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

Sep 5, 2023 – 09:47 AM EDT

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|---|---|---|
| PDB ID | : | 3ULY |
| Title | : | Crystal Structure of BROX Bro1 Domain in Complex with the C-Terminal Tails of CHMP5 |
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| Deposited on | : | 2011-11-11 |
| Resolution | : | 2.60 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:

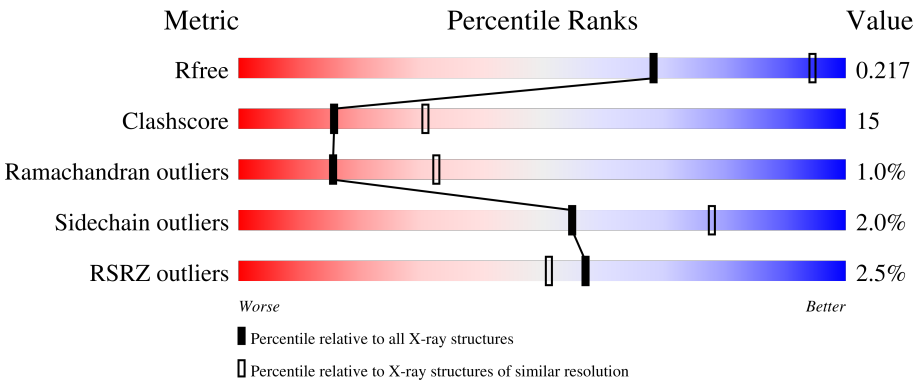
| | | |
|---|---|---|
| MolProbity | : | 4.02b-467 |
| Mogul | : | 1.8.5 (274361), CSD as541be (2020) |
| Xtriage (Phenix) | : | 1.13 |
| EDS | : | 2.35 |
| Percentile statistics | : | 20191225.v01 (using entries in the PDB archive December 25th 2019) |
| Refmac | : | 5.8.0158 |
| CCP4 | : | 7.0.044 (Gargrove) |
| Ideal geometry (proteins) | : | Engh & Huber (2001) |
| Ideal geometry (DNA, RNA) | : | Parkinson et al. (1996) |
| Validation Pipeline (wwPDB-VP) | : | 2.35 |

# 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 2.60 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)) |
|---|---|---|
| $R_{free}$ | 130704 | 3163 (2.60-2.60) |
| Clashscore | 141614 | 3518 (2.60-2.60) |
| Ramachandran outliers | 138981 | 3455 (2.60-2.60) |
| Sidechain outliers | 138945 | 3455 (2.60-2.60) |
| RSRZ outliers | 127900 | 3104 (2.60-2.60) |

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 | 410 | 2% 69% 25% • 5% |
| 2 | B | 69 | % 20% • • 75% |

# 2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 3325 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.

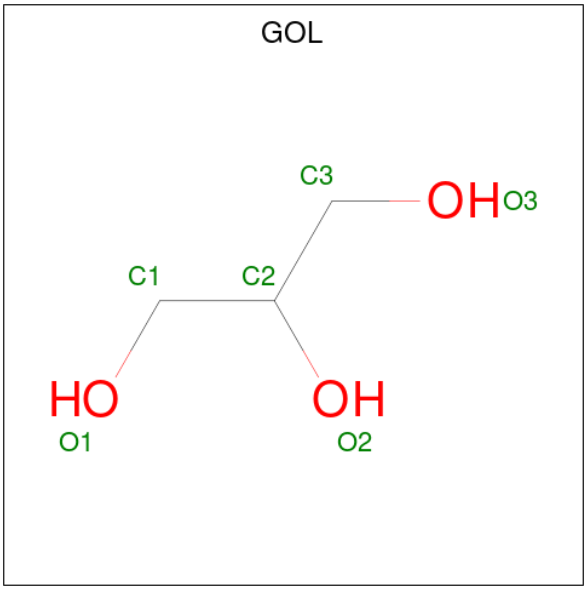
- Molecule 1 is a protein called BRO1 domain-containing protein BROX.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | | |
| 1 | A | 389 | 3104 | 1992 | 522 | 578 | 12 | 84 | 0 | 0 |

- Molecule 2 is a protein called Charged multivesicular body protein 5.

| Mol | Chain | Residues | Atoms | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | | | |
| 2 | B | 17 | 131 | 84 | 21 | 26 | 2 | 0 | 0 |

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).




| Mol | Chain | Residues | Atoms | | | ZeroOcc | AltConf |
|---|---|---|---|---|---|---|---|
| | | | Total | C | O | | |
| 3 | A | 1 | 6 | 3 | 3 | 0 | 0 |

- Molecule 4 is water.

| Mol | Chain | Residues | Atoms | | ZeroOcc | AltConf |
|---|---|---|---|---|---|---|
| | | | Total | O | | |
| 4 | A | 78 | 78 | 78 | 0 | 0 |
| | | | Total | O | | |
| 4 | B | 6 | 6 | 6 | 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: BRO1 domain-containing protein BROX

Chain A: 2% 69% 25% 5%

T2 H3 W4 N8 P9 A29 N53 P54 F65 Q69 G70 S74 L75 S76 T79 Q80 L84 R85 Y86 I87 Q88 N89 F90 K91 T95 S102 A103 Q104 Q105 E110 I111 I112 S113 M114 N117 V118 A119 L120 E133 N134 I135 E139 E142 R145

K148 I149 K155 E159 S160 H161 L162 P163 K164 L165 I166 T167 P168 A169 D174 L175 L179 I180 E181 A189 A197 I200 E201 E215 Y220 Q221 K222 E231 P232 A236 K240 Y241 L244 K245 M246 Y256 H257 T260 L261 L262 E269 E276

L280 C288 K289 E290 Y291 T300 P303 S304 L307 K311 L315 K322 C323 Q324 R325 E326 N327 G328 F329 I330 Y331 F332 Q333 K334 T337 E338 L342 E343 L344 K345 Y348 I354 W365 A372 F373 D374 L375 T376 K377 R378 P379 LYS ASP ASP SER T384

P388 V392 K393 P394 VAL LYS GLU PRO ASP ILE LYS PRO GLN LYS ASP THR GLY CYS TYR ILE SER

• Molecule 2: Charged multivesicular body protein 5

Chain B: % 20% 75%

ARG SER TYR GLY THR PRO GLU LEU ASP GLU ASP ASP LEU GLU ALA GLU LEU ASP ALA LEU GLY ASP GLU LEU LEU ALA ASP GLU ASP SER SER TYR LEU ASP GLU ALA ALA SER ALA PRO ALA ILE PRO GLU GLY VAL PRO THR ASP T200 V206 L207 E210 P214 Q215 I216 PRO

ALA SER

# 4 Data and refinement statistics (i)

| Property | Value | Source |
|---|---|---|
| Space group | C 1 2 1 | Depositor |
| Cell constants<br>a, b, c, $\alpha$, $\beta$, $\gamma$ | 172.38Å 46.03Å 68.56Å<br>90.00° 104.52° 90.00° | Depositor |
| Resolution (Å) | 41.72 – 2.60<br>41.72 – 2.60 | Depositor<br>EDS |
| % Data completeness<br>(in resolution range) | 90.1 (41.72-2.60)<br>97.2 (41.72-2.60) | Depositor<br>EDS |
| $R_{merge}$ | 0.09 | Depositor |
| $R_{sym}$ | (Not available) | Depositor |
| $< I/\sigma(I) >$ [1] | 2.20 (at 2.61Å) | Xtriage |
| Refinement program | PHENIX (phenix.refine: 1.7_650) | Depositor |
| R, $R_{free}$ | 0.166 , 0.211<br>0.175 , 0.217 | Depositor<br>DCC |
| $R_{free}$ test set | 803 reflections (5.04%) | wwPDB-VP |
| Wilson B-factor (Å$^2$) | 47.7 | Xtriage |
| Anisotropy | 0.628 | Xtriage |
| Bulk solvent $k_{sol}$(e/Å$^3$), $B_{sol}$(Å$^2$) | 0.35 , 74.1 | EDS |
| L-test for twinning[2] | $< \|L\| > = 0.48$, $< L^2 > = 0.32$ | Xtriage |
| Estimated twinning fraction | No twinning to report. | Xtriage |
| $F_o$,$F_c$ correlation | 0.96 | EDS |
| Total number of atoms | 3325 | wwPDB-VP |
| Average B, all atoms (Å$^2$) | 59.0 | wwPDB-VP |

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.10% 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: GOL

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 | 0.32 | 0/3182 | 0.51 | 0/4309 |
| 2 | B | 0.31 | 0/132 | 0.42 | 0/177 |
| All | All | 0.32 | 0/3314 | 0.51 | 0/4486 |

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 | 1 |

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

| Mol | Chain | Res | Type | Group |
|---|---|---|---|---|
| 1 | A | 78 | SER | Peptide |

## 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 | 3104 | 0 | 3082 | 91 | 0 |
| 2 | B | 131 | 0 | 133 | 3 | 0 |
| 3 | A | 6 | 0 | 8 | 3 | 0 |
| 4 | A | 78 | 0 | 0 | 2 | 0 |
| 4 | B | 6 | 0 | 0 | 0 | 0 |
| All | All | 3325 | 0 | 3223 | 92 | 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 15.

The worst 5 of 92 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:393:LYS:HB3 | 1:A:394:PRO:CD | 1.57 | 1.32 |
| 1:A:393:LYS:CB | 1:A:394:PRO:CD | 2.30 | 1.08 |
| 1:A:393:LYS:HB3 | 1:A:394:PRO:HD2 | 1.35 | 1.06 |
| 1:A:393:LYS:HB3 | 1:A:394:PRO:HD3 | 1.33 | 1.06 |
| 1:A:393:LYS:CB | 1:A:394:PRO:HD2 | 1.88 | 1.03 |

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 | 385/410 (94%) | 371 (96%) | 10 (3%) | 4 (1%) | 15 32 |
| 2 | B | 15/69 (22%) | 15 (100%) | 0 | 0 | 100 100 |
| All | All | 400/479 (84%) | 386 (96%) | 10 (2%) | 4 (1%) | 15 32 |

All (4) Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | A | 393 | LYS |
| 1 | A | 75 | LEU |
| 1 | A | 392 | VAL |
| 1 | A | 330 | ILE |

### 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 | 331/351 (94%) | 325 (98%) | 6 (2%) | 59 | 80 |
| 2 | B | 15/56 (27%) | 14 (93%) | 1 (7%) | 16 | 33 |
| All | All | 346/407 (85%) | 339 (98%) | 7 (2%) | 55 | 78 |

5 of 7 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | A | 120 | LEU |
| 1 | A | 300 | THR |
| 2 | B | 206 | VAL |
| 1 | A | 384 | THR |
| 1 | A | 117 | ASN |

Sometimes 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)

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 | GOL | A | 412 | - | 5,5,5 | 0.34 | 0 | 5,5,5 | 0.25 | 0 |

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 | GOL | A | 412 | - | - | 2/4/4/4 | - |

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

| Mol | Chain | Res | Type | Atoms |
|---|---|---|---|---|
| 3 | A | 412 | GOL | O1-C1-C2-C3 |
| 3 | A | 412 | GOL | O1-C1-C2-O2 |

There are no ring outliers.

1 monomer is involved in 3 short contacts:

| Mol | Chain | Res | Type | Clashes | Symm-Clashes |
|---|---|---|---|---|---|
| 3 | A | 412 | GOL | 3 | 0 |

## 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 | 388/410 (94%) | 0.00 | 9 (2%) | 60 | 54 | 28, 54, 102, 140 | 27 (6%) |
| 2 | B | 17/69 (24%) | 0.12 | 1 (5%) | 22 | 17 | 42, 56, 88, 88 | 1 (5%) |
| All | All | 405/479 (84%) | 0.01 | 10 (2%) | 57 | 51 | 28, 54, 101, 140 | 28 (6%) |

The worst 5 of 10 RSRZ outliers are listed below:

| Mol | Chain | Res | Type | RSRZ |
|---|---|---|---|---|
| 1 | A | 304 | SER | 5.2 |
| 1 | A | 394 | PRO | 4.9 |
| 1 | A | 384 | THR | 3.8 |
| 1 | A | 269 | GLU | 2.9 |
| 1 | A | 79 | THR | 2.6 |

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

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

## 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 | GOL | A | 412 | 6/6 | 0.74 | 0.24 | 70,87,88,93 | 0 |

## 6.5 Other polymers (i)

There are no such residues in this entry.