



Volume and models

Summary


MolProbity

Model vs. Data



Data

MolProbity


Clashes: All-atom contact analysis

Bad contacts from PROBE (l1st)  Save list as text 



CaBLAM

CaBLAM evaluation  

C-beta deviation analysis



No C-beta position outliers detected 

Cis and twisted peptides

Cis and Twisted peptides:  

Rotamers

No Rotamer outliers detected













Chi1-Chi2 graphs  

Rhamachandran

No Rhamachandran outliers detected

Rhamachandran graphs  

Geometry Restraints

Bond length  Bond angle  Dihedral angle  List of dihedral angle outliers  Chirality  Planarity  Parallelity  Non-bonded distance  

Display of rotamer and Rhamachandran outliers and clashes

Open In Coot 