

wwPDB X-ray Structure Validation Summary Report (i)

Oct 4, 2023 – 08:01 PM EDT

| PDB ID | : | 6PKE |
|--------------|---|---------------------------------|
| Title | : | Myocilin OLF mutant N428E/D478S |
| Authors | : | Lieberman, R.L.; Hill, S.E. |
| Deposited on | : | 2019-06-29 |
| Resolution | : | 1.88 Å(reported) |
| | | |

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org A user guide is available at https://www.wwpdb.org/validation/2017/XrayValidationReportHelp with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

| MolProbity | : | FAILED |
|--------------------------------|---|--|
| Xtriage (Phenix) | : | 1.13 |
| EDS | : | FAILED |
| Percentile statistics | : | 20191225.v01 (using entries in the PDB archive December 25th 2019) |
| Ideal geometry (proteins) | : | Engh & Huber (2001) |
| Ideal geometry (DNA, RNA) | : | Parkinson et al. (1996) |
| Validation Pipeline (wwPDB-VP) | : | 2.35.1 |

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\hbox{-}RAY\,DIFFRACTION$

The reported resolution of this entry is 1.88 Å.

There are no overall percentile quality scores available for this entry.

MolProbity and EDS failed to run properly - the sequence quality summary graphics cannot be shown.



2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 7722 atoms, of which 3323 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

• Molecule 1 is a protein called Myocilin.

| Mol | Chain | Residues | Atoms | | | | ZeroOcc | AltConf | Trace | | |
|-----|-------|----------|-------|------|------|-----|---------|---------|-------|---|---|
| 1 | Λ | 256 | Total | С | Η | Ν | 0 | S | 0 | 2 | 0 |
| | A | | 3716 | 1318 | 1663 | 326 | 403 | 6 | | | |
| 1 | В | 256 | Total | С | Η | Ν | 0 | S | 0 | 1 | 0 |
| | D 200 | 3699 | 1310 | 1660 | 324 | 399 | 6 | 0 | 1 | 0 | |

There are 4 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|---------------------|------------|
| А | 428 | GLU | ASN | engineered mutation | UNP Q99972 |
| А | 478 | SER | ASP | engineered mutation | UNP Q99972 |
| В | 428 | GLU | ASN | engineered mutation | UNP Q99972 |
| В | 478 | SER | ASP | engineered mutation | UNP Q99972 |

• Molecule 2 is water.

| Mol | Chain | Residues | Atoms | ZeroOcc | AltConf |
|-----|-------|----------|--------------------|---------|---------|
| 2 | А | 181 | Total O 181 181 | 0 | 0 |
| 2 | В | 126 | Total O 126 126 | 0 | 0 |

MolProbity and EDS failed to run properly - this section is therefore empty.



3 Data and refinement statistics (i)

| Property | Value | Source | |
|--|--|-----------|--|
| Space group | P 1 21 1 | Depositor | |
| Cell constants | 48.22Å 47.29Å 97.02Å | Depositor | |
| a, b, c, α , β , γ | 90.00° 100.28° 90.00° | Depositor | |
| Resolution (Å) | 33.60 - 1.88 | Depositor | |
| % Data completeness | 97.6 (33.60-1.88) | Depositor | |
| (in resolution range) | | - | |
| R _{merge} | 0.12 | Depositor | |
| R _{sym} | (Not available) | Depositor | |
| $< I/\sigma(I) > 1$ | 2.38 (at 1.88 Å) | Xtriage | |
| Refinement program | PHENIX 1.15.2_3472 | Depositor | |
| R, R_{free} | 0.176 , 0.218 | Depositor | |
| Wilson B-factor $(Å^2)$ | 25.5 | Xtriage | |
| Anisotropy | 0.211 | Xtriage | |
| L-test for twinning ² | $ < L >=0.49, < L^2>=0.32$ | Xtriage | |
| Estimated twinning fraction | No twinning to report. | Xtriage | |
| Total number of atoms | 7722 | wwPDB-VP | |
| Average B, all atoms $(Å^2)$ | 34.0 | wwPDB-VP | |

EDS failed to run properly - this section is therefore incomplete.

Xtriage's analysis on translational NCS is as follows: The analyses of the Patterson function reveals a significant off-origin peak that is 69.60 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 3.5979e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



¹Intensities estimated from amplitudes.

4 Model quality (i)

4.1 Standard geometry (i)

MolProbity failed to run properly - this section is therefore empty.

4.2 Too-close contacts (i)

MolProbity failed to run properly - this section is therefore empty.

4.3 Torsion angles (i)

4.3.1 Protein backbone (i)

MolProbity failed to run properly - this section is therefore empty.

4.3.2 Protein sidechains (i)

MolProbity failed to run properly - this section is therefore empty.

4.3.3 RNA (i)

MolProbity failed to run properly - this section is therefore empty.

4.4 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

4.5 Carbohydrates (i)

There are no monosaccharides in this entry.

4.6 Ligand geometry (i)

There are no ligands in this entry.

4.7 Other polymers (i)

There are no such residues in this entry.



4.8 Polymer linkage issues (i)

There are no chain breaks in this entry.



5 Fit of model and data (i)

5.1 Protein, DNA and RNA chains (i)

EDS failed to run properly - this section is therefore empty.

5.2 Non-standard residues in protein, DNA, RNA chains (i)

EDS failed to run properly - this section is therefore empty.

5.3 Carbohydrates (i)

EDS failed to run properly - this section is therefore empty.

5.4 Ligands (i)

EDS failed to run properly - this section is therefore empty.

5.5 Other polymers (i)

EDS failed to run properly - this section is therefore empty.

