Structural refinement using RSRef:

RSRef is a package of programs that enable an atomic model to be optimized by fitting to an electron density map. RSRef uses an electron density function that is resolution dependent, so that it accurately models a medium resolution map. When combined with TNT's (Tronrud *et al*., U. of Oregon) Geometry, or CNS (Brünger *et al*.), full stereochemical refinement is possible. RSRef can be used to quickly pre-refine a protein structure during or after model building, or to completely refine structures with high non-crystallographic symmetry, that have good electron density.

Typical model improvement:

Before (red) & after (green) refinement: