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

Dec 11, 2022 – 01:34 AM EST

| | | |
|---|---|---|
| PDB ID | : | 1JLQ |
| Title | : | CRYSTAL STRUCTURE OF HIV-1 REVERSE TRANSCRIPTASE IN COMPLEX WITH 739W94 |
| Authors | : | Ren, J.; Stuart, D.I.; Stammers, D.K. |
| Deposited on | : | 2001-07-16 |
| Resolution | : | 3.00 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.

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

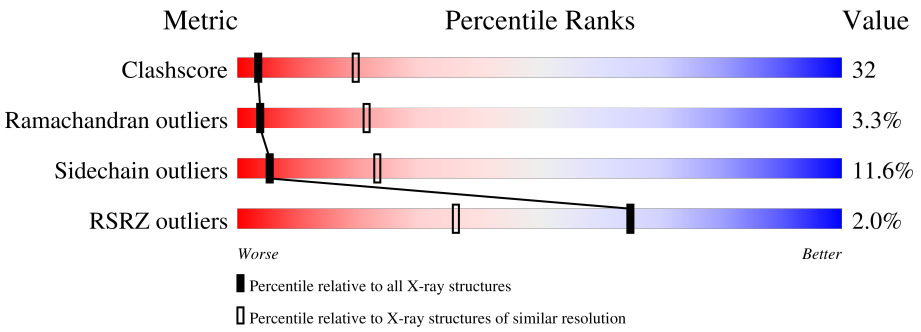
| | | |
|---|---|---|
| MolProbity | : | 4.02b-467 |
| Mogul | : | 1.8.5 (274361), CSD as541be (2020) |
| Xtriage (Phenix) | : | 1.13 |
| EDS | : | 2.31.2 |
| buster-report | : | 1.1.7 (2018) |
| Percentile statistics | : | 20191225.v01 (using entries in the PDB archive December 25th 2019) |
| Refmac | : | 5.8.0158 |
| CCP4 | : | 7.0.044 (Gargrove) |
| Ideal geometry (proteins) | : | Engh & Huber (2001) |
| Ideal geometry (DNA, RNA) | : | Parkinson et al. (1996) |
| Validation Pipeline (wwPDB-VP) | : | 2.31.2 |

# 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 3.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.




| Metric | Whole archive (#Entries) | Similar resolution (#Entries, resolution range(Å)) |
|---|---|---|
| Clashscore | 141614 | 2416 (3.00-3.00) |
| Ramachandran outliers | 138981 | 2333 (3.00-3.00) |
| Sidechain outliers | 138945 | 2336 (3.00-3.00) |
| RSRZ outliers | 127900 | 1990 (3.00-3.00) |

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 of 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% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

| Mol | Chain | Length | Quality of chain |
|---|---|---|---|
| 1 | A | 560 | 2%<br>37% 50% 7% • 5% |
| 2 | B | 440 | 2%<br>46% 38% 8% 8% |

# 2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 7722 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 HIV-1 RT, A-CHAIN.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | | |
| 1 | A | 534 | 4363 | 2823 | 724 | 808 | 8 | 0 | 0 | 0 |

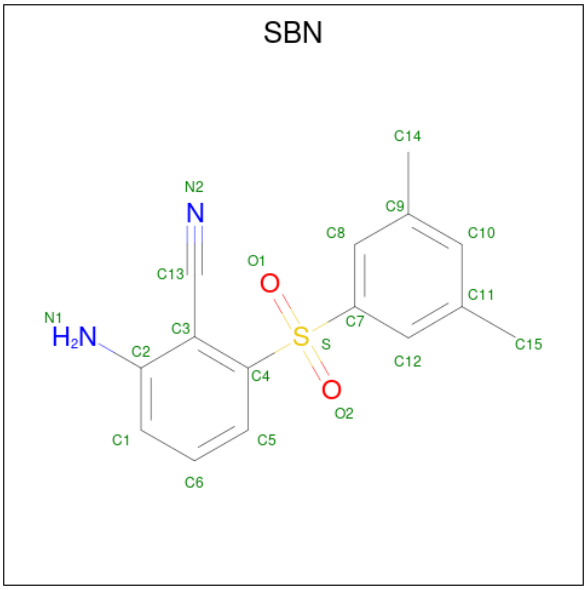
There is a discrepancy between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|---|---|---|---|---|---|
| A | 280 | CSD | CYS | modified residue | UNP P04585 |

- Molecule 2 is a protein called HIV-1 RT, B-CHAIN.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | | |
| 2 | B | 405 | 3339 | 2170 | 556 | 606 | 7 | 0 | 0 | 0 |

- Molecule 3 is 2-AMINO-6-(3,5-DIMETHYLPHENYL)SULFONYLBENZONITRILE (three-letter code: SBN) (formula: $C_{15}H_{14}N_2O_2S$).



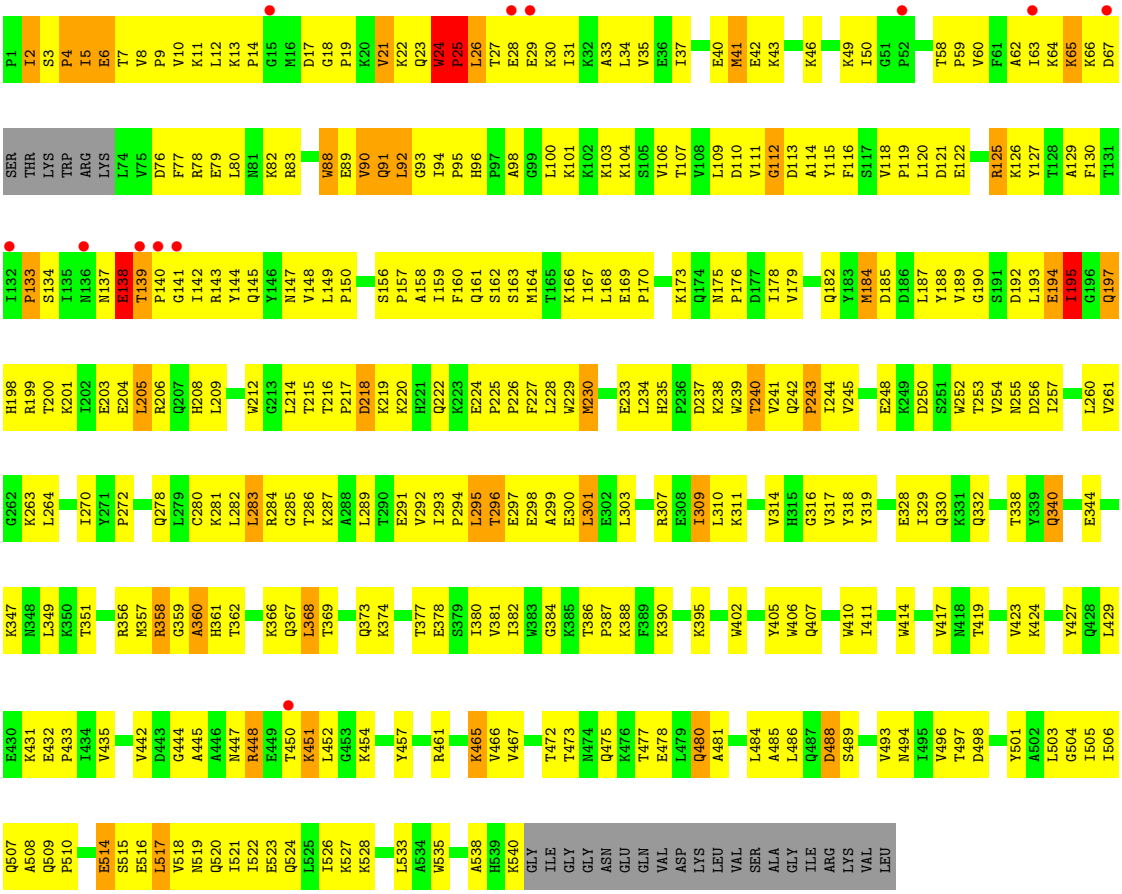
| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 3 | A | 1 | 20 | 15 | 2 | 2 | 1 | 0 | 0 |

# 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 and electron density. 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. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). 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.

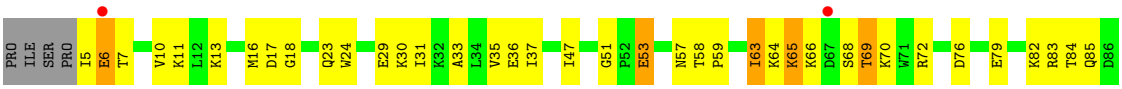
- Molecule 1: HIV-1 RT, A-CHAIN

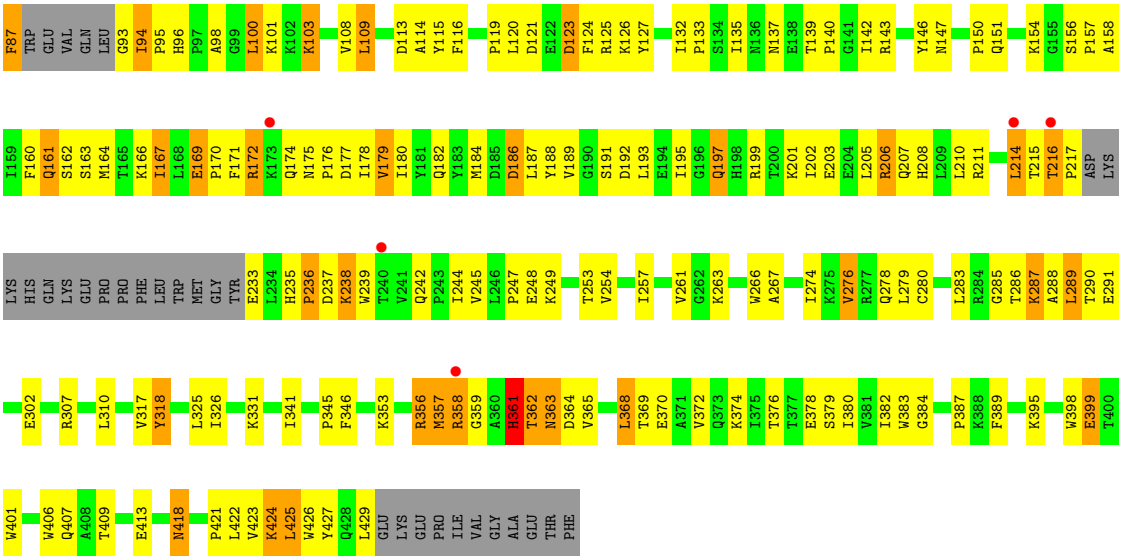
Chain A: 2% 37% 50% 7% 5%



- Molecule 2: HIV-1 RT, B-CHAIN

Chain B: 2% 46% 38% 8% 8%




F87 TRP GLU VAL GLN LEU G93 I94 P95 H96 P97 A98 G99 L100 K101 K102 K103 V108 L109 D113 A114 Y115 F116 P119 L120 D121 E122 D123 F124 R125 K126 Y127 I132 P133 S134 I135 N136 N137 E138 T139 P140 G141 I142 R143 Y146 N147 P150 Q151 K154 G155 S156 P157 A158
I159 F160 Q161 S162 S163 M164 T165 K166 I167 L168 E169 P170 F171 R172 K173 Q174 N175 P176 D177 I178 V179 I180 Y181 Q182 Y183 M184 D185 D186 L187 Y188 V189 G190 S191 D192 L193 E194 I195 G196 Q197 H198 R199 T200 K201 I202 E203 E204 L205 R206 Q207 H208 L209 L210 R211 L214 T215 T216 P217 ASP LYS
LYS HIS GLN LYS GLU PRO PRO PHE LEU TRP MET GLY TYR E233 L234 H235 P236 D237 K238 W239 T240 V241 Q242 P243 I244 V245 L246 P247 E248 K249 T253 V254 I257 V261 G262 K263 W266 A267 I274 K275 V276 R277 Q278 L279 C280 L283 R284 G285 T286 K287 A288 L289 T290 E291
E302 R307 L310 V317 Y318 L325 I326 K331 I341 P345 F346 K353 R356 M357 R358 G359 A360 H361 T362 N363 D364 V365 L368 T369 E370 A371 V372 Q373 K374 I375 T376 T377 E378 S379 I380 V381 I382 W383 G384 P387 K388 F389 K395 W398 E399 T400
W401 W406 Q407 A408 T409 E413 N418 P421 L422 V423 K424 L425 W426 Y427 Q428 L429 GLU LYS GLU PRO ILE VAL GLY ALA GLU THR PHE

# 4 Data and refinement statistics (i)

| Property | Value | Source |
|---|---|---|
| Space group | P 21 21 21 | Depositor |
| Cell constants<br>a, b, c, $\alpha$, $\beta$, $\gamma$ | 141.10Å 110.90Å 73.10Å<br>90.00° 90.00° 90.00° | Depositor |
| Resolution (Å) | 29.88 – 3.00<br>29.88 – 2.98 | Depositor<br>EDS |
| % Data completeness<br>(in resolution range) | 95.8 (29.88-3.00)<br>95.2 (29.88-2.98) | Depositor<br>EDS |
| $R_{merge}$ | 0.15 | Depositor |
| $R_{sym}$ | (Not available) | Depositor |
| $< I/\sigma(I) >$ [1] | 1.44 (at 3.00Å) | Xtriage |
| Refinement program | CNS | Depositor |
| R, $R_{free}$ | 0.219 , 0.267<br>0.210 , (Not available) | Depositor<br>DCC |
| $R_{free}$ test set | No test flags present. | wwPDB-VP |
| Wilson B-factor (Å$^2$) | 81.5 | Xtriage |
| Anisotropy | 0.297 | Xtriage |
| Bulk solvent $k_{sol}$(e/Å$^3$), $B_{sol}$(Å$^2$) | 0.30 , 82.2 | EDS |
| L-test for twinning[2] | $< \|L\| > = 0.47$, $< L^2 > = 0.30$ | Xtriage |
| Estimated twinning fraction | No twinning to report. | Xtriage |
| $F_o$,$F_c$ correlation | 0.95 | EDS |
| Total number of atoms | 7722 | wwPDB-VP |
| Average B, all atoms (Å$^2$) | 89.0 | wwPDB-VP |

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.19% 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.

# 5 Model quality (i)

## 5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: SBN, CSD

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 | 0.49 | 0/4469 | 0.73 | 2/6074 (0.0%) |
| 2 | B | 0.46 | 0/3431 | 0.71 | 1/4660 (0.0%) |
| All | All | 0.48 | 0/7900 | 0.72 | 3/10734 (0.0%) |

There are no bond length outliers.

All (3) bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 1 | A | 388 | LYS | N-CA-C | -5.66 | 95.71 | 111.00 |
| 2 | B | 238 | LYS | N-CA-C | -5.36 | 96.53 | 111.00 |
| 1 | A | 141 | GLY | N-CA-C | -5.21 | 100.08 | 113.10 |

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|---|---|---|---|---|---|---|
| 1 | A | 4363 | 0 | 4405 | 318 | 0 |
| 2 | B | 3339 | 0 | 3379 | 195 | 0 |
| 3 | A | 20 | 0 | 14 | 3 | 0 |
| All | All | 7722 | 0 | 7798 | 502 | 0 |

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including

hydrogen atoms). The all-atom clashscore for this structure is 32.

The worst 5 of 502 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:A:358:ARG:HH11 | 1:A:514:GLU:HA | 1.11 | 1.14 |
| 1:A:59:PRO:HG2 | 1:A:76:ASP:HB3 | 1.43 | 1.00 |
| 1:A:358:ARG:NH1 | 1:A:514:GLU:HA | 1.77 | 0.99 |
| 1:A:451:LYS:HG3 | 1:A:472:THR:O | 1.66 | 0.95 |
| 1:A:23:GLN:HE22 | 1:A:60:VAL:H | 1.15 | 0.94 |

There are no symmetry-related clashes.

## 5.3 Torsion angles (i)

### 5.3.1 Protein backbone (i)

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 | 529/560 (94%) | 452 (85%) | 58 (11%) | 19 (4%) | 3 19 |
| 2 | B | 399/440 (91%) | 342 (86%) | 45 (11%) | 12 (3%) | 4 24 |
| All | All | 928/1000 (93%) | 794 (86%) | 103 (11%) | 31 (3%) | 4 21 |

5 of 31 Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | A | 4 | PRO |
| 1 | A | 91 | GLN |
| 1 | A | 138 | GLU |
| 1 | A | 195 | ILE |
| 2 | B | 215 | THR |

### 5.3.2 Protein sidechains (i)

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 | 478/499 (96%) | 420 (88%) | 58 (12%) | 5 21 |
| 2 | B | 368/400 (92%) | 328 (89%) | 40 (11%) | 6 25 |
| All | All | 846/899 (94%) | 748 (88%) | 98 (12%) | 5 23 |

5 of 98 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | A | 540 | LYS |
| 2 | B | 172 | ARG |
| 2 | B | 10 | VAL |
| 2 | B | 70 | LYS |
| 2 | B | 206 | ARG |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 24 such sidechains are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | A | 519 | ASN |
| 2 | B | 161 | GLN |
| 2 | B | 85 | GLN |
| 2 | B | 207 | GLN |
| 1 | A | 222 | GLN |

### 5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The

Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

| Mol | Type | Chain | Res | Link | Bond lengths | | | Bond angles | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | Counts | RMSZ | $\#\|Z\| > 2$ | Counts | RMSZ | $\#\|Z\| > 2$ |
| 1 | CSD | A | 280 | 1 | 3,7,8 | 1.34 | 0 | 1,8,10 | 4.81 | 1 (100%) |

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

| Mol | Type | Chain | Res | Link | Chirals | Torsions | Rings |
|---|---|---|---|---|---|---|---|
| 1 | CSD | A | 280 | 1 | - | 2/2/6/8 | - |

There are no bond length outliers.

All (1) bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 1 | A | 280 | CSD | OD1-SG-CB | 4.81 | 114.69 | 105.54 |

There are no chirality outliers.

All (2) torsion outliers are listed below:

| Mol | Chain | Res | Type | Atoms |
|---|---|---|---|---|
| 1 | A | 280 | CSD | N-CA-CB-SG |
| 1 | A | 280 | CSD | CA-CB-SG-OD1 |

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry (i)

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

| Mol | Type | Chain | Res | Link | Bond lengths | | | Bond angles | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | Counts | RMSZ | $\#\|Z\| > 2$ | Counts | RMSZ | $\#\|Z\| > 2$ |
| 3 | SBN | A | 999 | - | 19,21,21 | 2.25 | 8 (42%) | 27,31,31 | 1.28 | 2 (7%) |

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

| Mol | Type | Chain | Res | Link | Chirals | Torsions | Rings |
|---|---|---|---|---|---|---|---|
| 3 | SBN | A | 999 | - | - | 0/14/14/14 | 0/2/2/2 |

The worst 5 of 8 bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|---|---|---|---|---|---|---|---|
| 3 | A | 999 | SBN | C5-C4 | 4.35 | 1.44 | 1.39 |
| 3 | A | 999 | SBN | C8-C7 | 3.21 | 1.44 | 1.39 |
| 3 | A | 999 | SBN | C10-C11 | 3.13 | 1.44 | 1.39 |
| 3 | A | 999 | SBN | C7-S | -3.12 | 1.72 | 1.77 |
| 3 | A | 999 | SBN | C4-S | -2.85 | 1.74 | 1.78 |

All (2) bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 3 | A | 999 | SBN | O2-S-O1 | -2.50 | 114.46 | 119.23 |
| 3 | A | 999 | SBN | C5-C4-S | 2.27 | 119.81 | 116.40 |

There are no chirality outliers.

There are no torsion outliers.

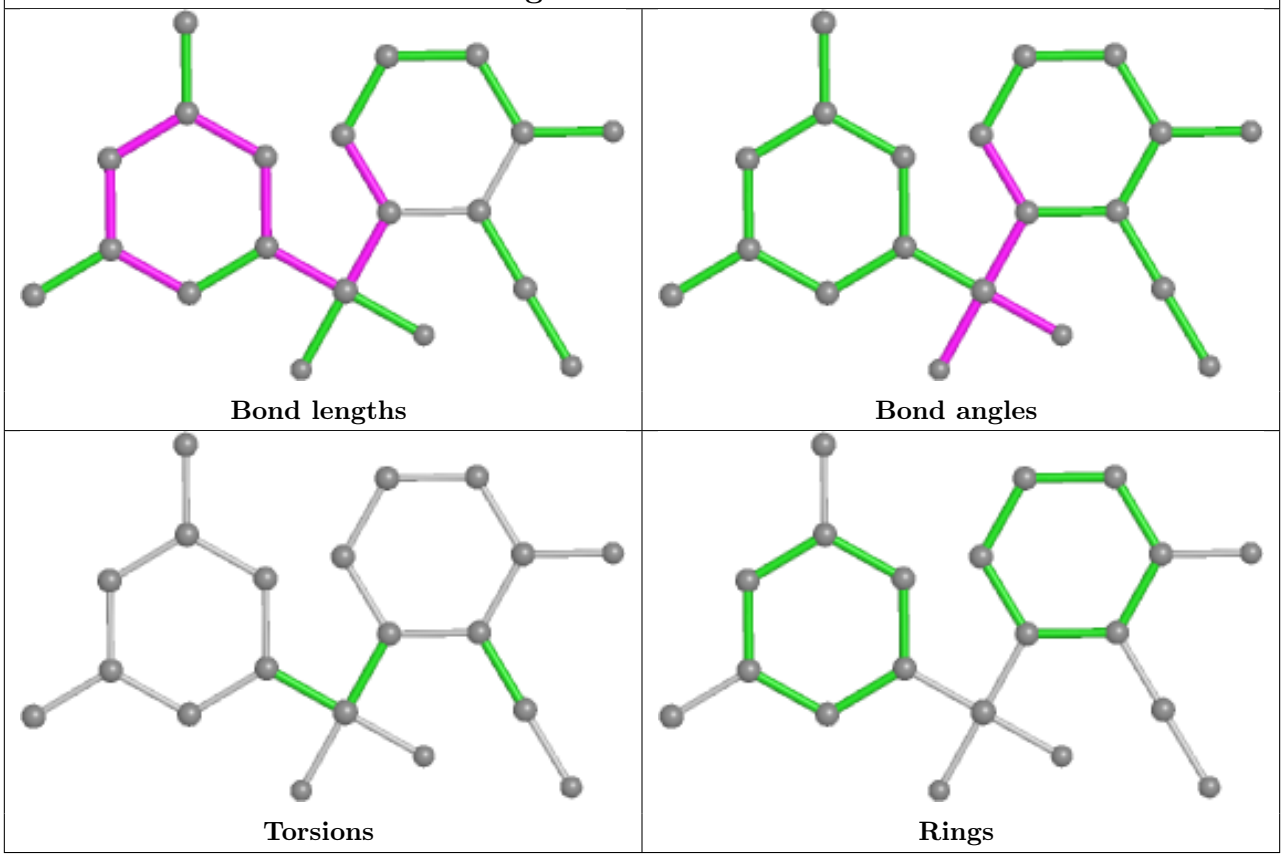
There are no ring outliers.

1 monomer is involved in 3 short contacts:

| Mol | Chain | Res | Type | Clashes | Symm-Clashes |
|---|---|---|---|---|---|
| 3 | A | 999 | SBN | 3 | 0 |

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

**Ligand SBN A 999**




## 5.7 Other polymers (i)

There are no such residues in this entry.

## 5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

# 6 Fit of model and data (i)

## 6.1 Protein, DNA and RNA chains (i)

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, $95^{th}$ percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

| Mol | Chain | Analysed | <RSRZ> | #RSRZ>2 | | | OWAB(Å$^2$) | Q<0.9 |
|---|---|---|---|---|---|---|---|---|
| 1 | A | 533/560 (95%) | -0.35 | 12 (2%) | 60 | 31 | 34, 86, 136, 150 | 0 |
| 2 | B | 405/440 (92%) | -0.38 | 7 (1%) | 70 | 41 | 41, 82, 134, 150 | 0 |
| All | All | 938/1000 (93%) | -0.36 | 19 (2%) | 65 | 36 | 34, 85, 136, 150 | 0 |

The worst 5 of 19 RSRZ outliers are listed below:

| Mol | Chain | Res | Type | RSRZ |
|---|---|---|---|---|
| 1 | A | 141 | GLY | 5.8 |
| 1 | A | 139 | THR | 4.5 |
| 1 | A | 28 | GLU | 3.8 |
| 1 | A | 67 | ASP | 3.6 |
| 1 | A | 140 | PRO | 3.3 |

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, $95^{th}$ percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

| Mol | Type | Chain | Res | Atoms | RSCC | RSR | B-factors(Å$^2$) | Q<0.9 |
|---|---|---|---|---|---|---|---|---|
| 1 | CSD | A | 280 | 8/9 | 0.91 | 0.17 | 73,78,82,83 | 0 |

## 6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

## 6.4 Ligands (i)

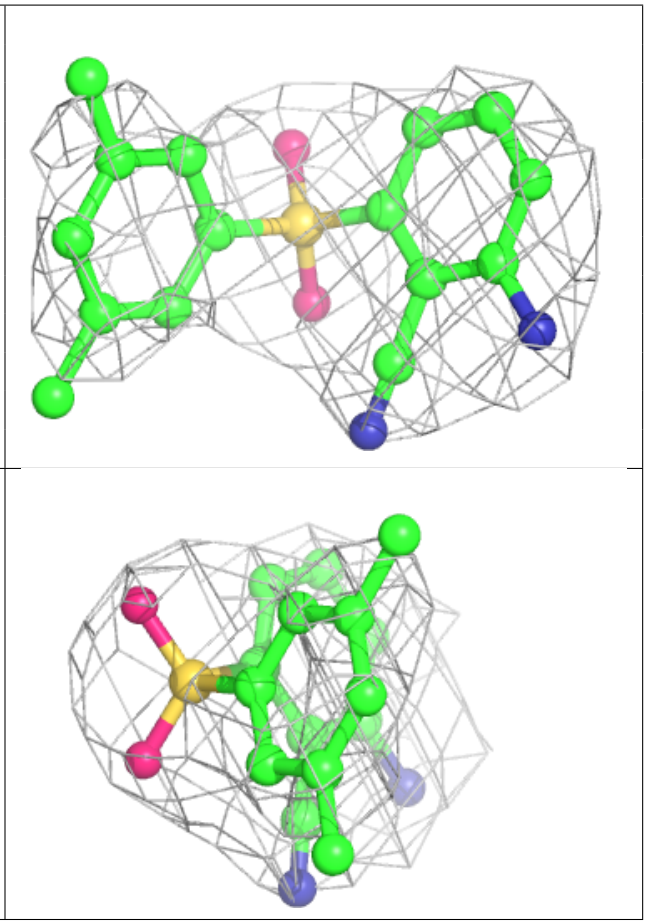
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, $95^{th}$ percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

| Mol | Type | Chain | Res | Atoms | RSCC | RSR | B-factors(Å$^2$) | Q<0.9 |
|---|---|---|---|---|---|---|---|---|
| 3 | SBN | A | 999 | 20/20 | 0.98 | 0.18 | 40,56,74,76 | 0 |

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

**Electron density around SBN A 999:**

2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative) and green (positive)



## 6.5 Other polymers (i)

There are no such residues in this entry.