# WORLDWIDE PDB
## PROTEIN DATA BANK

# wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 20, 2014 – 06:28 AM EDT

PDB ID : 4CCM

Title : 60S ribosomal protein L8 histidine hydroxylase (NO66) in complex with Mn(II), N-oxalylglycine (NOG) and 60S ribosomal protein L8 (RPL8 G220C) peptide fragment (complex-1)

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Deposited on : 2013-10-23

Resolution : 2.51 Å(reported)

# 1   Overall quality at a glance  ⓘ

The reported resolution of this entry is 2.51 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 | Percentile Ranks | Value |
|---|---|---|
| Rfree | | 0.243 |
| Clashscore | | 13 |
| Ramachandran outliers | | 0.2% |
| Sidechain outliers | | 3.2% |
| RSRZ outliers | | 2.3% |

*Worse* ← → *Better*

▮ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution
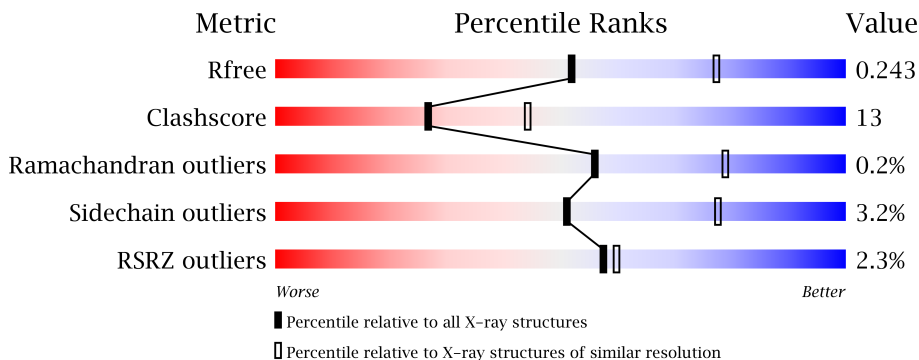
| Metric | Whole archive (#Entries) | Similar resolution (#Entries, resolution range(Å)) |
|---|---|---|
| $R_{free}$ | 66092 | 2784 (2.50-2.50) |
| Clashscore | 79885 | 3562 (2.50-2.50) |
| Ramachandran outliers | 78287 | 3480 (2.50-2.50) |
| Sidechain outliers | 78261 | 3482 (2.50-2.50) |
| RSRZ outliers | 66119 | 2785 (2.50-2.50) |

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

| Mol | Chain | Length | Quality of chain |
|---|---|---|---|
| 1 | A | 467 | |
| 1 | B | 467 | |
| 2 | C | 35 | |
| 2 | D | 35 | |

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

| Mol | Type | Chain | Res | Geometry | Electron density |
|---|---|---|---|---|---|
| 5 | EDO | A | 903 | - | X |
| 5 | EDO | B | 903 | - | X |

# 2 Entry composition ⓘ

There are 6 unique types of molecules in this entry. The entry contains 7841 atoms, of which 0 are hydrogen and 0 are deuterium.

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 BIFUNCTIONAL LYSINE-SPECIFIC DEMETHYLASE AND HISTIDYL-HYDROXYLASE NO66.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|------|------|------|---------|---------|-------|
| 1 | A | 457 | Total 3650 | C 2322 | N 644 | O 668 | S 16 | 0 | 1 | 0 |
| 1 | B | 459 | Total 3670 | C 2335 | N 649 | O 670 | S 16 | 0 | 1 | 0 |

There are 2 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|---------|-----------|
| A | 182 | MET | - | EXPRESSION TAG | UNP Q9H6W3 |
| B | 182 | MET | - | EXPRESSION TAG | UNP Q9H6W3 |

- Molecule 2 is a protein called 60S RIBOSOMAL PROTEIN L8.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|------|------|------|---------|---------|-------|
| 2 | C | 8 | Total 63 | C 38 | N 14 | O 10 | S 1 | 0 | 0 | 0 |
| 2 | D | 11 | Total 75 | C 44 | N 17 | O 13 | S 1 | 0 | 0 | 0 |

There are 2 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|---------|-----------|
| C | 220 | CYS | GLY | ENGINEERED MUTATION | UNP P62917 |
| D | 220 | CYS | GLY | ENGINEERED MUTATION | UNP P62917 |

- Molecule 3 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).
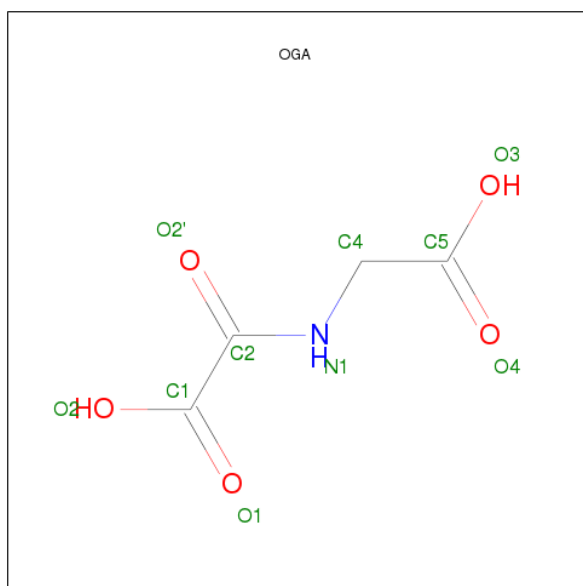
| Mol | Chain | Residues | Atoms | | ZeroOcc | AltConf |
|-----|-------|----------|-------|-----|---------|---------|
| 3 | B | 1 | Total 1 | Mn 1 | 0 | 0 |

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| Mol | Chain | Residues | Atoms | | ZeroOcc | AltConf |
|-----|-------|----------|-------|---|---------|---------|
| 3 | A | 1 | Total Mn<br>1  1 | | 0 | 0 |

- Molecule 4 is N-OXALYLGLYCINE (three-letter code: OGA) (formula: $C_4H_5NO_5$).



| Mol | Chain | Residues | Atoms | | | | ZeroOcc | AltConf |
|-----|-------|----------|-------|---|---|---|---------|---------|
| 4 | A | 1 | Total C N O<br>10  4  1  5 | | | | 0 | 0 |
| 4 | B | 1 | Total C N O<br>10  4  1  5 | | | | 0 | 0 |

- Molecule 5 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).

EDO
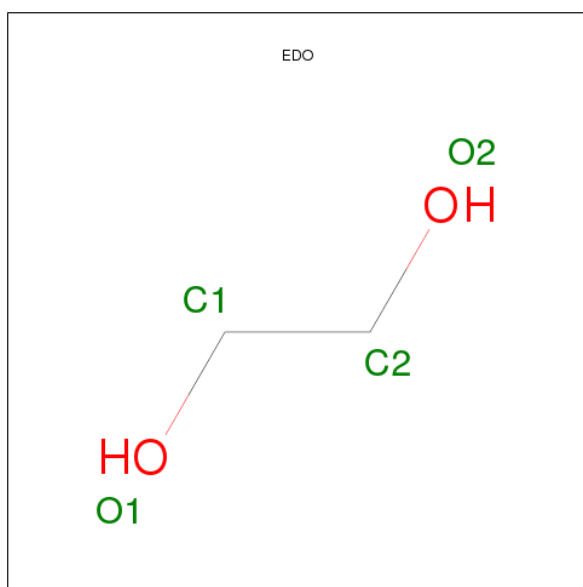
| Mol | Chain | Residues | Atoms | | | ZeroOcc | AltConf |
|-----|-------|----------|-------|---|---|---------|---------|
| 5 | A | 1 | Total<br>4 | C<br>2 | O<br>2 | 0 | 0 |
| 5 | B | 1 | Total<br>4 | C<br>2 | O<br>2 | 0 | 0 |
| 5 | B | 1 | Total<br>4 | C<br>2 | O<br>2 | 0 | 0 |

- Molecule 6 is water.

| Mol | Chain | Residues | Atoms | | ZeroOcc | AltConf |
|-----|-------|----------|-------|---|---------|---------|
| 6 | A | 189 | Total<br>189 | O<br>189 | 0 | 0 |
| 6 | B | 159 | Total<br>159 | O<br>159 | 0 | 0 |
| 6 | D | 1 | Total<br>1 | O<br>1 | 0 | 0 |

# 3 Residue-property plots ⓘ

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.
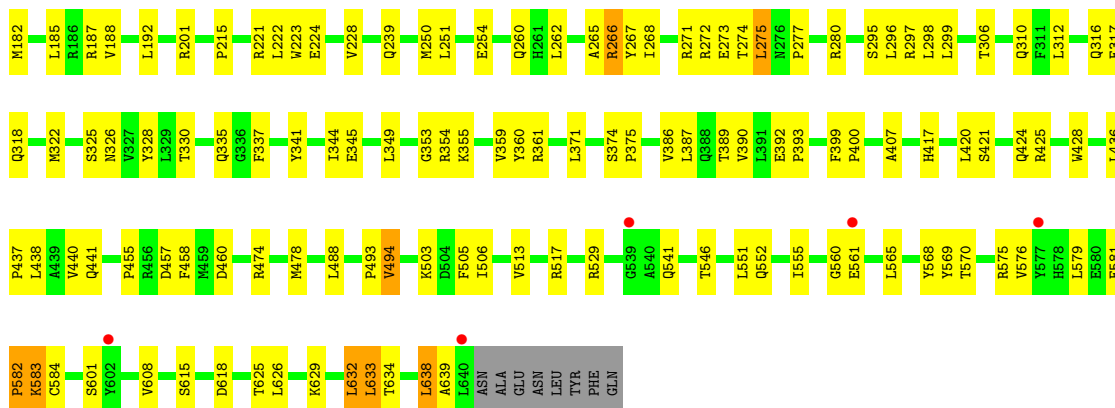
• Molecule 1: BIFUNCTIONAL LYSINE-SPECIFIC DEMETHYLASE AND HISTIDYL-HYDROXYLASE NO66
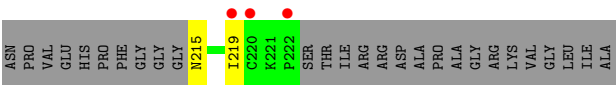
Chain A:
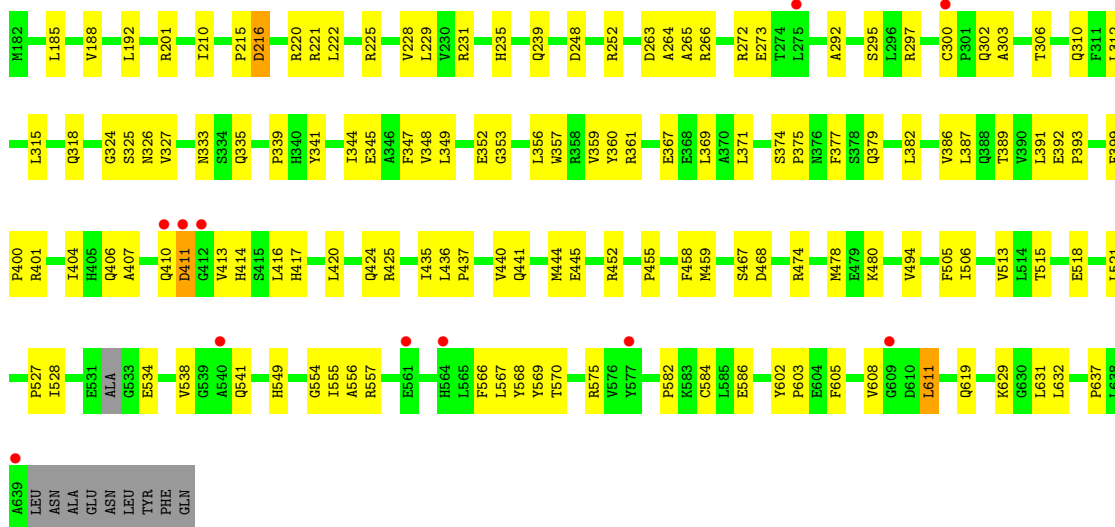


• Molecule 1: BIFUNCTIONAL LYSINE-SPECIFIC DEMETHYLASE AND HISTIDYL-HYDROXYLASE NO66

Chain B:



• Molecule 2: 60S RIBOSOMAL PROTEIN L8

Chain C:



• Molecule 2: 60S RIBOSOMAL PROTEIN L8

Chain D:

# 4 Data and refinement statistics (i)

| Property | Value | Source |
|---|---|---|
| Space group | C 1 2 1 | Depositor |
| Cell constants<br>a, b, c, $\alpha$, $\beta$, $\gamma$ | 154.77Å 83.50Å 96.87Å<br>90.00° 100.20° 90.00° | Depositor |
| Resolution (Å) | 44.07 – 2.51<br>44.07 – 2.51 | Depositor<br>EDS |
| % Data completeness<br>(in resolution range) | 99.2 (44.07-2.51)<br>98.8 (44.07-2.51) | Depositor<br>EDS |
| $R_{merge}$ | 0.13 | Depositor |
| $R_{sym}$ | (Not available) | Depositor |
| $< I/\sigma(I) >$ [1] | 2.19 (at 2.51Å) | Xtriage |
| Refinement program | CNS 1.3 | Depositor |
| R, $R_{free}$ | 0.228 , 0.236<br>0.236 , 0.243 | Depositor<br>DCC |
| $R_{free}$ test set | 2071 reflections (5.03%) | DCC |
| Wilson B-factor (Å$^2$) | 47.5 | Xtriage |
| Anisotropy | 0.643 | Xtriage |
| Bulk solvent $k_{sol}$(e/Å$^3$), $B_{sol}$(Å$^2$) | 0.32 , 32.8 | EDS |
| Estimated twinning fraction | No twinning to report. | Xtriage |
| L-test for twinning | $< |L| > = 0.48, < L^2 > = 0.32$ | Xtriage |
| Outliers | 1 of 41168 reflections (0.002%) | Xtriage |
| $F_o$,$F_c$ correlation | 0.94 | EDS |
| Total number of atoms | 7841 | wwPDB-VP |
| Average B, all atoms (Å$^2$) | 55.0 | wwPDB-VP |

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 13.35% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.

# 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: MN, OGA, EDO

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 | 0.41 | 0/3747 | 0.62 | 0/5100 |
| 1 | B | 0.42 | 0/3768 | 0.62 | 2/5129 (0.0%) |
| 2 | C | 0.37 | 0/65 | 0.49 | 0/88 |
| 2 | D | 0.74 | 0/77 | 0.76 | 0/103 |
| All | All | 0.42 | 0/7657 | 0.62 | 2/10420 (0.0%) |

There are no bond length outliers.

All (2) bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|-----|-------|-----|------|-------|---|----------------|-------------|
| 1 | B | 638 | LEU | CB-CA-C | -5.80 | 99.18 | 110.20 |
| 1 | B | 639 | ALA | N-CA-CB | -5.01 | 103.09 | 110.10 |

There are no chirality outliers.

There are no planarity outliers.

## 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 1 | A | 3650 | 0 | 3552 | 95 | 0 |
| 1 | B | 3670 | 0 | 3582 | 95 | 0 |
| 2 | C | 63 | 0 | 51 | 2 | 0 |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 2 | D | 75 | 0 | 60 | 12 | 0 |
| 3 | A | 1 | 0 | 0 | 0 | 0 |
| 3 | B | 1 | 0 | 0 | 0 | 0 |
| 4 | A | 10 | 0 | 3 | 0 | 0 |
| 4 | B | 10 | 0 | 4 | 0 | 0 |
| 5 | A | 4 | 0 | 6 | 1 | 0 |
| 5 | B | 8 | 0 | 12 | 2 | 0 |
| 6 | A | 189 | 0 | 0 | 7 | 0 |
| 6 | B | 159 | 0 | 0 | 5 | 0 |
| 6 | D | 1 | 0 | 0 | 0 | 0 |
| All | All | 7841 | 0 | 7270 | 193 | 0 |

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 13.

The worst 5 of 193 close contacts within the same asymmetric unit are listed below.

| Atom-1 | Atom-2 | Distance(Å) | Clash(Å) |
|--------|--------|-------------|----------|
| 1:B:280[B]:ARG:CG | 1:B:280[B]:ARG:HH11 | 1.73 | 1.01 |
| 1:B:310:GLN:HA | 1:B:513:VAL:HG21 | 1.57 | 0.86 |
| 1:B:280[B]:ARG:HG3 | 1:B:280[B]:ARG:HH11 | 1.43 | 0.82 |
| 1:B:280[B]:ARG:HG2 | 1:B:280[B]:ARG:HH11 | 1.48 | 0.79 |
| 2:D:221:LYS:H | 2:D:222:PRO:HA | 1.47 | 0.79 |

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 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 | 454/467 (97%) | 432 (95%) | 21 (5%) | 1 (0%) | 56 | 79 |
| 1 | B | 458/467 (98%) | 436 (95%) | 21 (5%) | 1 (0%) | 56 | 79 |
| 2 | C | 6/35 (17%) | 5 (83%) | 1 (17%) | 0 | 100 | 100 |
| 2 | D | 9/35 (26%) | 6 (67%) | 3 (33%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|----------|----------|---------|----------|-----|-----|
| All | All | 927/1004 (92%) | 879 (95%) | 46 (5%) | 2 (0%) | 56 | 79 |

All (2) Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | A | 527 | PRO |
| 1 | B | 582 | PRO |

### 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 | 386/400 (96%) | 374 (97%) | 12 (3%) | 52 | 79 |
| 1 | B | 388/400 (97%) | 375 (97%) | 13 (3%) | 49 | 75 |
| 2 | C | 7/27 (26%) | 7 (100%) | 0 | 100 | 100 |
| 2 | D | 7/27 (26%) | 6 (86%) | 1 (14%) | 5 | 8 |
| All | All | 788/854 (92%) | 762 (97%) | 26 (3%) | 51 | 76 |

5 of 26 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | A | 611 | LEU |
| 1 | B | 271 | ARG |
| 1 | B | 633 | LEU |
| 1 | B | 239 | GLN |
| 1 | B | 266 | ARG |

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 19 such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | A | 466 | HIS |
| 1 | A | 541 | GLN |
| 1 | B | 333 | ASN |
| 1 | A | 465 | GLN |
| 1 | B | 410 | GLN |

#### 5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

Mogul failed to run properly - this section will therefore be empty.

### 5.5 Carbohydrates ⓘ

Mogul failed to run properly - this section will therefore be empty.

### 5.6 Ligand geometry ⓘ

Mogul failed to run properly - this section will therefore be empty.

### 5.7 Other polymers ⓘ

Mogul failed to run properly - this section will therefore be empty.

### 5.8 Polymer linkage issues

There are no chain breaks in this entry.

# 6   Fit of model and data   ⓘ

## 6.1   Protein, DNA and RNA chains   ⓘ

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 | 457/467 (97%) | 0.25 | 11 (2%) | 56 | 58 | 31, 52, 92, 100 | 2 (0%) |
| 1 | B | 459/467 (98%) | 0.24 | 5 (1%) | 77 | 79 | 27, 51, 88, 100 | 2 (0%) |
| 2 | C | 8/35 (22%) | 1.35 | 3 (37%) | 1 | 1 | 82, 92, 100, 100 | 0 |
| 2 | D | 11/35 (31%) | 1.54 | 3 (27%) | 1 | 1 | 77, 82, 100, 100 | 0 |
| All | All | 935/1004 (93%) | 0.27 | 22 (2%) | 57 | 58 | 27, 52, 93, 100 | 4 (0%) |

The worst 5 of 22 RSRZ outliers are listed below:

| Mol | Chain | Res | Type | RSRZ |
|---|---|---|---|---|
| 1 | B | 640 | LEU | 6.6 |
| 1 | A | 275 | LEU | 4.2 |
| 2 | D | 216 | HIS | 3.1 |
| 1 | A | 639 | ALA | 3.0 |
| 1 | A | 577 | TYR | 3.0 |

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

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

## 6.3   Carbohydrates   ⓘ

There are no carbohydrates in this entry.

## 6.4   Ligands   ⓘ

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 | RSR | LLDF | B-factors(Å$^2$) | Q<0.9 |
|-----|------|-------|-----|-------|-----|------|------------------|-------|
| 5 | EDO | A | 903 | 4/4 | 0.23 | 5.79 | 66,68,69,71 | 0 |
| 5 | EDO | B | 903 | 4/4 | 0.19 | 2.16 | 49,51,52,53 | 0 |
| 5 | EDO | B | 904 | 4/4 | 0.16 | 1.28 | 45,49,49,50 | 0 |
| 4 | OGA | A | 902 | 10/10 | 0.16 | -0.23 | 41,43,50,50 | 0 |
| 4 | OGA | B | 902 | 10/10 | 0.14 | -0.33 | 37,42,50,51 | 0 |
| 3 | MN | B | 901 | 1/1 | 0.12 | -0.99 | 39,39,39,39 | 0 |
| 3 | MN | A | 901 | 1/1 | 0.11 | -1.76 | 38,38,38,38 | 0 |

## 6.5  Other polymers ⓘ

There are no such residues in this entry.