# Structure Assessment
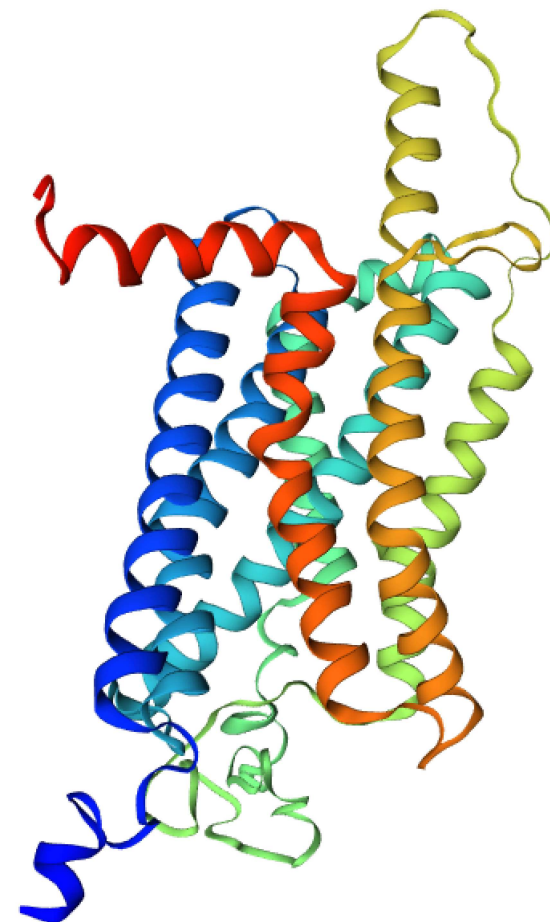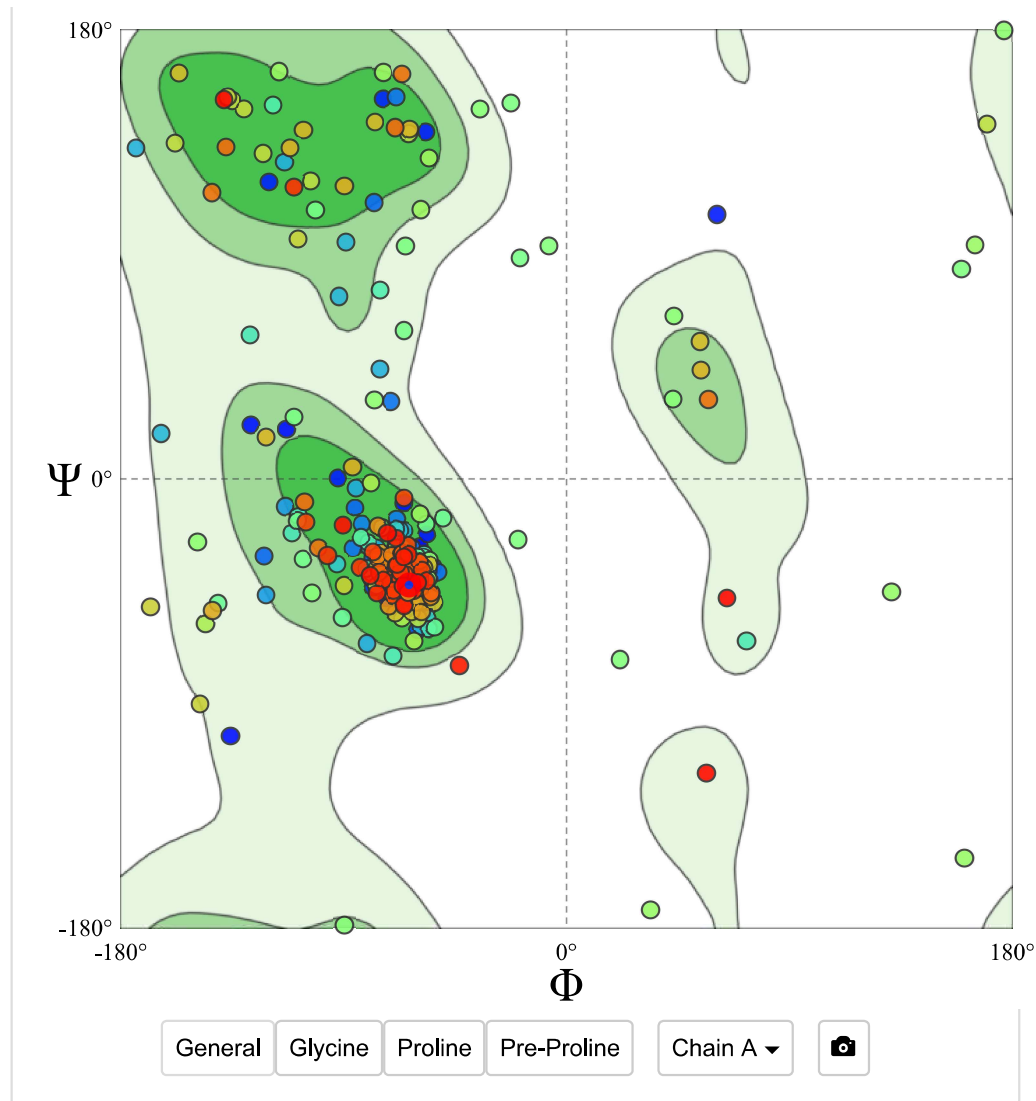
Help        Examples ▾

## DeepView-Project-Swiss-Model-LcOamb-Transmembrane-Agonist-3; Model 01;

Project Data ▾        ≡ ☐

Created: Fri 6th Aug, 19:30;

| Ramachandran Plots | ⌃ |
| --- | --- |

$\Psi$ 0°

$\Phi$

| General | Glycine | Proline | Pre-Proline | Chain A ▾ | 📷 |

## MolProbity Results

MolProbity is RUNNING

## Quality Estimate

QMEANDisCo Global:   0.55   ± 0.05 ❓

### QMEANDisCo Local



Local Quality Estimate

Predicted Local Similarity to Target

### QMEAN Z-Scores

| | | |
|---|---|---|
| QMEAN | | -9.27 |
| Cβ | | -6.24 |
| All Atom | | -3.96 |
| solvation | | -1.65 |
| torsion | | -7.62 |



Comparison with Non-redundant
Set of PDB Structures

Normalized QMEAN4

Protein Size (Residues)
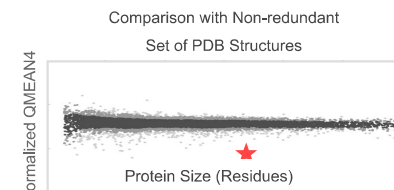
## Residue Quality

QMEAN

Chain:A  MNETECDNLIKSVKW-TEPSNLISLAILEFINVLVIGGNL   39

project_template_0.1.A  MNESECASLLASVQW-TDPTNLVSLAVLAFINVLVIVGNC   39

QMEAN

```
                          C H H H H T T T T T C C S S - C H H H H H H H H H H H H H H H H H H H H H
Chain:A            L V I A A V F C S N K L R S V T N F F I V N L A V A D L L V G L A V L P F S A T    79
project_template_0.1.A   L V I A A V L C S H K L R S V T N F F I V S L A V A D L L V G L A V L P F S A T    79
```

QMEAN

```
                          H H H H H H H C T T T C C H H H H H H H H H H H H H H H H H H H H H H H H
Chain:A            W E V F K V W I F G D V W C R I W L A V D V W M C T A S I L N L C A I S L D R Y   119
project_template_0.1.A   W E V F K V W I F G D V W C R I W L A V D V W M C T A S I L N L C A I S L D R Y   119
```

QMEAN

```
                          H H H S S S C T T H H H H H H H H H H H H H H H H H H H H H H H H H H H H
Chain:A            V A V T R P V T Y P S I M S T K K A K S L I A G I W V L S F V I C F P P L V G W   159
project_template_0.1.A   V A V T R P V T Y P S I M S T R R A K S L I A G L W V L S F V I C F P P L V G W   159
```

QMEAN

```
                          H H H H S T T H H H H H C C H H H H H H H H H H H H H H H H H H C T T T T S G
Chain:A            K D Q K P M I Q P T Y T R G N Y T L Y S M S S Y A T P P P P C P W K C E L T N D   199
project_template_0.1.A   K E Q K V K E N V Y Y Q Y G N Y T L V S V T P S P A P P L P C P W T C E L T N D   199
```

QMEAN

```
                          G G T S S S C C C T T T T T S T T C T T T T T S C S S S C T T T T C C C C C C C C
Chain:A            R G Y V L Y S A L G S F Y I P M F V M L F F Y W R I Y R A A V R T T - - R A I N   237
project_template_0.1.A   A G Y V V Y S A L G S F Y I P M F V M L F F Y W R I Y R A A V R T K - - K L G K   237
```

QMEAN

```
                          H H H H H H H H I I I I I H H H H H H H H H H H C C C S C C C C C - - C S S S
Chain:A            Q G F K T T G K R S V K F Q V K R F K V E T K A A K T L A I I V G G F I F C W L   277
project_template_0.1.A   K H L K V Q V K R F R M E T - - - - - - - - K A A K T L G I I V G G F I F C W L   269
```

QMEAN

```
                          H H H H H H H H H H H S S C C S T T C C C S H H H H H H H H H H H H H H H H
Chain:A            P F F T M Y L I R A F C D H C I Q P T V F S V L F W L G Y C N S A I N P L I Y A   317
```

project_template_0.1.A P F F T M Y L T R A F C A E C I N S L L F S V L F W L G Y C N S A V N P F I Y A   309

QMEAN   H H H H H H H H H H S T T C S C H H H H H H H H H H H H H H H H H H H H H H

Chain:A L F S H E F R I A F K R I V C R C V C T R S –   339

project_template_0.1.A L F S K D F R Q A F K R I I L R C L C S K R –   331

H H C H H H H H H H H H H H H T T C S C C –