



Visualization of Refmac results

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Refmac: Final Results Summary

Values for a good fitted 3D map.

R factor ~ 0.3,

Rms BondLength ~ 0.02.

	Initial	Final
R factor	0.3495	0.3484
Rms BondLength	0.0141	0.0150
Rms BondAngle	1.7022	1.8684
Rms ChirVolume	0.0797	0.0861

Volume and models



Display Mask



Final Results Table



Show log file



Results Table (last iteration)



R-factor vs. iteration



FOM vs. iteration



-LL vs. iteration



-LLfree vs. iteration



Geometry vs. iteration

