# Full wwPDB NMR Structure Validation Report (i)

Aug 30, 2020 – 11:51 AM BST

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|---|---|---|
| PDB ID | : | 1IOB |
| Title | : | INTERLEUKIN-1 BETA FROM JOINT X-RAY AND NMR REFINEMENT |
| Authors | : | Shaanan, B.; Clore, G.M. |
| Deposited on | : | 1996-03-14 |

This is a Full wwPDB NMR Structure Validation 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 following versions of software and data (see references (1)) were used in the production of this report:

| | | |
|---|---|---|
| Cyrange | : | NOT EXECUTED |
| NmrClust | : | NOT EXECUTED |
| MolProbity | : | 4.02b-467 |
| Percentile statistics | : | 20191225.v01 (using entries in the PDB archive December 25th 2019) |
| RCI | : | NOT EXECUTED |
| PANAV | : | NOT EXECUTED |
| ShiftChecker | : | NOT EXECUTED |
| Ideal geometry (proteins) | : | Engh & Huber (2001) |
| Ideal geometry (DNA, RNA) | : | Parkinson et al. (1996) |
| Validation Pipeline (wwPDB-VP) | : | 2.13 |

# 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
*X-RAY DIFFRACTION, SOLUTION NMR*

The reported resolution of this entry is 2.00 Å.

The overall completeness of chemical shifts assignment was not calculated.

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

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5%

Note EDS was not executed.

| Mol | Chain | Length | Quality of chain |
|---|---|---|---|
| 1 | A | 153 | 67% 26% 7% . |

## 2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 1335 atoms, of which 109 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called INTERLEUKIN-1 BETA.

| Mol | Chain | Residues | Atoms | | | | | | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 1 | A | 153 | Total | C | H | N | O | S | 0 |
| | | | 1328 | 773 | 109 | 201 | 237 | 8 | |

- Molecule 2 is water.

| Mol | Chain | Residues | Atoms | |
|---|---|---|---|---|
| 2 | A | 7 | Total | O |
| | | | 7 | 7 |

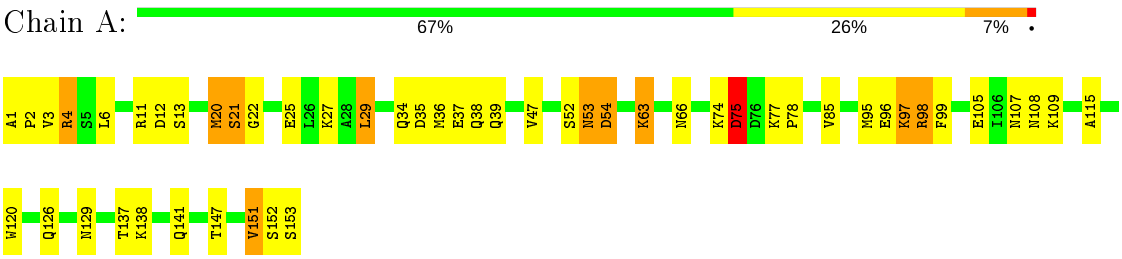
# 3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

Note EDS was not executed.

- Molecule 1: INTERLEUKIN-1 BETA

Chain A:



# 4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

| Property | Value | Source |
|---|---|---|
| Space group | P 43 | Depositor |
| Cell constants<br>a, b, c, $\alpha$, $\beta$, $\gamma$ | 55.14Å 55.14Å 76.66Å<br>90.00° 90.00° 90.00° | Depositor |
| Resolution (Å) | 6.00 – 2.00 | Depositor |
| % Data completeness<br>(in resolution range) | (Not available) (6.00-2.00) | Depositor |
| $R_{merge}$ | (Not available) | Depositor |
| $R_{sym}$ | (Not available) | Depositor |
| Refinement program | X-PLOR | Depositor |
| R, $R_{free}$ | 0.214 , 0.254 | Depositor |
| Estimated twinning fraction | No twinning to report. | Xtriage |
| Total number of atoms | 1335 | wwPDB-VP |
| Average B, all atoms (Å$^2$) | 33.0 | wwPDB-VP |

# 5 Model quality

## 5.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

| Mol | Chain | Bond lengths | | Bond angles | |
|---|---|---|---|---|---|
| | | RMSZ | $\#\|Z\| > 5$ | RMSZ | $\#\|Z\| > 5$ |
| 1 | A | 1.05 | 0/1242 | 1.25 | 5/1670 (0.3%) |

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

| Mol | Chain | #Chirality outliers | #Planarity outliers |
|---|---|---|---|
| 1 | A | 0 | 2 |

There are no bond length outliers.

All (5) bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 1 | A | 120 | TRP | CD1-NE1-CE2 | 7.85 | 116.07 | 109.00 |
| 1 | A | 120 | TRP | CG-CD1-NE1 | -6.56 | 103.54 | 110.10 |
| 1 | A | 120 | TRP | NE1-CE2-CZ2 | 5.86 | 136.84 | 130.40 |
| 1 | A | 11 | ARG | NE-CZ-NH2 | -5.43 | 117.58 | 120.30 |
| 1 | A | 120 | TRP | NE1-CE2-CD2 | -5.07 | 102.23 | 107.30 |

There are no chirality outliers.

All (2) planarity outliers are listed below:

| Mol | Chain | Res | Type | Group |
|---|---|---|---|---|
| 1 | A | 4 | ARG | Sidechain |
| 1 | A | 98 | ARG | Sidechain |

## 5.2 Too-close contacts

Due to software issues we are unable to calculate clashes - this section is therefore empty.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles |
|---|---|---|---|---|---|---|
| 1 | A | 151/153 (99%) | 134 (89%) | 14 (9%) | 3 (2%) | 7 3 |

All (3) Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | A | 151 | VAL |
| 1 | A | 63 | LYS |
| 1 | A | 75 | ASP |

### 5.3.2 Protein sidechains

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles |
|---|---|---|---|---|---|
| 1 | A | 140/140 (100%) | 118 (84%) | 22 (16%) | 2 1 |

All (22) residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | A | 3 | VAL |
| 1 | A | 4 | ARG |
| 1 | A | 6 | LEU |
| 1 | A | 20 | MET |
| 1 | A | 21 | SER |
| 1 | A | 25 | GLU |
| 1 | A | 27 | LYS |
| 1 | A | 29 | LEU |

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| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | A | 36 | MET |
| 1 | A | 38 | GLN |
| 1 | A | 53 | ASN |
| 1 | A | 54 | ASP |
| 1 | A | 63 | LYS |
| 1 | A | 75 | ASP |
| 1 | A | 97 | LYS |
| 1 | A | 105 | GLU |
| 1 | A | 126 | GLN |
| 1 | A | 129 | ASN |
| 1 | A | 138 | LYS |
| 1 | A | 141 | GLN |
| 1 | A | 147 | THR |
| 1 | A | 153 | SER |

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

#### 5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

### 5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

### 5.6 Ligand geometry (i)

There are no ligands in this entry.

### 5.7 Other polymers (i)

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.