# Full wwPDB X-ray Structure Validation Report ⓘ

Nov 13, 2023 – 12:48 PM JST

| | | |
|---|---|---|
| PDB ID | : | 5X9Y |
| Title | : | Crystal structure of the ATPase domain from bacterial mismatch repair endonuclease Aquifex aeolicus MutL. |
| Authors | : | Fukui, K.; Yano, T. |
| Deposited on | : | 2017-03-10 |
| Resolution | : | 3.44 Å(reported) |

This is a Full wwPDB X-ray 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 ⓘ 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 ⓘ) were used in the production of this report:

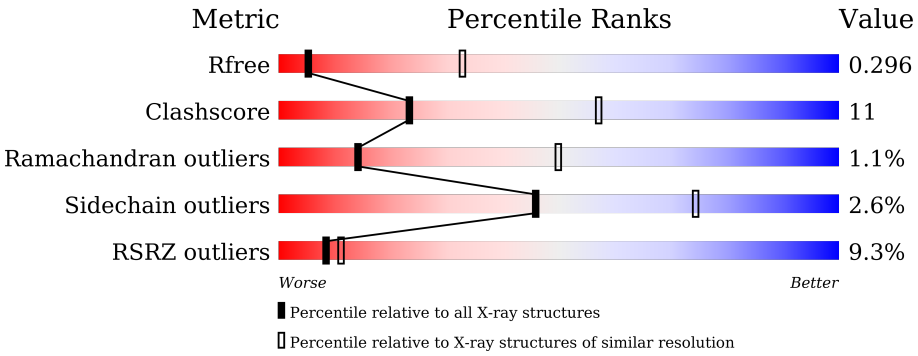
| | | |
|---|---|---|
| MolProbity | : | 4.02b-467 |
| Mogul | : | 1.8.5 (274361), CSD as541be (2020) |
| Xtriage (Phenix) | : | 1.13 |
| EDS | : | 2.36 |
| Percentile statistics | : | 20191225.v01 (using entries in the PDB archive December 25th 2019) |
| Refmac | : | 5.8.0158 |
| CCP4 | : | 7.0.044 (Gargrove) |
| Ideal geometry (proteins) | : | Engh & Huber (2001) |
| Ideal geometry (DNA, RNA) | : | Parkinson et al. (1996) |
| Validation Pipeline (wwPDB-VP) | : | 2.36 |

# 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 3.44 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 | 1278 (3.50-3.38) |
| Clashscore | 141614 | 1361 (3.50-3.38) |
| Ramachandran outliers | 138981 | 1327 (3.50-3.38) |
| Sidechain outliers | 138945 | 1328 (3.50-3.38) |
| RSRZ outliers | 127900 | 1192 (3.50-3.38) |

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 | 308 | 7% 57% 20% • 20% |
| 1 | B | 308 | 13% 51% 26% • • 20% |
| 1 | C | 308 | 2% 57% 19% • 20% |

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 |
|---|---|---|---|---|---|---|---|
| 2 | PEG | B | 401 | - | - | - | X |

## 2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 6141 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.

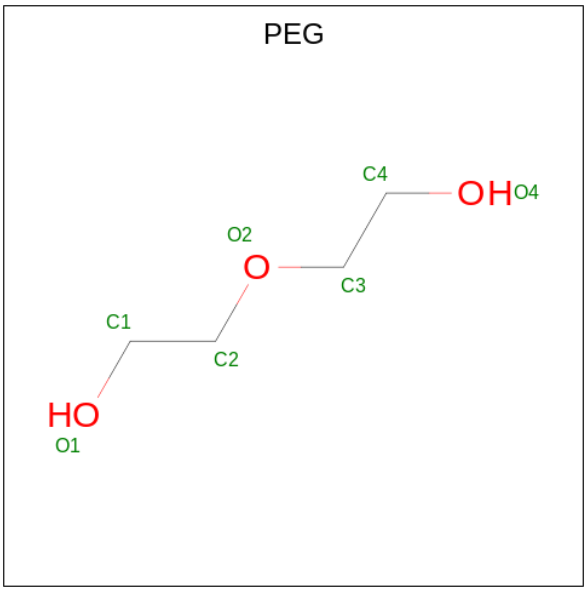
- Molecule 1 is a protein called DNA mismatch repair protein MutL.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| 1 | C | 247 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 2036 | 1310 | 355 | 369 | 2 | | | |
| 1 | A | 247 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 2036 | 1310 | 355 | 369 | 2 | | | |
| 1 | B | 247 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 2036 | 1310 | 355 | 369 | 2 | | | |

There are 3 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|---|---|---|---|---|---|
| C | 1 | MET | - | initiating methionine | UNP O67518 |
| A | 1 | MET | - | initiating methionine | UNP O67518 |
| B | 1 | MET | - | initiating methionine | UNP O67518 |

- Molecule 2 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$).



| Mol | Chain | Residues | Atoms | ZeroOcc | AltConf |
|---|---|---|---|---|---|
| 2 | C | 1 | Total C O<br>7 4 3 | 0 | 0 |
| 2 | B | 1 | Total C O<br>7 4 3 | 0 | 0 |

- Molecule 3 is water.

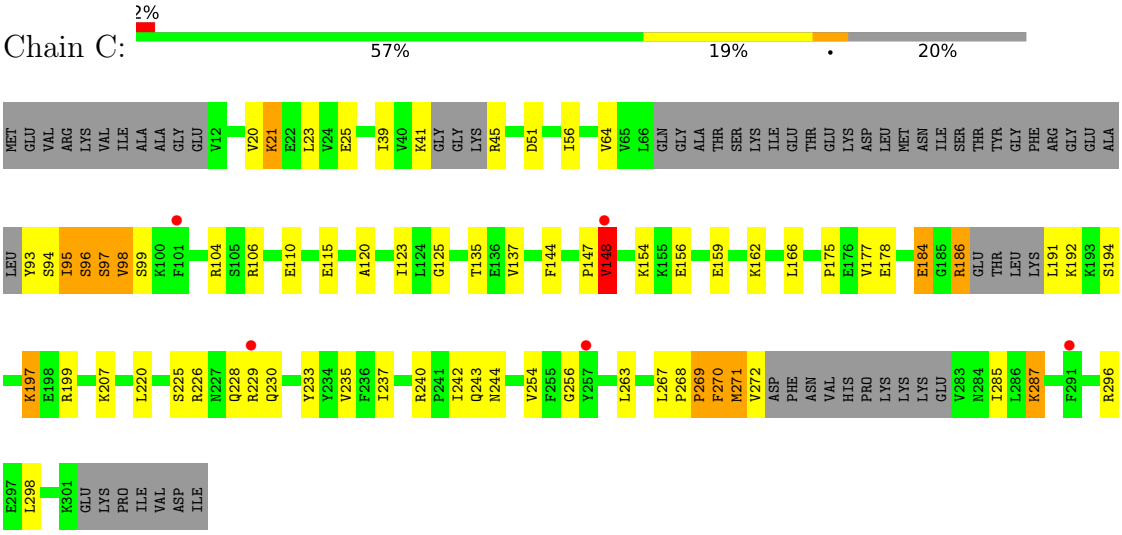
| Mol | Chain | Residues | Atoms | ZeroOcc | AltConf |
|---|---|---|---|---|---|
| 3 | C | 10 | Total O<br>10 10 | 0 | 0 |
| 3 | A | 3 | Total O<br>3 3 | 0 | 0 |
| 3 | B | 6 | Total O<br>6 6 | 0 | 0 |

# 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.

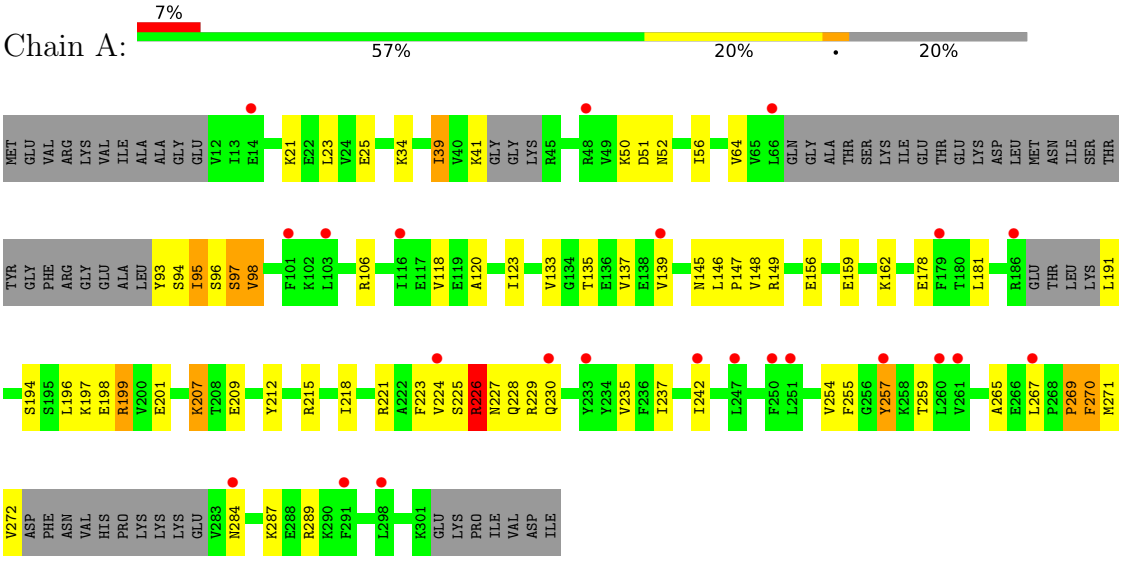
• Molecule 1: DNA mismatch repair protein MutL

Chain C:



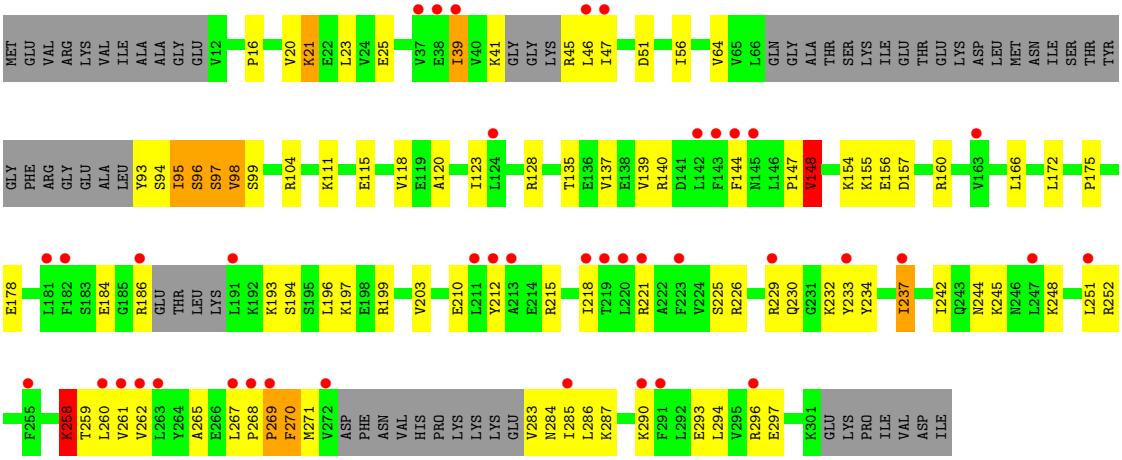

• Molecule 1: DNA mismatch repair protein MutL

Chain A:




• Molecule 1: DNA mismatch repair protein MutL

Chain B:


MET GLU VAL ARG LYS VAL ILE ALA ALA GLY GLU V12 P16 V20 K21 E22 L23 V24 E25 V37 E38 I39 V40 K41 GLY GLY LYS R45 L46 I47 D51 I56 V64 V65 L66 GLN GLY ALA THR SER LYS ILE GLU THR GLU LYS ASP LEU MET ASN ILE SER THR TYR
GLY PHE ARG GLY GLU ALA LEU Y93 S94 I95 S96 S97 V98 S99 R104 K111 E115 V118 E119 A120 I123 L124 R128 T135 E136 V137 E138 V139 R140 D141 L142 F143 F144 N145 L146 P147 V148 K154 K155 E156 D157 R160 V163 L166 L172 P175
E178 L181 F182 S183 E184 G185 R186 GLU THR LEU LYS L191 K192 K193 S194 S195 L196 K197 E198 R199 V203 E210 L211 Y212 A213 E214 R215 I218 T219 L220 R221 A222 F223 V224 S225 R226 R229 Q230 G231 K232 Y233 Y234 I237 I242 Q243 N244 K245 N246 L247 K248 L251 R252
F255 R258 T259 L260 V261 V262 L263 Y264 A265 E266 L267 P268 P269 F270 M271 V272 ASP PHE ASN VAL HIS PRO LYS LYS LYS GLU V283 N284 I285 L286 K287 K290 F291 L292 E293 L294 V295 R296 E297 K301 GLU LYS PRO ILE VAL ASP ILE

# 4 Data and refinement statistics (i)

| Property | Value | Source |
|---|---|---|
| Space group | I 21 21 21 | Depositor |
| Cell constants<br>a, b, c, $\alpha$, $\beta$, $\gamma$ | 126.93Å 145.25Å 176.77Å<br>90.00° 90.00° 90.00° | Depositor |
| Resolution (Å) | 43.05 – 3.44<br>44.19 – 3.44 | Depositor<br>EDS |
| % Data completeness<br>(in resolution range) | 92.8 (43.05-3.44)<br>91.5 (44.19-3.44) | Depositor<br>EDS |
| $R_{merge}$ | 0.13 | Depositor |
| $R_{sym}$ | (Not available) | Depositor |
| $< I/\sigma(I) >$ [1] | 2.67 (at 3.48Å) | Xtriage |
| Refinement program | PHENIX (1.10.1_2155) | Depositor |
| R, $R_{free}$ | 0.256 , 0.295<br>0.256 , 0.296 | Depositor<br>DCC |
| $R_{free}$ test set | 2000 reflections (9.16%) | wwPDB-VP |
| Wilson B-factor (Å$^2$) | 97.4 | Xtriage |
| Anisotropy | 0.096 | Xtriage |
| Bulk solvent $k_{sol}$(e/Å$^3$), $B_{sol}$(Å$^2$) | 0.32 , 76.7 | EDS |
| L-test for twinning[2] | $< \|L\| > = 0.48$, $< L^2 > = 0.31$ | Xtriage |
| Estimated twinning fraction | No twinning to report. | Xtriage |
| $F_o$,$F_c$ correlation | 0.89 | EDS |
| Total number of atoms | 6141 | wwPDB-VP |
| Average B, all atoms (Å$^2$) | 119.0 | wwPDB-VP |

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.16% 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

## 5.1 Standard geometry

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

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 | 0/2062 | 0.45 | 0/2758 |
| 1 | B | 0.24 | 0/2062 | 0.44 | 0/2758 |
| 1 | C | 0.24 | 0/2062 | 0.43 | 0/2758 |
| All | All | 0.24 | 0/6186 | 0.44 | 0/8274 |

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 | 14 |
| 1 | B | 0 | 13 |
| 1 | C | 0 | 10 |
| All | All | 0 | 37 |

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (37) planarity outliers are listed below:

| Mol | Chain | Res | Type | Group |
|---|---|---|---|---|
| 1 | A | 139 | VAL | Peptide |
| 1 | A | 223 | PHE | Peptide |
| 1 | A | 224 | VAL | Peptide |
| 1 | A | 227 | ASN | Peptide |
| 1 | A | 257 | TYR | Peptide |
| 1 | A | 270 | PHE | Peptide |
| 1 | A | 287 | LYS | Peptide |

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| Mol | Chain | Res | Type | Group |
|---|---|---|---|---|
| 1 | A | 39 | ILE | Peptide |
| 1 | A | 50 | LYS | Peptide |
| 1 | A | 94 | SER | Peptide |
| 1 | A | 95 | ILE | Peptide |
| 1 | A | 96 | SER | Peptide |
| 1 | A | 97 | SER | Peptide |
| 1 | A | 98 | VAL | Peptide |
| 1 | B | 111 | LYS | Peptide |
| 1 | B | 139 | VAL | Peptide |
| 1 | B | 148 | VAL | Peptide |
| 1 | B | 237 | ILE | Peptide |
| 1 | B | 258 | LYS | Peptide |
| 1 | B | 270 | PHE | Peptide |
| 1 | B | 271 | MET | Peptide |
| 1 | B | 39 | ILE | Peptide |
| 1 | B | 94 | SER | Peptide |
| 1 | B | 95 | ILE | Peptide |
| 1 | B | 96 | SER | Peptide |
| 1 | B | 97 | SER | Peptide |
| 1 | B | 98 | VAL | Peptide |
| 1 | C | 148 | VAL | Peptide |
| 1 | C | 184 | GLU | Peptide |
| 1 | C | 237 | ILE | Peptide |
| 1 | C | 270 | PHE | Peptide |
| 1 | C | 287 | LYS | Peptide |
| 1 | C | 94 | SER | Peptide |
| 1 | C | 95 | ILE | Peptide |
| 1 | C | 96 | SER | Peptide |
| 1 | C | 97 | SER | Peptide |
| 1 | C | 98 | VAL | 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 | 2036 | 0 | 2138 | 37 | 0 |
| 1 | B | 2036 | 0 | 2138 | 68 | 0 |
| 1 | C | 2036 | 0 | 2138 | 38 | 0 |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|---|---|---|---|---|---|---|
| 2 | B | 7 | 0 | 10 | 0 | 0 |
| 2 | C | 7 | 0 | 10 | 0 | 0 |
| 3 | A | 3 | 0 | 0 | 0 | 0 |
| 3 | B | 6 | 0 | 0 | 0 | 0 |
| 3 | C | 10 | 0 | 0 | 0 | 0 |
| All | All | 6141 | 0 | 6434 | 142 | 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 11.

All (142) 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:B:193:LYS:HD2 | 1:B:199:ARG:HE | 1.20 | 1.04 |
| 1:B:193:LYS:HD2 | 1:B:199:ARG:NE | 1.77 | 0.98 |
| 1:B:95:ILE:HA | 1:B:97:SER:H | 1.46 | 0.79 |
| 1:B:41:LYS:HB2 | 1:B:156:GLU:HG2 | 1.64 | 0.79 |
| 1:C:95:ILE:HA | 1:C:97:SER:H | 1.48 | 0.78 |
| 1:A:225:SER:OG | 1:A:226:ARG:NH1 | 2.21 | 0.74 |
| 1:A:41:LYS:HB2 | 1:A:156:GLU:HG3 | 1.70 | 0.73 |
| 1:C:270:PHE:HE1 | 1:C:287:LYS:HD3 | 1.55 | 0.70 |
| 1:C:39:ILE:HB | 1:C:41:LYS:HE3 | 1.74 | 0.70 |
| 1:C:41:LYS:HB2 | 1:C:156:GLU:HG3 | 1.74 | 0.69 |
| 1:A:95:ILE:HA | 1:A:97:SER:H | 1.55 | 0.69 |
| 1:A:39:ILE:HB | 1:A:41:LYS:HE3 | 1.75 | 0.68 |
| 1:B:215:ARG:HH21 | 1:B:294:LEU:HD12 | 1.58 | 0.68 |
| 1:B:147:PRO:O | 1:B:148:VAL:HG12 | 1.96 | 0.65 |
| 1:C:147:PRO:O | 1:C:148:VAL:HG12 | 1.97 | 0.65 |
| 1:C:106:ARG:NH1 | 1:C:110:GLU:O | 2.30 | 0.65 |
| 1:B:39:ILE:HB | 1:B:41:LYS:HE3 | 1.80 | 0.64 |
| 1:B:233:TYR:CE1 | 1:B:261:VAL:HG12 | 2.33 | 0.64 |
| 1:A:196:LEU:HB2 | 1:A:199:ARG:HB2 | 1.80 | 0.64 |
| 1:B:225:SER:HB3 | 1:B:260:LEU:HD13 | 1.81 | 0.62 |
| 1:C:233:TYR:OH | 1:C:256:GLY:O | 2.17 | 0.62 |
| 1:A:98:VAL:HG13 | 1:A:120:ALA:HA | 1.81 | 0.62 |
| 1:B:210:GLU:OE2 | 1:B:221:ARG:NH2 | 2.30 | 0.61 |
| 1:B:287:LYS:HD2 | 1:B:290:LYS:HG2 | 1.83 | 0.61 |
| 1:C:229:ARG:HG3 | 1:C:230:GLN:HG2 | 1.83 | 0.60 |
| 1:A:194:SER:O | 1:A:199:ARG:NH1 | 2.34 | 0.60 |
| 1:C:51:ASP:HB3 | 1:C:135:THR:H | 1.67 | 0.60 |
| 1:C:178:GLU:HG2 | 1:C:194:SER:HA | 1.83 | 0.59 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:B:248:LYS:HA | 1:B:251:LEU:HB2 | 1.84 | 0.59 |
| 1:C:98:VAL:HG13 | 1:C:120:ALA:HA | 1.86 | 0.58 |
| 1:B:175:PRO:O | 1:B:199:ARG:NH1 | 2.36 | 0.58 |
| 1:B:157:ASP:OD1 | 1:B:160:ARG:NH2 | 2.37 | 0.58 |
| 1:B:51:ASP:HB3 | 1:B:135:THR:H | 1.68 | 0.58 |
| 1:A:51:ASP:HB3 | 1:A:135:THR:H | 1.68 | 0.57 |
| 1:C:23:LEU:HD22 | 1:C:137:VAL:HG21 | 1.87 | 0.57 |
| 1:C:225:SER:HB3 | 1:C:228:GLN:HE22 | 1.70 | 0.57 |
| 1:C:186:ARG:HH12 | 1:C:192:LYS:HD2 | 1.71 | 0.56 |
| 1:B:23:LEU:HD22 | 1:B:137:VAL:HG21 | 1.87 | 0.55 |
| 1:B:99:SER:HB3 | 1:B:144:PHE:HD1 | 1.71 | 0.55 |
| 1:B:99:SER:HB3 | 1:B:144:PHE:CD1 | 2.41 | 0.55 |
| 1:A:209:GLU:H | 1:A:225:SER:HB3 | 1.72 | 0.54 |
| 1:A:23:LEU:HD22 | 1:A:137:VAL:HG21 | 1.88 | 0.54 |
| 1:B:154:LYS:HG3 | 1:B:155:LYS:H | 1.72 | 0.54 |
| 1:C:269:PRO:HD2 | 1:C:270:PHE:CE2 | 2.43 | 0.54 |
| 1:A:218:ILE:HD12 | 1:A:267:LEU:HG | 1.89 | 0.54 |
| 1:A:207:LYS:O | 1:A:226:ARG:NH2 | 2.36 | 0.54 |
| 1:B:269:PRO:HD2 | 1:B:270:PHE:CE2 | 2.42 | 0.54 |
| 1:B:178:GLU:HG2 | 1:B:194:SER:HA | 1.91 | 0.53 |
| 1:B:283:VAL:N | 1:B:284:ASN:OD1 | 2.42 | 0.53 |
| 1:B:233:TYR:CD1 | 1:B:259:THR:HG23 | 2.44 | 0.53 |
| 1:C:220:LEU:HD12 | 1:C:298:LEU:HD13 | 1.92 | 0.52 |
| 1:A:56:ILE:HD13 | 1:A:64:VAL:HG21 | 1.93 | 0.51 |
| 1:A:212:TYR:HD1 | 1:A:221:ARG:HG2 | 1.76 | 0.51 |
| 1:C:228:GLN:O | 1:C:230:GLN:N | 2.44 | 0.50 |
| 1:C:242:ILE:HG22 | 1:C:244:ASN:H | 1.77 | 0.50 |
| 1:B:258:LYS:O | 1:B:258:LYS:HG2 | 2.12 | 0.49 |
| 1:B:242:ILE:HG22 | 1:B:244:ASN:H | 1.77 | 0.49 |
| 1:A:235:VAL:HG13 | 1:A:242:ILE:HG13 | 1.94 | 0.49 |
| 1:B:234:TYR:HB2 | 1:B:262:VAL:HG13 | 1.95 | 0.49 |
| 1:C:235:VAL:HG23 | 1:C:263:LEU:HD22 | 1.94 | 0.49 |
| 1:A:226:ARG:HB2 | 1:A:228:GLN:OE1 | 2.12 | 0.49 |
| 1:B:20:VAL:HG23 | 1:B:166:LEU:HD23 | 1.95 | 0.49 |
| 1:B:270:PHE:CD1 | 1:B:286:LEU:HD12 | 2.49 | 0.48 |
| 1:B:16:PRO:HB3 | 1:B:47:ILE:HD11 | 1.95 | 0.48 |
| 1:B:41:LYS:HE2 | 1:B:45:ARG:HH12 | 1.78 | 0.48 |
| 1:B:56:ILE:HD13 | 1:B:64:VAL:HG21 | 1.96 | 0.48 |
| 1:B:98:VAL:HG12 | 1:B:120:ALA:HA | 1.95 | 0.48 |
| 1:A:181:LEU:HB3 | 1:A:191:LEU:HA | 1.96 | 0.47 |
| 1:C:175:PRO:O | 1:C:199:ARG:NH1 | 2.47 | 0.47 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:A:225:SER:O | 1:A:226:ARG:HG2 | 2.14 | 0.47 |
| 1:B:294:LEU:HA | 1:B:297:GLU:HG2 | 1.96 | 0.47 |
| 1:B:215:ARG:HB2 | 1:B:294:LEU:HD21 | 1.97 | 0.47 |
| 1:B:212:TYR:HD1 | 1:B:221:ARG:HG2 | 1.80 | 0.47 |
| 1:B:226:ARG:C | 1:B:258:LYS:HE2 | 2.35 | 0.46 |
| 1:B:233:TYR:CD1 | 1:B:261:VAL:HG12 | 2.50 | 0.46 |
| 1:B:96:SER:HA | 1:B:98:VAL:O | 2.16 | 0.46 |
| 1:A:178:GLU:HG2 | 1:A:194:SER:HA | 1.97 | 0.46 |
| 1:B:245:LYS:HA | 1:B:248:LYS:HE3 | 1.97 | 0.46 |
| 1:C:226:ARG:HD3 | 1:C:226:ARG:HA | 1.73 | 0.46 |
| 1:B:233:TYR:CG | 1:B:259:THR:HG23 | 2.51 | 0.46 |
| 1:B:218:ILE:HD12 | 1:B:294:LEU:HD22 | 1.98 | 0.45 |
| 1:A:269:PRO:HD2 | 1:A:270:PHE:CE2 | 2.51 | 0.45 |
| 1:C:41:LYS:HE2 | 1:C:45:ARG:HH12 | 1.81 | 0.45 |
| 1:B:172:LEU:HD11 | 1:B:203:VAL:HG11 | 1.97 | 0.45 |
| 1:B:285:ILE:O | 1:B:286:LEU:HD13 | 2.17 | 0.45 |
| 1:B:156:GLU:OE2 | 1:B:160:ARG:NH1 | 2.50 | 0.45 |
| 1:C:104:ARG:HB3 | 1:C:115:GLU:HB2 | 1.98 | 0.45 |
| 1:C:159:GLU:HA | 1:C:162:LYS:HD3 | 1.98 | 0.45 |
| 1:C:254:VAL:HG11 | 1:C:296:ARG:HA | 1.98 | 0.45 |
| 1:C:99:SER:HB3 | 1:C:144:PHE:CD1 | 2.51 | 0.44 |
| 1:C:240:ARG:HD2 | 1:C:272:VAL:HG21 | 2.00 | 0.44 |
| 1:B:229:ARG:HE | 1:B:230:GLN:HG2 | 1.82 | 0.44 |
| 1:A:198:GLU:HG2 | 1:A:201:GLU:HG3 | 2.00 | 0.44 |
| 1:A:271:MET:HG3 | 1:A:272:VAL:H | 1.82 | 0.44 |
| 1:B:154:LYS:HA | 1:B:154:LYS:HD2 | 1.85 | 0.44 |
| 1:B:21:LYS:O | 1:B:25:GLU:HB2 | 2.17 | 0.44 |
| 1:A:159:GLU:HA | 1:A:162:LYS:HD3 | 1.99 | 0.44 |
| 1:B:218:ILE:HB | 1:B:294:LEU:CD2 | 2.48 | 0.44 |
| 1:B:104:ARG:NH1 | 1:B:115:GLU:OE1 | 2.51 | 0.44 |
| 1:B:233:TYR:HE2 | 1:B:252:ARG:HG3 | 1.83 | 0.43 |
| 1:B:237:ILE:HD13 | 1:B:265:ALA:HB3 | 2.00 | 0.43 |
| 1:A:269:PRO:HD2 | 1:A:270:PHE:CD2 | 2.53 | 0.43 |
| 1:C:186:ARG:HA | 1:C:191:LEU:HD12 | 2.00 | 0.43 |
| 1:B:212:TYR:CD1 | 1:B:221:ARG:HG2 | 2.53 | 0.43 |
| 1:B:118:VAL:HG12 | 1:B:123:ILE:HG12 | 2.01 | 0.43 |
| 1:B:233:TYR:HD2 | 1:B:248:LYS:HB2 | 1.83 | 0.43 |
| 1:B:196:LEU:HD12 | 1:B:199:ARG:HG3 | 2.00 | 0.43 |
| 1:C:123:ILE:HG22 | 1:C:125:GLY:H | 1.83 | 0.43 |
| 1:C:177:VAL:O | 1:C:199:ARG:NH2 | 2.51 | 0.43 |
| 1:B:225:SER:H | 1:B:260:LEU:HD22 | 1.84 | 0.43 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:B:233:TYR:CE1 | 1:B:259:THR:HG23 | 2.54 | 0.42 |
| 1:A:229:ARG:HA | 1:A:230:GLN:HA | 1.64 | 0.42 |
| 1:A:118:VAL:HG12 | 1:A:123:ILE:HA | 2.02 | 0.42 |
| 1:B:232:LYS:HB3 | 1:B:234:TYR:CE1 | 2.55 | 0.42 |
| 1:C:197:LYS:HE2 | 1:A:215:ARG:HH21 | 1.84 | 0.42 |
| 1:A:145:ASN:OD1 | 1:A:146:LEU:HD23 | 2.20 | 0.42 |
| 1:C:20:VAL:HG23 | 1:C:166:LEU:HD23 | 2.02 | 0.42 |
| 1:C:21:LYS:O | 1:C:25:GLU:HB2 | 2.20 | 0.42 |
| 1:A:237:ILE:HG12 | 1:A:265:ALA:HB3 | 2.02 | 0.42 |
| 1:B:269:PRO:HD2 | 1:B:270:PHE:CD2 | 2.55 | 0.42 |
| 1:B:258:LYS:HB3 | 1:B:258:LYS:HE3 | 1.75 | 0.41 |
| 1:C:96:SER:HA | 1:C:98:VAL:O | 2.19 | 0.41 |
| 1:A:21:LYS:O | 1:A:25:GLU:HB2 | 2.20 | 0.41 |
| 1:B:233:TYR:CD2 | 1:B:248:LYS:HB2 | 2.56 | 0.41 |
| 1:B:267:LEU:HA | 1:B:268:PRO:HD3 | 1.93 | 0.41 |
| 1:C:267:LEU:HA | 1:C:268:PRO:HD3 | 1.88 | 0.41 |
| 1:A:106:ARG:HB3 | 1:A:133:VAL:HA | 2.02 | 0.41 |
| 1:A:147:PRO:C | 1:A:149:ARG:H | 2.24 | 0.41 |
| 1:B:293:GLU:OE1 | 1:B:296:ARG:NE | 2.49 | 0.41 |
| 1:B:46:LEU:HD22 | 1:B:140:ARG:HH21 | 1.86 | 0.41 |
| 1:B:184:GLU:OE1 | 1:B:184:GLU:N | 2.54 | 0.41 |
| 1:B:225:SER:N | 1:B:260:LEU:HD22 | 2.36 | 0.41 |
| 1:C:184:GLU:OE1 | 1:C:184:GLU:N | 2.54 | 0.41 |
| 1:B:232:LYS:HE3 | 1:B:232:LYS:HB2 | 1.90 | 0.41 |
| 1:C:56:ILE:HD13 | 1:C:64:VAL:HG21 | 2.03 | 0.41 |
| 1:A:34:LYS:HB2 | 1:A:52:ASN:HB2 | 2.03 | 0.41 |
| 1:A:289:ARG:HD2 | 1:A:289:ARG:H | 1.85 | 0.41 |
| 1:B:128:ARG:HA | 1:B:128:ARG:HD2 | 1.87 | 0.41 |
| 1:A:254:VAL:HG23 | 1:A:255:PHE:CD1 | 2.56 | 0.40 |
| 1:A:226:ARG:O | 1:A:259:THR:HG23 | 2.21 | 0.40 |
| 1:C:271:MET:HB2 | 1:C:285:ILE:O | 2.22 | 0.40 |
| 1:A:242:ILE:HG21 | 1:A:284:ASN:HD21 | 1.87 | 0.40 |

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 | 237/308 (77%) | 218 (92%) | 15 (6%) | 4 (2%) | 9 41 |
| 1 | B | 237/308 (77%) | 218 (92%) | 17 (7%) | 2 (1%) | 19 57 |
| 1 | C | 237/308 (77%) | 218 (92%) | 17 (7%) | 2 (1%) | 19 57 |
| All | All | 711/924 (77%) | 654 (92%) | 49 (7%) | 8 (1%) | 14 50 |

All (8) Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | C | 148 | VAL |
| 1 | A | 148 | VAL |
| 1 | B | 148 | VAL |
| 1 | A | 226 | ARG |
| 1 | C | 269 | PRO |
| 1 | A | 269 | PRO |
| 1 | B | 269 | PRO |
| 1 | A | 199 | ARG |

### 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 | 227/278 (82%) | 222 (98%) | 5 (2%) | 52 77 |
| 1 | B | 227/278 (82%) | 222 (98%) | 5 (2%) | 52 77 |
| 1 | C | 227/278 (82%) | 219 (96%) | 8 (4%) | 36 67 |
| All | All | 681/834 (82%) | 663 (97%) | 18 (3%) | 46 74 |

All (18) residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | C | 21 | LYS |

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| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | C | 93 | TYR |
| 1 | C | 154 | LYS |
| 1 | C | 186 | ARG |
| 1 | C | 197 | LYS |
| 1 | C | 207 | LYS |
| 1 | C | 243 | GLN |
| 1 | C | 271 | MET |
| 1 | A | 93 | TYR |
| 1 | A | 197 | LYS |
| 1 | A | 207 | LYS |
| 1 | A | 226 | ARG |
| 1 | A | 257 | TYR |
| 1 | B | 21 | LYS |
| 1 | B | 93 | TYR |
| 1 | B | 186 | ARG |
| 1 | B | 197 | LYS |
| 1 | B | 258 | LYS |

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)

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 | $\#\|Z\| > 2$ |
| 2 | PEG | C | 401 | - | 6,6,6 | 0.45 | 0 | 5,5,5 | 0.33 | 0 |
| 2 | PEG | B | 401 | - | 6,6,6 | 0.42 | 0 | 5,5,5 | 0.36 | 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 |
|---|---|---|---|---|---|---|---|
| 2 | PEG | C | 401 | - | - | 2/4/4/4 | - |
| 2 | PEG | B | 401 | - | - | 1/4/4/4 | - |

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

| Mol | Chain | Res | Type | Atoms |
|---|---|---|---|---|
| 2 | C | 401 | PEG | O1-C1-C2-O2 |
| 2 | C | 401 | PEG | C1-C2-O2-C3 |
| 2 | B | 401 | PEG | C1-C2-O2-C3 |

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

## 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 | 247/308 (80%) | 0.68 | 23 (9%) 8 11 | 81, 127, 185, 238 | 0 |
| 1 | B | 247/308 (80%) | 0.84 | 41 (16%) 1 2 | 65, 129, 223, 261 | 0 |
| 1 | C | 247/308 (80%) | 0.29 | 5 (2%) 65 63 | 52, 78, 127, 187 | 0 |
| All | All | 741/924 (80%) | 0.60 | 69 (9%) 8 11 | 52, 111, 199, 261 | 0 |

All (69) RSRZ outliers are listed below:

| Mol | Chain | Res | Type | RSRZ |
|---|---|---|---|---|
| 1 | B | 218 | ILE | 6.0 |
| 1 | A | 284 | ASN | 5.0 |
| 1 | B | 223 | PHE | 5.0 |
| 1 | B | 261 | VAL | 4.7 |
| 1 | B | 260 | LEU | 4.5 |
| 1 | B | 262 | VAL | 4.0 |
| 1 | B | 285 | ILE | 3.9 |
| 1 | B | 144 | PHE | 3.8 |
| 1 | B | 233 | TYR | 3.7 |
| 1 | A | 224 | VAL | 3.7 |
| 1 | B | 267 | LEU | 3.6 |
| 1 | B | 38 | GLU | 3.5 |
| 1 | B | 181 | LEU | 3.5 |
| 1 | B | 145 | ASN | 3.5 |
| 1 | B | 268 | PRO | 3.4 |
| 1 | B | 263 | LEU | 3.4 |
| 1 | B | 290 | LYS | 3.4 |
| 1 | A | 291 | PHE | 3.3 |
| 1 | B | 291 | PHE | 3.3 |
| 1 | B | 212 | TYR | 3.3 |
| 1 | C | 101 | PHE | 3.3 |
| 1 | A | 139 | VAL | 3.2 |
| 1 | B | 247 | LEU | 3.2 |

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| Mol | Chain | Res | Type | RSRZ |
|---|---|---|---|---|
| 1 | B | 220 | LEU | 3.2 |
| 1 | A | 257 | TYR | 3.1 |
| 1 | B | 211 | LEU | 3.1 |
| 1 | B | 46 | LEU | 3.0 |
| 1 | A | 250 | PHE | 3.0 |
| 1 | B | 213 | ALA | 2.9 |
| 1 | A | 242 | ILE | 2.9 |
| 1 | B | 255 | PHE | 2.8 |
| 1 | A | 101 | PHE | 2.8 |
| 1 | A | 251 | LEU | 2.8 |
| 1 | A | 66 | LEU | 2.7 |
| 1 | B | 182 | PHE | 2.7 |
| 1 | B | 296 | ARG | 2.7 |
| 1 | A | 261 | VAL | 2.7 |
| 1 | A | 14 | GLU | 2.6 |
| 1 | C | 257 | TYR | 2.6 |
| 1 | B | 251 | LEU | 2.6 |
| 1 | B | 142 | LEU | 2.6 |
| 1 | B | 269 | PRO | 2.6 |
| 1 | B | 237 | ILE | 2.5 |
| 1 | B | 221 | ARG | 2.5 |
| 1 | A | 298 | LEU | 2.5 |
| 1 | B | 219 | THR | 2.5 |
| 1 | A | 247 | LEU | 2.4 |
| 1 | A | 230 | GLN | 2.4 |
| 1 | C | 229 | ARG | 2.4 |
| 1 | B | 186 | ARG | 2.4 |
| 1 | B | 272 | VAL | 2.3 |
| 1 | B | 47 | ILE | 2.3 |
| 1 | B | 143 | PHE | 2.3 |
| 1 | B | 124 | LEU | 2.3 |
| 1 | B | 163 | VAL | 2.2 |
| 1 | A | 267 | LEU | 2.2 |
| 1 | C | 291 | PHE | 2.2 |
| 1 | A | 179 | PHE | 2.2 |
| 1 | A | 116 | ILE | 2.2 |
| 1 | A | 103 | LEU | 2.2 |
| 1 | C | 148 | VAL | 2.1 |
| 1 | A | 233 | TYR | 2.1 |
| 1 | A | 260 | LEU | 2.1 |
| 1 | B | 37 | VAL | 2.1 |
| 1 | B | 191 | LEU | 2.0 |

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| Mol | Chain | Res | Type | RSRZ |
|---|---|---|---|---|
| 1 | B | 229 | ARG | 2.0 |
| 1 | A | 186 | ARG | 2.0 |
| 1 | A | 48 | ARG | 2.0 |
| 1 | B | 39 | ILE | 2.0 |

## 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 |
|---|---|---|---|---|---|---|---|---|
| 2 | PEG | B | 401 | 7/7 | 0.69 | 0.54 | 117,138,145,146 | 0 |
| 2 | PEG | C | 401 | 7/7 | 0.87 | 0.33 | 133,136,143,144 | 0 |

## 6.5 Other polymers (i)

There are no such residues in this entry.