# Full wwPDB X-ray Structure Validation Report ⓘ

Apr 30, 2024 – 07:14 PM JST

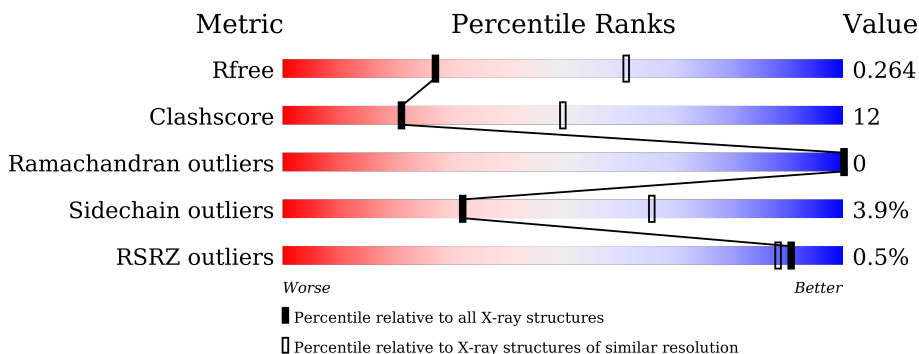|            |   |                                                           |
|-----------:|:-:|:----------------------------------------------------------|
| PDB ID     | : | 8WTC                                                      |
| Title      | : | Crystal structure of McsB kinase domain complexed with McsA. |
| Authors    | : | Arifuzzaman, M.; Kwon, E.; Kim, D.Y.                      |
| Deposited on | : | 2023-10-18                                              |
| Resolution | : | 2.80 Å(reported)                                         |

# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:
*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.80 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 | | 0.264 |
| Clashscore | | 12 |
| Ramachandran outliers | | 0 |
| Sidechain outliers | | 3.9% |
| RSRZ outliers | | 0.5% |

*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$_{free}$ | 130704 | 3140 (2.80-2.80) |
| Clashscore | 141614 | 3569 (2.80-2.80) |
| Ramachandran outliers | 138981 | 3498 (2.80-2.80) |
| Sidechain outliers | 138945 | 3500 (2.80-2.80) |
| RSRZ outliers | 127900 | 3078 (2.80-2.80) |

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 | 243 | 67% 26% • 5% |
| 1 | C | 243 | 68% 25% • 5% |
| 2 | B | 187 | % 40% 13% • 47% |
| 2 | D | 187 | % 38% 13% • 47% |

## 2 Entry composition ⓘ

There are 3 unique types of molecules in this entry. The entry contains 5265 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 Protein-arginine kinase.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|---|---|---|---|---------|---------|-------|
| 1 | A | 231 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1829 | 1146 | 322 | 353 | 8 | | | |
| 1 | C | 231 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1829 | 1146 | 322 | 353 | 8 | | | |

There are 4 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|---------|-----------|
| A | 16 | GLY | - | expression tag | UNP P37570 |
| A | 17 | SER | - | expression tag | UNP P37570 |
| C | 16 | GLY | - | expression tag | UNP P37570 |
| C | 17 | SER | - | expression tag | UNP P37570 |

- Molecule 2 is a protein called Protein-arginine kinase activator protein.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|---|---|---|---|---------|---------|-------|
| 2 | B | 100 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 807 | 505 | 156 | 140 | 6 | | | |
| 2 | D | 99 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 798 | 499 | 154 | 139 | 6 | | | |

There are 4 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|---------|-----------|
| B | -1 | GLY | - | expression tag | UNP P37569 |
| B | 0 | SER | - | expression tag | UNP P37569 |
| D | -1 | GLY | - | expression tag | UNP P37569 |
| D | 0 | SER | - | expression tag | UNP P37569 |

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

| Mol | Chain | Residues | Atoms | | ZeroOcc | AltConf |
|---|---|---|---|---|---|---|
| 3 | B | 1 | Total 1 | Zn 1 | 1 | 0 |
| 3 | D | 1 | Total 1 | Zn 1 | 1 | 0 |

# 3 Residue-property plots ⓘ

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.
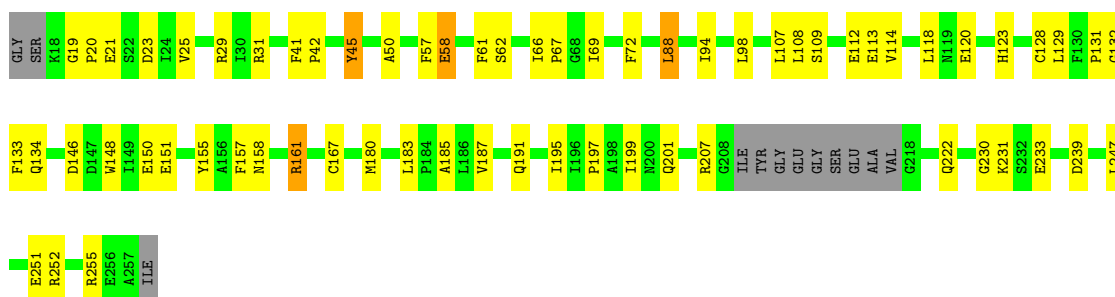
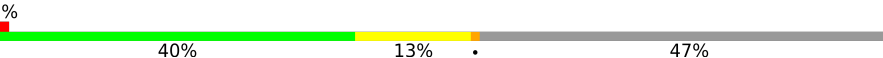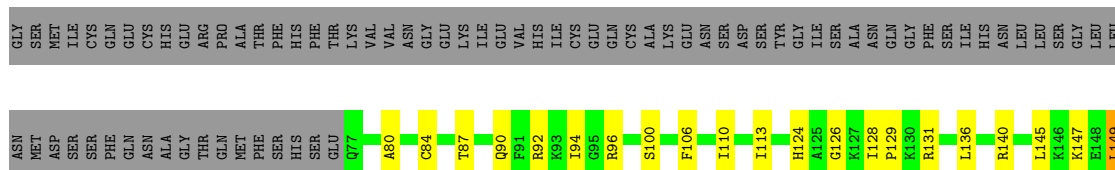• Molecule 1: Protein-arginine kinase



Chain A:
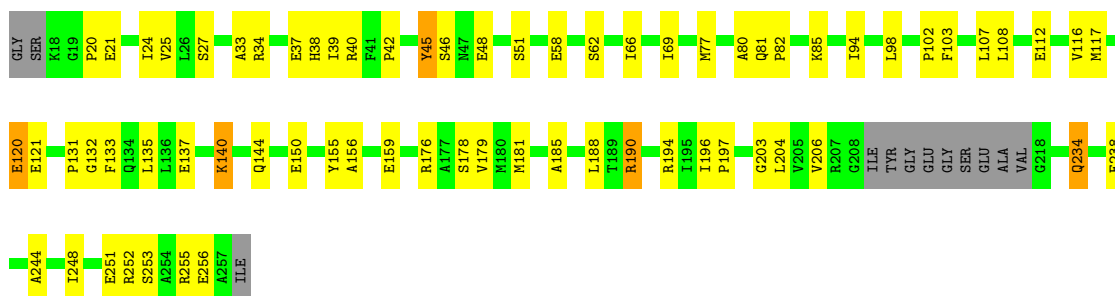
• Molecule 1: Protein-arginine kinase



Chain C:

• Molecule 2: Protein-arginine kinase activator protein



Chain B:

I153 H163 V164 Q167 Q173 K176 SER THR ASP SER GLU GLU GLU GLN GLU

• Molecule 2: Protein-arginine kinase activator protein

Chain D:

GLY SER MET ILE CYS GLN GLU CYS HIS GLU ARG PRO ALA THR PHE HIS PHE THR LYS VAL VAL ASN GLY GLU LYS ILE GLU VAL HIS ILE CYS GLU GLN CYS ALA LYS GLU ASN SER ASP SER TYR GLY ILE SER ALA ASN GLN GLY PHE SER ILE HIS ASN LEU LEU SER GLY LEU LEU

ASN MET ASP SER PHE GLN ASN ALA GLY THR GLN MET PHE SER HIS SER GLU Q77 I78 K83 C84 G85 M86 T87 F88 Q89 C99 S100 E101 C102 Y103 K104 T105 F106 M109 I110 T111 P112 I113 L114 N121 H124 K127 I128 R131 I132 G133 G134 N135 D143 M144

I153 R165 R169 Q173 S174 L175 LYS SER THR ASP SER GLU GLU GLU GLN GLU

# 4 Data and refinement statistics ⓘ

| Property | Value | Source |
|---|---|---|
| Space group | C 1 2 1 | Depositor |
| Cell constants<br>a, b, c, $\alpha$, $\beta$, $\gamma$ | 188.10Å     74.21Å     79.94Å<br>90.00°     100.84°     90.00° | Depositor |
| Resolution (Å) | 43.45   –   2.80<br>43.45   –   2.80 | Depositor<br>EDS |
| % Data completeness<br>(in resolution range) | 95.4 (43.45-2.80)<br>95.4 (43.45-2.80) | Depositor<br>EDS |
| $R_{merge}$ | 0.10 | Depositor |
| $R_{sym}$ | (Not available) | Depositor |
| $< I/\sigma(I) >$ [1] | 2.10 (at 2.81Å) | Xtriage |
| Refinement program | PHENIX (1.19rc5_4047: ???) | Depositor |
| R, $R_{free}$ | 0.216   ,   0.266<br>0.216   ,   0.264 | Depositor<br>DCC |
| $R_{free}$ test set | 1970 reflections (7.69%) | wwPDB-VP |
| Wilson B-factor (Å$^2$) | 63.4 | Xtriage |
| Anisotropy | 0.254 | Xtriage |
| Bulk solvent $k_{sol}$(e/Å$^3$), $B_{sol}$(Å$^2$) | 0.30 , 35.2 | EDS |
| L-test for twinning[2] | $< |L| > = 0.49, < L^2 > = 0.33$ | Xtriage |
| Estimated twinning fraction | No twinning to report. | Xtriage |
| $F_o,F_c$ correlation | 0.93 | EDS |
| Total number of atoms | 5265 | wwPDB-VP |
| Average B, all atoms (Å$^2$) | 62.0 | wwPDB-VP |

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.67% of the height of the origin peak. No significant pseudotranslation is detected.*

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[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: ZN

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 | 0.52 | 0/1856 | 0.73 | 0/2507 |
| 1 | C | 0.55 | 0/1856 | 0.72 | 0/2507 |
| 2 | B | 0.53 | 0/821 | 0.72 | 0/1096 |
| 2 | D | 0.58 | 1/812 (0.1%) | 0.71 | 0/1085 |
| All | All | 0.54 | 1/5345 (0.0%) | 0.72 | 0/7195 |

All (1) bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|---|---|---|---|---|---|---|---|
| 2 | D | 102 | CYS | CB-SG | 8.82 | 1.97 | 1.82 |

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2    Too-close contacts ⓘ

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 | 1829 | 0 | 1820 | 48 | 0 |
| 1 | C | 1829 | 0 | 1820 | 50 | 0 |
| 2 | B | 807 | 0 | 823 | 18 | 0 |
| 2 | D | 798 | 0 | 809 | 18 | 0 |
| 3 | B | 1 | 0 | 0 | 0 | 0 |
| 3 | D | 1 | 0 | 0 | 0 | 0 |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| All | All | 5265 | 0 | 5272 | 127 | 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 12.

All (127) 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:25:VAL:HG21 | 1:A:133:PHE:HB2 | 1.59 | 0.83 |
| 1:C:42:PRO:HA | 1:C:45:TYR:CD1 | 2.16 | 0.78 |
| 1:A:94:ILE:HB | 1:A:98:LEU:HD23 | 1.65 | 0.78 |
| 1:A:21:GLU:HG3 | 1:A:252:ARG:HH21 | 1.49 | 0.77 |
| 1:A:108:LEU:HD21 | 1:A:112:GLU:HG2 | 1.66 | 0.76 |
| 1:C:42:PRO:HA | 1:C:45:TYR:CE1 | 2.22 | 0.74 |
| 1:C:132:GLY:H | 1:C:134:GLN:HE21 | 1.37 | 0.72 |
| 1:A:102:PRO:HD3 | 2:D:89:GLN:HG2 | 1.72 | 0.71 |
| 2:D:165:ARG:HD2 | 2:D:169:ARG:HH11 | 1.55 | 0.71 |
| 2:B:80:ALA:HB2 | 2:B:87:THR:HG22 | 1.73 | 0.69 |
| 1:C:88:LEU:HB3 | 1:C:94:ILE:HG12 | 1.75 | 0.69 |
| 1:A:150:GLU:OE2 | 2:B:129:PRO:HB2 | 1.92 | 0.68 |
| 1:A:150:GLU:O | 2:B:131:ARG:NH2 | 2.27 | 0.67 |
| 1:C:23:ASP:OD1 | 1:C:252:ARG:NH1 | 2.28 | 0.67 |
| 1:A:98:LEU:HD22 | 1:A:117:MET:SD | 2.36 | 0.66 |
| 1:A:159:GLU:HB3 | 2:B:136:LEU:HD11 | 1.77 | 0.65 |
| 2:D:84:CYS:HB2 | 2:D:86:MET:H | 1.63 | 0.63 |
| 1:A:33:ALA:O | 1:A:34:ARG:HD3 | 1.99 | 0.63 |
| 2:D:165:ARG:HD2 | 2:D:169:ARG:NH1 | 2.16 | 0.61 |
| 1:C:185:ALA:HB3 | 1:C:251:GLU:OE2 | 2.01 | 0.61 |
| 1:C:183:LEU:O | 1:C:187:VAL:HG23 | 2.01 | 0.60 |
| 1:C:231:LYS:NZ | 1:C:239:ASP:OD2 | 2.30 | 0.60 |
| 2:B:149:LEU:O | 2:B:153:ILE:HG12 | 2.01 | 0.60 |
| 1:C:114:VAL:HG23 | 1:C:128:CYS:SG | 2.43 | 0.59 |
| 1:A:234:GLN:O | 1:A:238:GLU:HB2 | 2.02 | 0.59 |
| 1:C:29:ARG:NH1 | 1:C:31:ARG:CZ | 2.67 | 0.58 |
| 2:D:106:PHE:O | 2:D:110:ILE:HG13 | 2.02 | 0.58 |
| 1:C:29:ARG:NH2 | 1:C:222:GLN:HE22 | 2.02 | 0.57 |
| 2:B:90:GLN:O | 2:B:94:ILE:HG13 | 2.04 | 0.57 |
| 1:C:29:ARG:NH1 | 1:C:31:ARG:NH2 | 2.53 | 0.56 |
| 2:B:87:THR:OG1 | 2:B:90:GLN:HG3 | 2.05 | 0.56 |
| 1:C:72:PHE:HB3 | 1:C:107:LEU:HG | 1.88 | 0.56 |
| 1:A:80:ALA:HB3 | 1:A:85:LYS:HE3 | 1.88 | 0.55 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:A:20:PRO:HD2 | 1:A:132:GLY:HA3 | 1.88 | 0.55 |
| 1:A:81:GLN:HG3 | 1:A:82:PRO:HD2 | 1.88 | 0.55 |
| 1:C:148:TRP:O | 1:C:151:GLU:HG2 | 2.06 | 0.55 |
| 1:C:161:ARG:HG2 | 1:C:161:ARG:HH11 | 1.71 | 0.55 |
| 1:C:29:ARG:HH21 | 1:C:222:GLN:HE22 | 1.56 | 0.54 |
| 1:C:98:LEU:HD13 | 1:C:120:GLU:HB2 | 1.90 | 0.54 |
| 1:C:233:GLU:OE1 | 1:C:233:GLU:N | 2.26 | 0.54 |
| 1:A:137:GLU:OE1 | 1:A:137:GLU:N | 2.28 | 0.54 |
| 2:B:149:LEU:HB2 | 2:B:164:VAL:HG11 | 1.89 | 0.54 |
| 2:B:124:HIS:CE1 | 2:B:126:GLY:HA3 | 2.42 | 0.53 |
| 1:C:112:GLU:O | 1:C:113:GLU:HB2 | 2.09 | 0.53 |
| 1:A:137:GLU:H | 1:A:137:GLU:CD | 2.11 | 0.52 |
| 2:D:124:HIS:HE1 | 2:D:127:LYS:O | 1.91 | 0.52 |
| 1:C:150:GLU:O | 2:D:131:ARG:NH2 | 2.38 | 0.52 |
| 1:C:180:MET:HG2 | 1:C:222:GLN:HG3 | 1.92 | 0.51 |
| 1:A:66:ILE:CG2 | 1:A:69:ILE:HB | 2.41 | 0.51 |
| 1:C:20:PRO:HD2 | 1:C:132:GLY:HA3 | 1.93 | 0.51 |
| 1:C:66:ILE:HD12 | 1:C:67:PRO:HD2 | 1.93 | 0.50 |
| 1:A:107:LEU:HB3 | 1:A:116:VAL:HB | 1.94 | 0.50 |
| 2:D:88:PHE:CZ | 2:D:109:ASN:HB3 | 2.47 | 0.50 |
| 1:A:21:GLU:HG3 | 1:A:252:ARG:NH2 | 2.25 | 0.49 |
| 1:C:199:ILE:HD11 | 1:C:247:LEU:HD11 | 1.95 | 0.49 |
| 1:A:46:SER:OG | 1:A:48:GLU:OE1 | 2.29 | 0.49 |
| 1:C:23:ASP:OD2 | 1:C:255:ARG:NH1 | 2.46 | 0.49 |
| 1:C:21:GLU:HG3 | 1:C:252:ARG:NH2 | 2.27 | 0.49 |
| 1:A:24:ILE:HD11 | 1:A:255:ARG:HE | 1.78 | 0.48 |
| 2:D:77:GLN:CD | 2:D:78:ILE:H | 2.16 | 0.48 |
| 1:C:191:GLN:O | 1:C:195:ILE:HG13 | 2.14 | 0.48 |
| 1:A:140:LYS:O | 1:A:144:GLN:HG3 | 2.14 | 0.48 |
| 2:D:128:ILE:HG22 | 2:D:133:GLY:HA3 | 1.96 | 0.47 |
| 1:A:203:GLY:O | 1:A:204:LEU:HD23 | 2.14 | 0.47 |
| 1:C:197:PRO:O | 1:C:201:GLN:HG3 | 2.14 | 0.47 |
| 1:C:25:VAL:HG21 | 1:C:133:PHE:HB2 | 1.96 | 0.47 |
| 1:C:29:ARG:HH12 | 1:C:31:ARG:NH2 | 2.13 | 0.47 |
| 1:C:57:PHE:HA | 1:C:61:PHE:HD2 | 1.80 | 0.46 |
| 1:C:45:TYR:CE2 | 1:C:50:ALA:HB2 | 2.50 | 0.46 |
| 1:A:38:HIS:O | 1:A:39:ILE:HD13 | 2.16 | 0.46 |
| 1:A:66:ILE:HD12 | 1:A:66:ILE:HA | 1.86 | 0.46 |
| 2:D:110:ILE:HG22 | 2:D:114:LEU:HD13 | 1.96 | 0.46 |
| 2:D:109:ASN:O | 2:D:112:PRO:HD2 | 2.16 | 0.45 |
| 1:C:146:ASP:OD2 | 1:C:155:TYR:HE2 | 2.00 | 0.45 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:C:19:GLY:HA3 | 1:C:132:GLY:HA3 | 1.99 | 0.45 |
| 1:C:69:ILE:CG2 | 1:C:114:VAL:HG11 | 2.46 | 0.45 |
| 2:B:149:LEU:HB2 | 2:B:164:VAL:CG1 | 2.46 | 0.45 |
| 1:C:157:PHE:CG | 1:C:158:ASN:N | 2.85 | 0.45 |
| 2:D:83:LYS:HE3 | 2:D:99:CYS:SG | 2.56 | 0.45 |
| 1:A:196:ILE:HD12 | 1:A:206:VAL:HG11 | 1.99 | 0.44 |
| 1:A:244:ALA:O | 1:A:248:ILE:HG13 | 2.16 | 0.44 |
| 2:D:101:GLU:HA | 2:D:104:LYS:HZ3 | 1.82 | 0.44 |
| 1:A:42:PRO:HA | 1:A:45:TYR:CD1 | 2.53 | 0.44 |
| 1:C:157:PHE:CD1 | 1:C:158:ASN:N | 2.85 | 0.44 |
| 1:A:135:LEU:HD23 | 1:A:135:LEU:HA | 1.85 | 0.44 |
| 1:A:190:ARG:HD3 | 1:A:190:ARG:N | 2.33 | 0.44 |
| 1:C:230:GLY:HA3 | 2:D:121:ASN:OD1 | 2.18 | 0.44 |
| 2:B:145:LEU:HD21 | 2:B:167:GLN:HB3 | 2.00 | 0.43 |
| 1:A:253:SER:O | 1:A:256:GLU:HG2 | 2.18 | 0.43 |
| 1:C:207:ARG:HD3 | 1:C:207:ARG:HA | 1.86 | 0.43 |
| 1:A:121:GLU:HG3 | 2:B:96:ARG:HH21 | 1.84 | 0.43 |
| 1:A:77:MET:HG3 | 1:A:85:LYS:HE2 | 1.99 | 0.43 |
| 1:C:131:PRO:HD2 | 1:C:134:GLN:NE2 | 2.33 | 0.43 |
| 2:D:101:GLU:HA | 2:D:104:LYS:NZ | 2.33 | 0.43 |
| 1:A:185:ALA:N | 1:A:251:GLU:OE2 | 2.47 | 0.43 |
| 1:A:120:GLU:CD | 1:A:121:GLU:H | 2.20 | 0.43 |
| 1:C:41:PHE:N | 1:C:41:PHE:CD1 | 2.86 | 0.43 |
| 2:D:135:ASN:N | 2:D:135:ASN:OD1 | 2.52 | 0.42 |
| 1:A:48:GLU:H | 1:A:48:GLU:CD | 2.23 | 0.42 |
| 1:C:108:LEU:HD22 | 1:C:112:GLU:HA | 2.02 | 0.42 |
| 1:C:29:ARG:HD3 | 1:C:129:LEU:HD12 | 2.01 | 0.42 |
| 1:C:66:ILE:HG23 | 1:C:69:ILE:HB | 2.02 | 0.42 |
| 2:B:163:HIS:O | 2:B:167:GLN:HG3 | 2.20 | 0.42 |
| 1:A:176:ARG:HD3 | 1:A:176:ARG:HA | 1.91 | 0.42 |
| 2:B:110:ILE:O | 2:B:113:ILE:HB | 2.20 | 0.42 |
| 1:C:109:SER:OG | 1:C:114:VAL:HG12 | 2.20 | 0.42 |
| 1:C:118:LEU:HA | 1:C:123:HIS:O | 2.20 | 0.42 |
| 1:A:58:GLU:HA | 1:A:62:SER:HB2 | 2.02 | 0.42 |
| 2:B:147:LYS:C | 2:B:147:LYS:HD3 | 2.39 | 0.42 |
| 1:A:40:ARG:O | 1:A:45:TYR:HB3 | 2.20 | 0.41 |
| 2:B:106:PHE:O | 2:B:110:ILE:HG12 | 2.19 | 0.41 |
| 1:C:72:PHE:CE1 | 1:C:114:VAL:HG13 | 2.55 | 0.41 |
| 1:C:233:GLU:H | 1:C:233:GLU:CD | 2.14 | 0.41 |
| 2:D:89:GLN:H | 2:D:89:GLN:CD | 2.23 | 0.41 |
| 1:A:27:SER:HA | 1:A:131:PRO:O | 2.19 | 0.41 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:A:37:GLU:HA | 1:A:156:ALA:HB2 | 2.01 | 0.41 |
| 1:A:196:ILE:HB | 1:A:197:PRO:HD3 | 2.02 | 0.41 |
| 1:A:188:LEU:HD12 | 1:A:188:LEU:HA | 1.89 | 0.41 |
| 1:A:179:VAL:HG12 | 1:A:181:MET:HG3 | 2.03 | 0.41 |
| 1:A:251:GLU:O | 1:A:255:ARG:HG3 | 2.21 | 0.41 |
| 1:A:159:GLU:H | 1:A:159:GLU:CD | 2.24 | 0.40 |
| 1:A:103:PHE:CD2 | 1:A:103:PHE:N | 2.90 | 0.40 |
| 2:B:136:LEU:HD21 | 2:B:140:ARG:HH12 | 1.87 | 0.40 |
| 1:C:58:GLU:HA | 1:C:62:SER:HB2 | 2.03 | 0.40 |
| 1:C:161:ARG:HG2 | 1:C:161:ARG:NH1 | 2.36 | 0.40 |
| 1:A:155:TYR:HD1 | 1:A:155:TYR:HA | 1.77 | 0.40 |
| 2:B:128:ILE:HD12 | 2:B:128:ILE:HG23 | 1.82 | 0.40 |

There are no symmetry-related clashes.

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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 | 227/243 (93%) | 220 (97%) | 7 (3%) | 0 | 100 | 100 |
| 1 | C | 227/243 (93%) | 216 (95%) | 11 (5%) | 0 | 100 | 100 |
| 2 | B | 98/187 (52%) | 92 (94%) | 6 (6%) | 0 | 100 | 100 |
| 2 | D | 97/187 (52%) | 89 (92%) | 8 (8%) | 0 | 100 | 100 |
| All | All | 649/860 (76%) | 617 (95%) | 32 (5%) | 0 | 100 | 100 |

There are no Ramachandran outliers to report.

### 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 | 203/212 (96%) | 195 (96%) | 8 (4%) | 32 | 66 |
| 1 | C | 203/212 (96%) | 198 (98%) | 5 (2%) | 47 | 80 |
| 2 | B | 89/166 (54%) | 85 (96%) | 4 (4%) | 27 | 60 |
| 2 | D | 88/166 (53%) | 82 (93%) | 6 (7%) | 16 | 42 |
| All | All | 583/756 (77%) | 560 (96%) | 23 (4%) | 32 | 66 |

All (23) residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | A | 45 | TYR |
| 1 | A | 51 | SER |
| 1 | A | 120 | GLU |
| 1 | A | 140 | LYS |
| 1 | A | 178 | SER |
| 1 | A | 190 | ARG |
| 1 | A | 194 | ARG |
| 1 | A | 234 | GLN |
| 2 | B | 84 | CYS |
| 2 | B | 92 | ARG |
| 2 | B | 100 | SER |
| 2 | B | 149 | LEU |
| 1 | C | 45 | TYR |
| 1 | C | 58 | GLU |
| 1 | C | 88 | LEU |
| 1 | C | 161 | ARG |
| 1 | C | 167 | CYS |
| 2 | D | 77 | GLN |
| 2 | D | 84 | CYS |
| 2 | D | 104 | LYS |
| 2 | D | 143 | ASP |
| 2 | D | 144 | MET |
| 2 | D | 174 | SER |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 2 | B | 89 | GLN |
| 2 | B | 154 | HIS |
| 1 | C | 56 | GLN |
| 1 | C | 81 | GLN |
| 1 | C | 97 | ASN |
| 1 | C | 134 | GLN |
| 1 | C | 222 | GLN |
| 2 | D | 124 | HIS |

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

## 5.6 Ligand geometry ⓘ

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

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 ⓘ

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 | 231/243 (95%) | -0.27 | 0 | 100 | 100 | 40, 54, 76, 99 | 0 |
| 1 | C | 231/243 (95%) | -0.06 | 0 | 100 | 100 | 40, 56, 82, 105 | 0 |
| 2 | B | 100/187 (53%) | 0.07 | 1 (1%) | 82 | 77 | 46, 69, 94, 103 | 0 |
| 2 | D | 99/187 (52%) | 0.16 | 2 (2%) | 65 | 56 | 47, 68, 101, 111 | 0 |
| All | All | 661/860 (76%) | -0.08 | 3 (0%) | 91 | 88 | 40, 60, 93, 111 | 0 |

All (3) RSRZ outliers are listed below:

| Mol | Chain | Res | Type | RSRZ |
| --- | --- | --- | --- | --- |
| 2 | D | 173 | GLN | 4.0 |
| 2 | D | 153 | ILE | 2.4 |
| 2 | B | 173 | GLN | 2.1 |

## 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 monosaccharides in this entry.

## 6.4 Ligands ⓘ

LIGAND-RSR INFOmissingINFO

## 6.5 Other polymers ⓘ

There are no such residues in this entry.