser, molecular replacement, maximum likelihood, pruning