Phenix

Protocol: phenix - Validation cryoEM viewer   ⧉Cite ❓Help

| Volume and models | Summary | MolProbity | Model vs. Data | Data |

MolProbity

Clashes: All-atom contact analysis

Bad contacts from PROBE (list) 👁 ❓

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 list 👁 ❓

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 👁 ❓

✖ Close