

Refmac: Final Results Summary

Values for a good fitted 3D
map.

R factor ~ 0.3,

Rms BondLength ~ 0.02.

	Initial	Final
R factor	0.3865	0.3441
Rms BondLength	0.0142	0.0165
Rms BondAngle	2.0081	1.9697
Rms ChirVolume	0.1401	0.0844