# wwPDB X-ray Structure Validation Summary Report (i)

Oct 2, 2023 – 06:09 AM EDT

| | | |
|---|---|---|
| PDB ID | : | 6N81 |
| Title | : | Crystal structure of GII.4 2002 norovirus P domain in complex with cross-reactive human antibody A1227 |
| Authors | : | Changela, A.; Verardi, R.; Kwong, P.D. |
| Deposited on | : | 2018-11-28 |
| Resolution | : | 2.58 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 (i)) 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-RAY DIFFRACTION*

The reported resolution of this entry is 2.58 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 4 unique types of molecules in this entry. The entry contains 11539 atoms, of which 0 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 Major capsid protein.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | | |
| 1 | A | 306 | 2375 | 1503 | 411 | 450 | 11 | 0 | 0 | 0 |
| 1 | B | 306 | 2375 | 1503 | 411 | 450 | 11 | 0 | 0 | 0 |

There are 6 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|---|---|---|---|---|---|
| A | 222 | GLY | - | expression tag | UNP R4I4P2 |
| A | 223 | PRO | - | expression tag | UNP R4I4P2 |
| A | 224 | SER | - | expression tag | UNP R4I4P2 |
| B | 222 | GLY | - | expression tag | UNP R4I4P2 |
| B | 223 | PRO | - | expression tag | UNP R4I4P2 |
| B | 224 | SER | - | expression tag | UNP R4I4P2 |

- Molecule 2 is a protein called A1227 Fab light chain.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | | |
| 2 | D | 211 | 1619 | 1009 | 275 | 331 | 4 | 0 | 0 | 0 |
| 2 | L | 211 | 1619 | 1009 | 275 | 331 | 4 | 0 | 0 | 0 |

- Molecule 3 is a protein called A1227 Fab heavy chain.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | | |
| 3 | C | 217 | 1598 | 1004 | 270 | 315 | 9 | 0 | 0 | 0 |
| 3 | H | 225 | 1646 | 1030 | 279 | 328 | 9 | 0 | 0 | 0 |

- Molecule 4 is water.

| Mol | Chain | Residues | Atoms | | ZeroOcc | AltConf |
|---|---|---|---|---|---|---|
| | | | Total | O | | |
| 4 | A | 75 | 75 | 75 | 0 | 0 |
| | | | Total | O | | |
| 4 | B | 109 | 109 | 109 | 0 | 0 |
| | | | Total | O | | |
| 4 | D | 13 | 13 | 13 | 0 | 0 |
| | | | Total | O | | |
| 4 | C | 18 | 18 | 18 | 0 | 0 |
| | | | Total | O | | |
| 4 | H | 46 | 46 | 46 | 0 | 0 |
| | | | Total | O | | |
| 4 | L | 46 | 46 | 46 | 0 | 0 |

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

# 3 Data and refinement statistics (i)

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

| Property | Value | Source |
|---|---|---|
| Space group | P 1 21 1 | Depositor |
| Cell constants<br>a, b, c, $\alpha$, $\beta$, $\gamma$ | 82.60Å 150.10Å 117.25Å<br>90.00° 95.06° 90.00° | Depositor |
| Resolution (Å) | 46.09 – 2.58 | Depositor |
| % Data completeness<br>(in resolution range) | 94.7 (46.09-2.58) | Depositor |
| $R_{merge}$ | 0.12 | Depositor |
| $R_{sym}$ | (Not available) | Depositor |
| $< I/\sigma(I) >$ [1] | 1.84 (at 2.58Å) | Xtriage |
| Refinement program | PHENIX 1.9_1692 | Depositor |
| R, $R_{free}$ | 0.173 , 0.211 | Depositor |
| Wilson B-factor (Å$^2$) | 31.0 | Xtriage |
| Anisotropy | 1.151 | 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 | 11539 | wwPDB-VP |
| Average B, all atoms (Å$^2$) | 47.0 | wwPDB-VP |

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.33% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

# 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.