



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.

[Save Data](#)

	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   Close