






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

No non-trans peptides detected 

Rotamers













Rotamer outlier l1st  Chi1-1-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 