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

Feb 1, 2016 – 05:34 PM GMT

| | | |
|---|---|---|
| PDB ID | : | 4IML |
| Title | : | CrossFab binding to human Angiopoietin 2 |
| Authors | : | Fenn, S.; Schiller, C.; Griese, J.; Hopfner, K.-P.; Kettenberger, H. |
| Deposited on | : | 2013-01-03 |
| Resolution | : | 2.93 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
http://wwpdb.org/validation/2016/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:

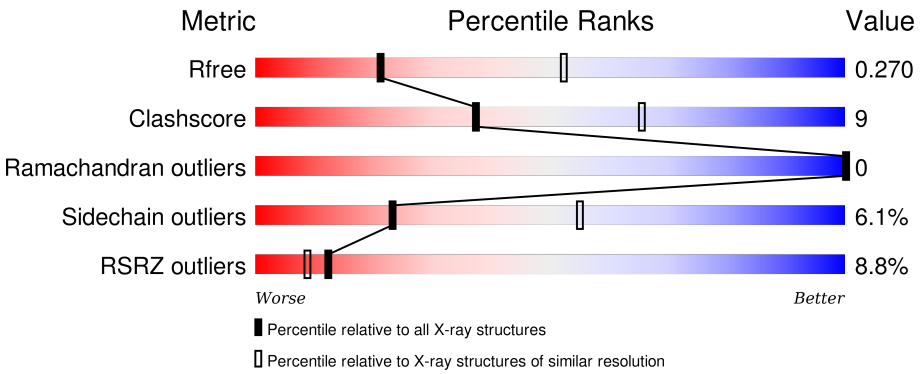
| | | |
|---|---|---|
| MolProbity | : | 4.02b-467 |
| Mogul | : | 1.7 (RC4), CSD as536be (2015) |
| Xtriage (Phenix) | : | 1.9-1692 |
| EDS | : | rb-20026688 |
| Percentile statistics | : | 20151230.v01 (using entries in the PDB archive December 30th 2015) |
| Refmac | : | 5.8.0135 |
| CCP4 | : | 6.5.0 |
| Ideal geometry (proteins) | : | Engh & Huber (2001) |
| Ideal geometry (DNA, RNA) | : | Parkinson et al. (1996) |
| Validation Pipeline (wwPDB-VP) | : | trunk26865 |

# 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 2.93 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)) |
|---|---|---|
| $R_{free}$ | 91344 | 2057 (2.98-2.90) |
| Clashscore | 102246 | 2308 (2.98-2.90) |
| Ramachandran outliers | 100387 | 2245 (2.98-2.90) |
| Sidechain outliers | 100360 | 2247 (2.98-2.90) |
| RSRZ outliers | 91569 | 2065 (2.98-2.90) |

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. 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 | 245 | 11% 75% 20% • |
| 1 | H | 245 | 3% 70% 24% • • |
| 2 | B | 213 | 13% 82% 16% • |
| 2 | L | 213 | 8% 80% 17% • • |

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

| Mol | Type | Chain | Res | Chirality | Geometry | Clashes | Electron density |
|---|---|---|---|---|---|---|---|
| 3 | GOL | B | 301 | - | - | - | X |

# 2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 6743 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.

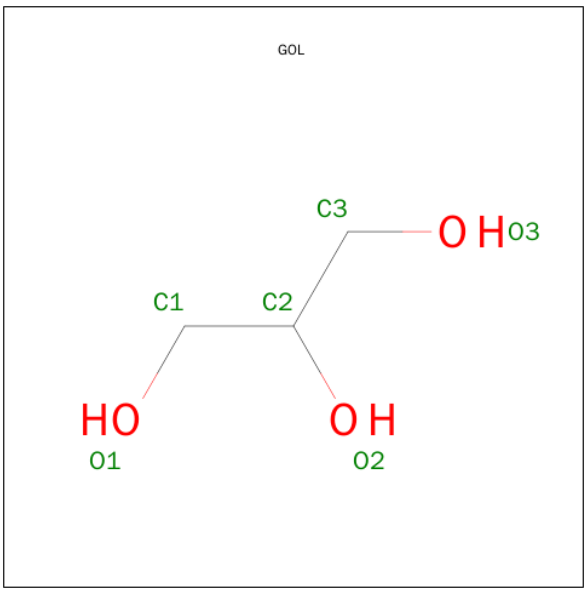
- Molecule 1 is a protein called Crossed heavy chain (VH-Ckappa).

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | | |
| 1 | H | 234 | 1816 | 1142 | 305 | 360 | 9 | 81 | 0 | 0 |
| 1 | A | 234 | 1816 | 1142 | 305 | 360 | 9 | 95 | 0 | 0 |

- Molecule 2 is a protein called Crossed light chain (VL-CH1).

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | | |
| 2 | L | 210 | 1540 | 961 | 260 | 315 | 4 | 18 | 0 | 0 |
| 2 | B | 212 | 1552 | 968 | 262 | 317 | 5 | 16 | 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 | H | 1 | 6 | 3 | 3 | 0 | 0 |
| | | | Total | C | O | | |
| 3 | B | 1 | 6 | 3 | 3 | 0 | 0 |

- Molecule 4 is water.

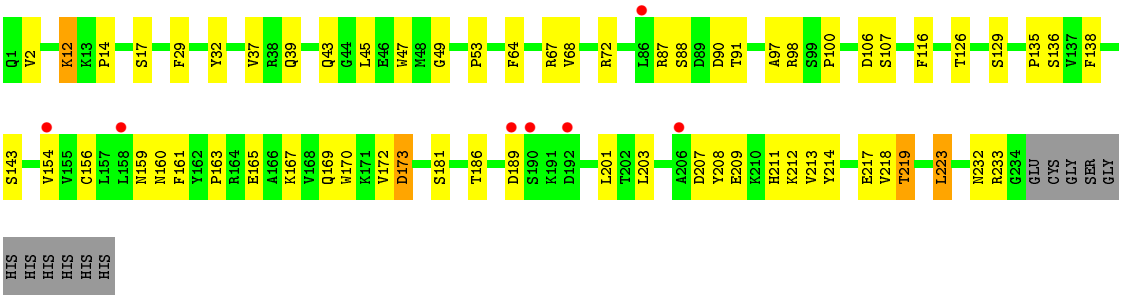
| Mol | Chain | Residues | Atoms | | ZeroOcc | AltConf |
|---|---|---|---|---|---|---|
| | | | Total | O | | |
| 4 | H | 2 | 2 | 2 | 0 | 0 |
| | | | Total | O | | |
| 4 | L | 2 | 2 | 2 | 0 | 0 |
| | | | Total | O | | |
| 4 | A | 2 | 2 | 2 | 0 | 0 |
| | | | Total | O | | |
| 4 | B | 1 | 1 | 1 | 0 | 0 |

# 3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

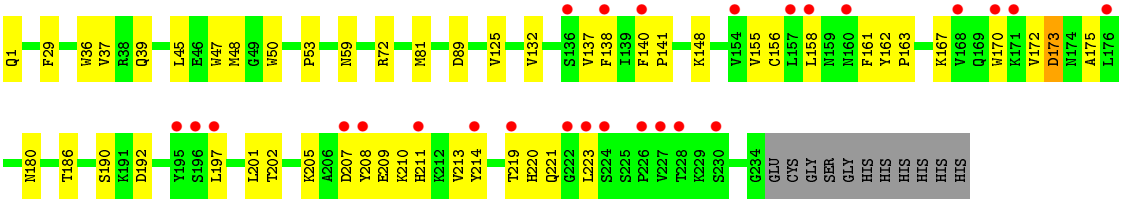
- Molecule 1: Crossed heavy chain (VH-Ckappa)

Chain H:



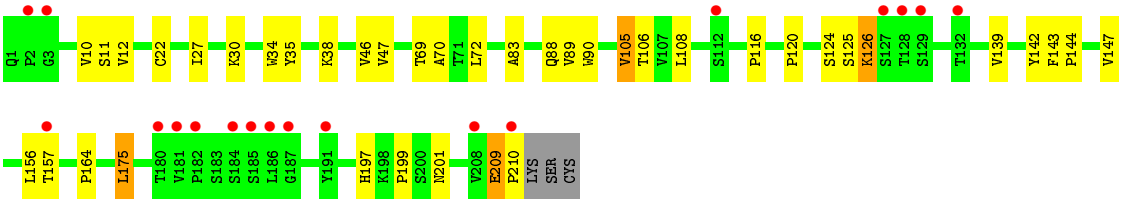

- Molecule 1: Crossed heavy chain (VH-Ckappa)

Chain A:



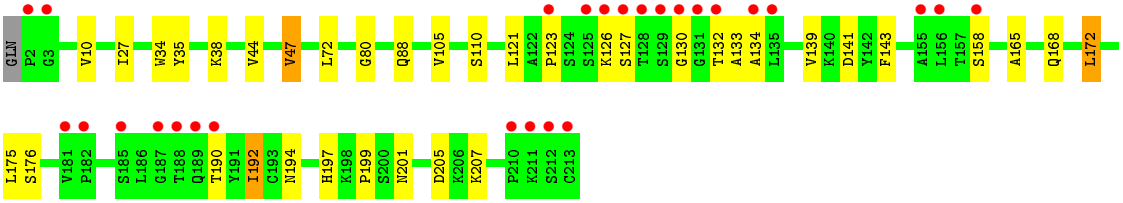

- Molecule 2: Crossed light chain (VL-CH1)

Chain L:




- Molecule 2: Crossed light chain (VL-CH1)

Chain B:


GLM
P2
G3
V10
I27
W34
Y35
K38
V44
V47
L72
G80
Q88
V105
S110
L121
A122
P123
S124
S125
K126
S127
T128
S129
G130
G131
T132
A133
A134
L135
V139
K140
D141
Y142
F143
A155
L156
T157
S158
A165
Q168
L172
L175
S176
V181
P182
S185
L186
G187
T188
Q189
T190
Y191
I192
G193
N194
H197
K198
P199
S200
N201
D205
R206
K207
P210
K211
S212
C213

# 4 Data and refinement statistics (i)

| Property | Value | Source |
|---|---|---|
| Space group | P 21 21 21 | Depositor |
| Cell constants<br>a, b, c, $\alpha$, $\beta$, $\gamma$ | 75.75Å 80.55Å 158.27Å<br>90.00° 90.00° 90.00° | Depositor |
| Resolution (Å) | 44.13 – 2.93<br>44.13 – 2.93 | Depositor<br>EDS |
| % Data completeness<br>(in resolution range) | 98.6 (44.13-2.93)<br>98.7 (44.13-2.93) | Depositor<br>EDS |
| $R_{merge}$ | (Not available) | Depositor |
| $R_{sym}$ | (Not available) | Depositor |
| $< I/\sigma(I) >$ [1] | 2.03 (at 2.96Å) | Xtriage |
| Refinement program | PHENIX (phenix.refine: 1.8.1_1168) | Depositor |
| R, $R_{free}$ | 0.237 , 0.269<br>0.237 , 0.270 | Depositor<br>DCC |
| $R_{free}$ test set | 1059 reflections (5.01%) | DCC |
| Wilson B-factor (Å$^2$) | 59.0 | Xtriage |
| Anisotropy | 0.421 | Xtriage |
| Bulk solvent $k_{sol}$(e/Å$^3$), $B_{sol}$(Å$^2$) | 0.35 , 63.8 | EDS |
| Estimated twinning fraction | No twinning to report. | Xtriage |
| L-test for twinning[2] | $< \|L\| > = 0.46$, $< L^2 > = 0.29$ | Xtriage |
| Outliers | 2 of 21186 reflections (0.009%) | Xtriage |
| $F_o$,$F_c$ correlation | 0.93 | EDS |
| Total number of atoms | 6743 | wwPDB-VP |
| Average B, all atoms (Å$^2$) | 71.0 | wwPDB-VP |

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 47.94 % 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 9.2315e-05.The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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 | 0.24 | 0/1863 | 0.47 | 0/2532 |
| 1 | H | 0.23 | 0/1863 | 0.46 | 1/2532 (0.0%) |
| 2 | B | 0.23 | 0/1591 | 0.46 | 0/2176 |
| 2 | L | 0.23 | 0/1579 | 0.45 | 0/2162 |
| All | All | 0.23 | 0/6896 | 0.46 | 1/9402 (0.0%) |

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 | H | 223 | LEU | CA-CB-CG | 5.80 | 128.63 | 115.30 |

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 | 1816 | 0 | 1729 | 41 | 0 |
| 1 | H | 1816 | 0 | 1729 | 36 | 0 |
| 2 | B | 1552 | 0 | 1505 | 27 | 0 |
| 2 | L | 1540 | 0 | 1492 | 21 | 0 |
| 3 | B | 6 | 0 | 8 | 0 | 0 |
| 3 | H | 6 | 0 | 8 | 0 | 0 |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|---|---|---|---|---|---|---|
| 4 | A | 2 | 0 | 0 | 0 | 0 |
| 4 | B | 1 | 0 | 0 | 0 | 0 |
| 4 | H | 2 | 0 | 0 | 0 | 0 |
| 4 | L | 2 | 0 | 0 | 0 | 0 |
| All | All | 6743 | 0 | 6471 | 118 | 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 9.

The worst 5 of 118 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:173:ASP:H | 1:A:213:VAL:CG2 | 1.51 | 1.23 |
| 1:A:173:ASP:H | 1:A:213:VAL:HG23 | 1.21 | 1.05 |
| 1:A:173:ASP:N | 1:A:213:VAL:CG2 | 2.21 | 1.04 |
| 2:B:127:SER:HB2 | 2:B:133:ALA:HB2 | 1.41 | 1.01 |
| 1:A:173:ASP:HA | 1:A:213:VAL:HG21 | 1.58 | 0.85 |

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 | 232/245 (95%) | 223 (96%) | 9 (4%) | 0 | 100 | 100 |
| 1 | H | 232/245 (95%) | 225 (97%) | 7 (3%) | 0 | 100 | 100 |
| 2 | B | 210/213 (99%) | 203 (97%) | 7 (3%) | 0 | 100 | 100 |
| 2 | L | 208/213 (98%) | 198 (95%) | 10 (5%) | 0 | 100 | 100 |
| All | All | 882/916 (96%) | 849 (96%) | 33 (4%) | 0 | 100 | 100 |

There are no Ramachandran outliers to report.

### 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 | 199/208 (96%) | 188 (94%) | 11 (6%) | 27 | 60 |
| 1 | H | 199/208 (96%) | 185 (93%) | 14 (7%) | 19 | 47 |
| 2 | B | 180/181 (99%) | 170 (94%) | 10 (6%) | 26 | 59 |
| 2 | L | 178/181 (98%) | 167 (94%) | 11 (6%) | 23 | 54 |
| All | All | 756/778 (97%) | 710 (94%) | 46 (6%) | 23 | 55 |

5 of 46 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 2 | L | 156 | LEU |
| 1 | A | 1 | GLN |
| 2 | B | 176 | SER |
| 2 | L | 157 | THR |
| 2 | L | 201 | ASN |

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | A | 62 | GLN |
| 1 | A | 146 | 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)

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

## 5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry (i)

2 ligands are 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 | B | 301 | - | 5,5,5 | 0.35 | 0 | 5,5,5 | 0.28 | 0 |
| 3 | GOL | H | 301 | - | 5,5,5 | 0.36 | 0 | 5,5,5 | 0.23 | 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 | B | 301 | - | - | 0/4/4/4 | 0/0/0/0 |
| 3 | GOL | H | 301 | - | - | 0/4/4/4 | 0/0/0/0 |

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 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 | 234/245 (95%) | 0.67 | 26 (11%) | 7 | 5 | 32, 70, 134, 161 | 24 (10%) |
| 1 | H | 234/245 (95%) | 0.45 | 7 (2%) | 54 | 50 | 31, 74, 111, 127 | 21 (8%) |
| 2 | B | 212/213 (99%) | 0.63 | 27 (12%) | 5 | 3 | 24, 57, 147, 253 | 4 (1%) |
| 2 | L | 210/213 (98%) | 0.47 | 18 (8%) | 13 | 9 | 27, 56, 136, 180 | 5 (2%) |
| All | All | 890/916 (97%) | 0.56 | 78 (8%) | 12 | 9 | 24, 64, 131, 253 | 54 (6%) |

The worst 5 of 78 RSRZ outliers are listed below:

| Mol | Chain | Res | Type | RSRZ |
|---|---|---|---|---|
| 2 | B | 127 | SER | 11.9 |
| 2 | B | 128 | THR | 7.4 |
| 2 | B | 185 | SER | 6.5 |
| 2 | B | 135 | LEU | 5.2 |
| 1 | A | 154 | VAL | 5.1 |

## 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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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 | LLDF | B-factors(Å$^2$) | Q<0.9 |
|---|---|---|---|---|---|---|---|---|---|
| 3 | GOL | B | 301 | 6/6 | 0.92 | 0.25 | 3.29 | 47,49,51,54 | 0 |
| 3 | GOL | H | 301 | 6/6 | 0.95 | 0.16 | -0.51 | 43,44,45,45 | 0 |

## 6.5 Other polymers (i)

There are no such residues in this entry.