# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 19, 2024 – 03:49 PM EST

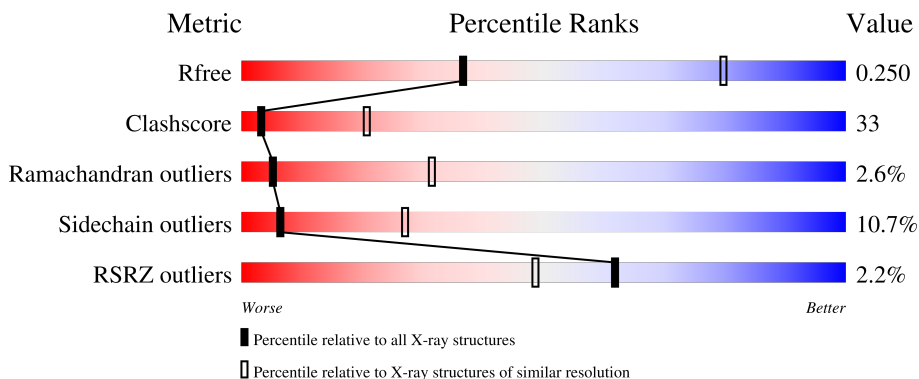|  |  |  |
|---|---|---|
| PDB ID | : | 4KIS |
| Title | : | Crystal Structure of a LSR-DNA Complex |
| Authors | : | Rutherford, K.; Yuan, P.; Perry, K.; Van Duyne, G.D. |
| Deposited on | : | 2013-05-02 |
| Resolution | : | 3.20 Å(reported) |

# 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 3.20 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.
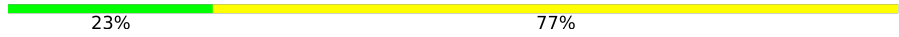
| Metric | Percentile Ranks | Value |
|--------|-----------------|-------|
| Rfree | | 0.250 |
| Clashscore | | 33 |
| Ramachandran outliers | | 2.6% |
| Sidechain outliers | | 10.7% |
| RSRZ outliers | | 2.2% |

*Worse*                                                                 *Better*

▊ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution
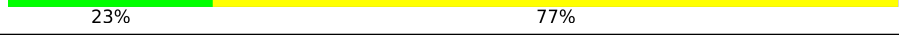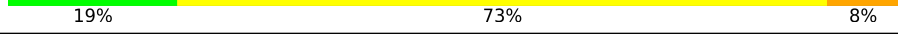
| Metric | Whole archive (#Entries) | Similar resolution (#Entries, resolution range(Å)) |
|--------|--------------------------|-----------------------------------------------------|
| $R_{free}$ | 130704 | 1133 (3.20-3.20) |
| Clashscore | 141614 | 1253 (3.20-3.20) |
| Ramachandran outliers | 138981 | 1234 (3.20-3.20) |
| Sidechain outliers | 138945 | 1233 (3.20-3.20) |
| RSRZ outliers | 127900 | 1095 (3.20-3.20) |

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 | 328 | 3% / 42% 49% 5% · |
| 1 | B | 328 | .% / 43% 39% 10% 7% |
| 1 | C | 328 | 4% / 36% 50% 8% · 6% |
| 1 | D | 328 | 2% / 44% 37% 7% 12% |
| 2 | E | 26 | 23% 77% |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 2 | G | 26 | 58% 42% |
| 2 | I | 26 | 23% 77% |
| 2 | K | 26 | 23% 77% |
| 3 | F | 26 | 35% 58% 8% |
| 3 | H | 26 | 27% 69% . |
| 3 | J | 26 | 23% 77% |
| 3 | L | 26 | 19% 73% 8% |

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 |
|-----|------|-------|-----|-----------|----------|---------|------------------|
| 5 | CA | A | 505 | - | - | - | X |

# 2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 14347 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 Putative integrase [Bacteriophage A118].

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| 1 | A | 315 | Total 2651 | C 1683 | N 464 | O 493 | S 11 | 0 | 0 | 0 |
| 1 | B | 305 | Total 2557 | C 1630 | N 439 | O 477 | S 11 | 0 | 0 | 0 |
| 1 | C | 309 | Total 2589 | C 1646 | N 448 | O 484 | S 11 | 0 | 0 | 0 |
| 1 | D | 287 | Total 2289 | C 1454 | N 413 | O 413 | S 9 | 0 | 0 | 0 |

There are 32 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|---|---|---|---|---|---|
| A | 453 | LEU | - | expression tag | UNP Q928V6 |
| A | 454 | GLU | - | expression tag | UNP Q928V6 |
| A | 455 | HIS | - | expression tag | UNP Q928V6 |
| A | 456 | HIS | - | expression tag | UNP Q928V6 |
| A | 457 | HIS | - | expression tag | UNP Q928V6 |
| A | 458 | HIS | - | expression tag | UNP Q928V6 |
| A | 459 | HIS | - | expression tag | UNP Q928V6 |
| A | 460 | HIS | - | expression tag | UNP Q928V6 |
| B | 453 | LEU | - | expression tag | UNP Q928V6 |
| B | 454 | GLU | - | expression tag | UNP Q928V6 |
| B | 455 | HIS | - | expression tag | UNP Q928V6 |
| B | 456 | HIS | - | expression tag | UNP Q928V6 |
| B | 457 | HIS | - | expression tag | UNP Q928V6 |
| B | 458 | HIS | - | expression tag | UNP Q928V6 |
| B | 459 | HIS | - | expression tag | UNP Q928V6 |
| B | 460 | HIS | - | expression tag | UNP Q928V6 |
| C | 453 | LEU | - | expression tag | UNP Q928V6 |
| C | 454 | GLU | - | expression tag | UNP Q928V6 |
| C | 455 | HIS | - | expression tag | UNP Q928V6 |
| C | 456 | HIS | - | expression tag | UNP Q928V6 |
| C | 457 | HIS | - | expression tag | UNP Q928V6 |

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| Chain | Residue | Modelled | Actual | Comment | Reference |
|---|---|---|---|---|---|
| C | 458 | HIS | - | expression tag | UNP Q928V6 |
| C | 459 | HIS | - | expression tag | UNP Q928V6 |
| C | 460 | HIS | - | expression tag | UNP Q928V6 |
| D | 453 | LEU | - | expression tag | UNP Q928V6 |
| D | 454 | GLU | - | expression tag | UNP Q928V6 |
| D | 455 | HIS | - | expression tag | UNP Q928V6 |
| D | 456 | HIS | - | expression tag | UNP Q928V6 |
| D | 457 | HIS | - | expression tag | UNP Q928V6 |
| D | 458 | HIS | - | expression tag | UNP Q928V6 |
| D | 459 | HIS | - | expression tag | UNP Q928V6 |
| D | 460 | HIS | - | expression tag | UNP Q928V6 |

- Molecule 2 is a DNA chain called DNA (26-MER).

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| 2 | E | 26 | Total 522 | C 254 | N 76 | O 167 | P 25 | 0 | 0 | 0 |
| 2 | G | 26 | Total 522 | C 254 | N 76 | O 167 | P 25 | 0 | 0 | 0 |
| 2 | I | 26 | Total 522 | C 254 | N 76 | O 167 | P 25 | 0 | 0 | 0 |
| 2 | K | 26 | Total 522 | C 254 | N 76 | O 167 | P 25 | 0 | 0 | 0 |

- Molecule 3 is a DNA chain called DNA (26-MER).

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| 3 | F | 26 | Total 538 | C 255 | N 117 | O 141 | P 25 | 0 | 0 | 0 |
| 3 | H | 26 | Total 538 | C 255 | N 117 | O 141 | P 25 | 0 | 0 | 0 |
| 3 | J | 26 | Total 538 | C 255 | N 117 | O 141 | P 25 | 0 | 0 | 0 |
| 3 | L | 26 | Total 538 | C 255 | N 117 | O 141 | P 25 | 0 | 0 | 0 |

- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

| Mol | Chain | Residues | Atoms | | ZeroOcc | AltConf |
|---|---|---|---|---|---|---|
| 4 | A | 3 | Total 3 | Zn 3 | 0 | 0 |

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| Mol | Chain | Residues | Atoms | | ZeroOcc | AltConf |
|---|---|---|---|---|---|---|
| 4 | B | 1 | Total 1 | Zn 1 | 0 | 0 |
| 4 | C | 1 | Total 1 | Zn 1 | 0 | 0 |
| 4 | D | 1 | Total 1 | Zn 1 | 0 | 0 |

- Molecule 5 is CALCIUM ION (three-letter code: CA) (formula: Ca).

| Mol | Chain | Residues | Atoms | | ZeroOcc | AltConf |
|---|---|---|---|---|---|---|
| 5 | A | 2 | Total 2 | Ca 2 | 0 | 0 |
| 5 | E | 1 | Total 1 | Ca 1 | 0 | 0 |
| 5 | B | 2 | Total 2 | Ca 2 | 0 | 0 |
| 5 | C | 1 | Total 1 | Ca 1 | 0 | 0 |
| 5 | D | 1 | Total 1 | Ca 1 | 0 | 0 |

- Molecule 6 is water.

| Mol | Chain | Residues | Atoms | | ZeroOcc | AltConf |
|---|---|---|---|---|---|---|
| 6 | E | 2 | Total 2 | O 2 | 0 | 0 |
| 6 | F | 1 | Total 1 | O 1 | 0 | 0 |
| 6 | G | 2 | Total 2 | O 2 | 0 | 0 |
| 6 | H | 1 | Total 1 | O 1 | 0 | 0 |
| 6 | I | 1 | Total 1 | O 1 | 0 | 0 |
| 6 | J | 1 | Total 1 | O 1 | 0 | 0 |

# 3 Residue-property plots ⓘ

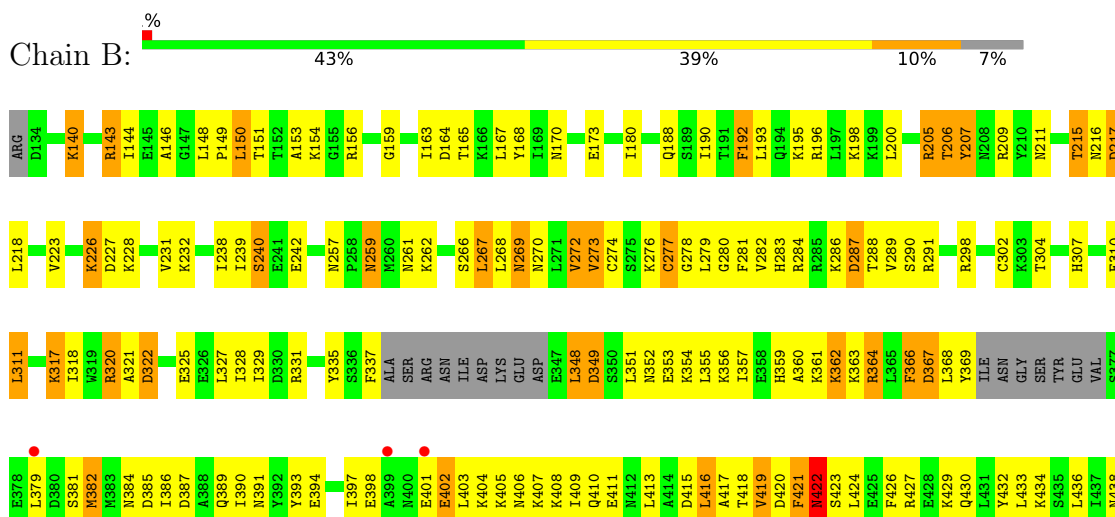These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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.
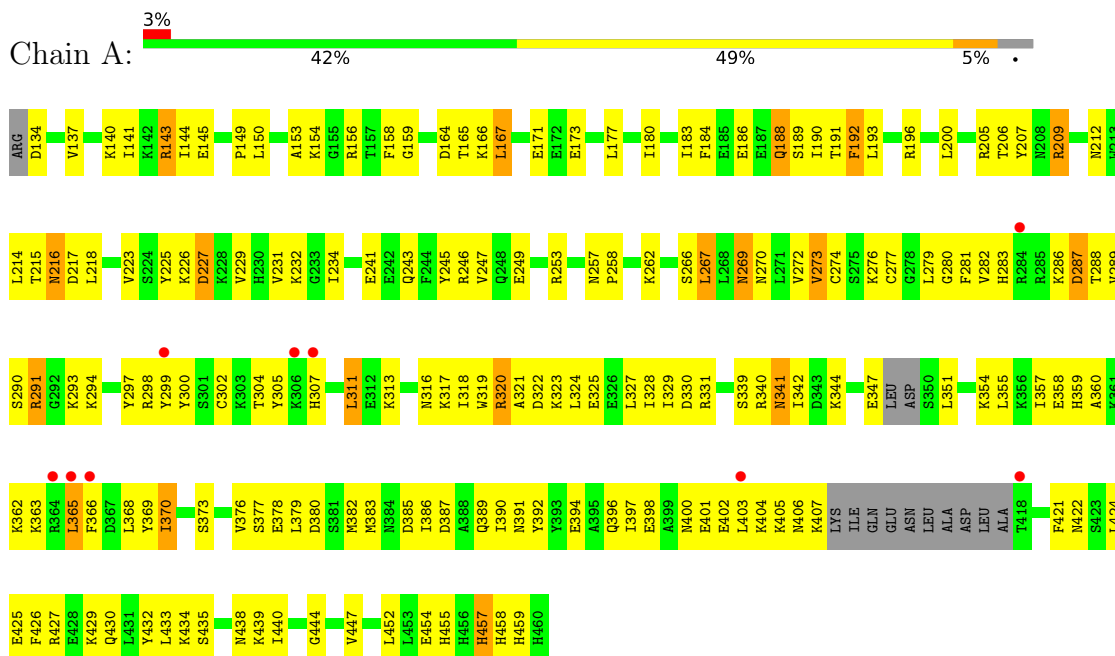
• Molecule 1: Putative integrase [Bacteriophage A118]



• Molecule 1: Putative integrase [Bacteriophage A118]

K439 I440 Y441 I442 Q446 V447 L452 L453 E454 HIS HIS HIS HIS HIS
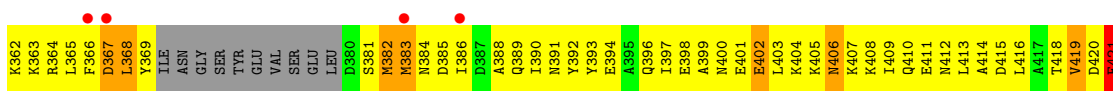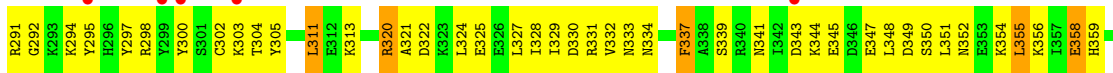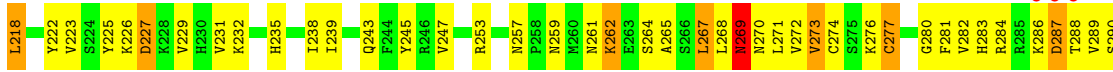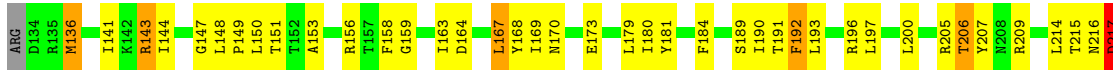
• Molecule 1: Putative integrase [Bacteriophage A118]
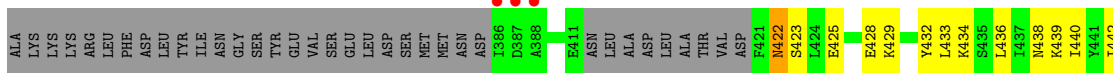
Chain C:



• Molecule 1: Putative integrase [Bacteriophage A118]

Chain D:



• Molecule 2: DNA (26-MER)

Chain E:

G25 T26 T27 T28 A29 G30 T31 T32 C33 C34 T35 C36 G37 T38 T39 T40 T43 C44 T45 C46 G47 T48 T49 G50

• Molecule 2: DNA (26-MER)

Chain G:

```
58%                                    42%
```

G25 T28 A29 G30 T31 T32 C33 C34 T35 C36 G37 G47 T48 T49 G50

• Molecule 2: DNA (26-MER)

Chain I:

```
23%                         77%
```

G25 T26 T27 T28 A29 G30 T31 T32 C33 C34 T35 C36 G37 T38 C42 T43 C44 T45 C46 G47 T48 T49 G50

• Molecule 2: DNA (26-MER)

Chain K:

```
23%                         77%
```

G25 T26 T27 T28 A29 G30 T31 T32 C33 C34 G37 T38 T39 T40 T41 C42 T43 C44 T45 C46 G47 T48 T49 G50

• Molecule 3: DNA (26-MER)

Chain F:

```
35%                         58%                         8%
```

C-1 C0 A1 A5 G6 A7 G8 A11 A12 C13 G14 A15 G16 G17 A18 A19 C20 T21 A22 A23 A24

• Molecule 3: DNA (26-MER)

Chain H:

```
27%                         69%                         .
```

C-1 C0 A1 A2 A5 G6 A7 G8 A9 A10 A11 A12 C13 G16 G17 A18 A19 C20 A23 A24

• Molecule 3: DNA (26-MER)

Chain J:

```
23%                         77%
```

C-1 C0 A5 G6 A7 G8 A11 A12 C13 G14 A15 G16 G17 A18 A19 C20 T21 A22 A23 A24

• Molecule 3: DNA (26-MER)

Chain L:

```
19%                         73%                         8%
```

C-1 C0 A1 A2 A5 G6 A7 G8 A9 A10 A11 A12 C13 G14 A15 G16 G17 A18 A19 C20 T21 A22 A23 A24

# 4 Data and refinement statistics ⓘ

| Property | Value | Source |
|---|---|---|
| Space group | I 2 3 | Depositor |
| Cell constants<br>a, b, c, $\alpha$, $\beta$, $\gamma$ | 290.75Å    290.75Å    290.75Å<br>90.00°      90.00°       90.00° | Depositor |
| Resolution (Å) | 49.86   –   3.20<br>49.86   –   3.15 | Depositor<br>EDS |
| % Data completeness<br>(in resolution range) | (Not available) (49.86-3.20)<br>96.7 (49.86-3.15) | Depositor<br>EDS |
| $R_{merge}$ | 0.12 | Depositor |
| $R_{sym}$ | 0.12 | Depositor |
| $< I/\sigma(I) >$ [1] | 1.24 (at 3.12Å) | Xtriage |
| Refinement program | CNS 1.3 | Depositor |
| R, $R_{free}$ | 0.236   ,   0.256<br>0.219   ,   0.250 | Depositor<br>DCC |
| $R_{free}$ test set | 3353 reflections (4.94%) | wwPDB-VP |
| Wilson B-factor (Å$^2$) | 92.3 | Xtriage |
| Anisotropy | 0.000 | Xtriage |
| Bulk solvent $k_{sol}$(e/Å$^3$), $B_{sol}$(Å$^2$) | 0.27 , 66.5 | EDS |
| L-test for twinning[2] | $< |L| > = 0.47, < L^2 > = 0.30$ | Xtriage |
| Estimated twinning fraction | 0.002 for -l,-k,-h | Xtriage |
| $F_o$,$F_c$ correlation | 0.93 | EDS |
| Total number of atoms | 14347 | wwPDB-VP |
| Average B, all atoms (Å$^2$) | 100.0 | wwPDB-VP |

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.19% 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, CA

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 | 0.43 | 0/2702 | 0.69 | 0/3620 |
| 1 | B | 0.49 | 0/2601 | 0.72 | 0/3485 |
| 1 | C | 0.41 | 0/2634 | 0.66 | 0/3530 |
| 1 | D | 0.44 | 0/2333 | 0.70 | 1/3136 (0.0%) |
| 2 | E | 0.57 | 0/579 | 0.83 | 0/892 |
| 2 | G | 0.60 | 0/579 | 0.84 | 0/892 |
| 2 | I | 0.42 | 0/579 | 0.75 | 0/892 |
| 2 | K | 0.57 | 0/579 | 0.80 | 0/892 |
| 3 | F | 0.52 | 0/609 | 0.71 | 0/938 |
| 3 | H | 0.60 | 0/609 | 0.76 | 0/938 |
| 3 | J | 0.39 | 0/609 | 0.70 | 0/938 |
| 3 | L | 0.53 | 0/609 | 0.74 | 0/938 |
| All | All | 0.47 | 0/15022 | 0.72 | 1/21091 (0.0%) |

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 | B | 0 | 1 |
| 1 | D | 0 | 1 |
| 3 | F | 0 | 2 |
| 3 | H | 0 | 1 |
| 3 | L | 0 | 2 |
| All | All | 0 | 7 |

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 | D | 451 | TRP | N-CA-C | 5.61 | 126.16 | 111.00 |

There are no chirality outliers.

5 of 7 planarity outliers are listed below:

| Mol | Chain | Res | Type | Group |
|-----|-------|-----|------|-------|
| 1 | B | 168 | TYR | Sidechain |
| 1 | D | 168 | TYR | Sidechain |
| 3 | F | -1 | DC | Sidechain |
| 3 | F | 16 | DG | Sidechain |
| 3 | H | -1 | DC | Sidechain |

## 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 | 2651 | 0 | 2628 | 179 | 0 |
| 1 | B | 2557 | 0 | 2565 | 169 | 0 |
| 1 | C | 2589 | 0 | 2594 | 213 | 0 |
| 1 | D | 2289 | 0 | 2170 | 149 | 0 |
| 2 | E | 522 | 0 | 302 | 44 | 0 |
| 2 | G | 522 | 0 | 302 | 17 | 0 |
| 2 | I | 522 | 0 | 302 | 35 | 0 |
| 2 | K | 522 | 0 | 302 | 29 | 0 |
| 3 | F | 538 | 0 | 289 | 28 | 0 |
| 3 | H | 538 | 0 | 289 | 25 | 0 |
| 3 | J | 538 | 0 | 289 | 24 | 0 |
| 3 | L | 538 | 0 | 289 | 33 | 0 |
| 4 | A | 3 | 0 | 0 | 0 | 0 |
| 4 | B | 1 | 0 | 0 | 0 | 0 |
| 4 | C | 1 | 0 | 0 | 0 | 0 |
| 4 | D | 1 | 0 | 0 | 0 | 0 |
| 5 | A | 2 | 0 | 0 | 0 | 0 |
| 5 | B | 2 | 0 | 0 | 0 | 0 |
| 5 | C | 1 | 0 | 0 | 0 | 0 |
| 5 | D | 1 | 0 | 0 | 0 | 0 |
| 5 | E | 1 | 0 | 0 | 0 | 0 |
| 6 | E | 2 | 0 | 0 | 0 | 0 |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 6 | F | 1 | 0 | 0 | 0 | 0 |
| 6 | G | 2 | 0 | 0 | 0 | 0 |
| 6 | H | 1 | 0 | 0 | 0 | 0 |
| 6 | I | 1 | 0 | 0 | 0 | 0 |
| 6 | J | 1 | 0 | 0 | 0 | 0 |
| All | All | 14347 | 0 | 12321 | 880 | 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 33.

The worst 5 of 880 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:C:415:ASP:HA | 1:C:418:THR:HG23 | 1.36 | 1.08 |
| 3:J:18:DA:H2" | 3:J:19:DA:H5" | 1.37 | 1.07 |
| 2:E:30:DG:H2" | 2:E:31:DT:H5" | 1.37 | 1.02 |
| 2:K:25:DG:H2" | 2:K:26:DT:H5' | 1.39 | 1.01 |
| 2:I:44:DC:H2" | 2:I:45:DT:H5" | 1.43 | 1.00 |

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 | 309/328 (94%) | 263 (85%) | 43 (14%) | 3 (1%) | 15 | 54 |
| 1 | B | 299/328 (91%) | 256 (86%) | 34 (11%) | 9 (3%) | 4 | 28 |
| 1 | C | 305/328 (93%) | 251 (82%) | 47 (15%) | 7 (2%) | 6 | 34 |
| 1 | D | 279/328 (85%) | 228 (82%) | 39 (14%) | 12 (4%) | 2 | 20 |
| All | All | 1192/1312 (91%) | 998 (84%) | 163 (14%) | 31 (3%) | 5 | 31 |

5 of 31 Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | A | 341 | ASN |
| 1 | B | 227 | ASP |
| 1 | B | 278 | GLY |
| 1 | B | 419 | VAL |
| 1 | B | 421 | PHE |

### 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 | 291/302 (96%) | 266 (91%) | 25 (9%) | 10 | 38 |
| 1 | B | 281/302 (93%) | 246 (88%) | 35 (12%) | 4 | 21 |
| 1 | C | 284/302 (94%) | 251 (88%) | 33 (12%) | 5 | 24 |
| 1 | D | 228/302 (76%) | 205 (90%) | 23 (10%) | 7 | 29 |
| All | All | 1084/1208 (90%) | 968 (89%) | 116 (11%) | 6 | 27 |

5 of 116 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | B | 416 | LEU |
| 1 | D | 311 | LEU |
| 1 | C | 273 | VAL |
| 1 | D | 302 | CYS |
| 1 | D | 217 | ASP |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 28 such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | B | 384 | ASN |
| 1 | D | 270 | ASN |
| 1 | C | 270 | ASN |
| 1 | D | 230 | HIS |
| 1 | C | 269 | ASN |

### 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 13 ligands modelled in this entry, 13 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 ⓘ

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 | 315/328 (96%) | -0.01 | 9 (2%) | 51 | 36 | 45, 87, 156, 171 | 3 (0%) |
| 1 | B | 305/328 (92%) | -0.24 | 3 (0%) | 82 | 72 | 43, 81, 149, 167 | 2 (0%) |
| 1 | C | 309/328 (94%) | 0.08 | 12 (3%) | 39 | 25 | 52, 117, 167, 190 | 0 |
| 1 | D | 287/328 (87%) | 0.00 | 8 (2%) | 53 | 37 | 51, 91, 166, 184 | 1 (0%) |
| 2 | E | 26/26 (100%) | -0.45 | 0 | 100 | 100 | 68, 87, 115, 116 | 0 |
| 2 | G | 26/26 (100%) | -0.50 | 0 | 100 | 100 | 64, 82, 99, 109 | 0 |
| 2 | I | 26/26 (100%) | -0.41 | 0 | 100 | 100 | 89, 116, 157, 165 | 0 |
| 2 | K | 26/26 (100%) | -0.39 | 0 | 100 | 100 | 77, 93, 118, 121 | 0 |
| 3 | F | 26/26 (100%) | -0.30 | 0 | 100 | 100 | 69, 96, 128, 135 | 0 |
| 3 | H | 26/26 (100%) | -0.52 | 0 | 100 | 100 | 69, 85, 108, 111 | 0 |
| 3 | J | 26/26 (100%) | -0.43 | 0 | 100 | 100 | 96, 120, 174, 188 | 0 |
| 3 | L | 26/26 (100%) | -0.42 | 0 | 100 | 100 | 72, 96, 123, 131 | 0 |
| All | All | 1424/1520 (93%) | -0.10 | 32 (2%) | 62 | 48 | 43, 94, 161, 190 | 6 (0%) |

The worst 5 of 32 RSRZ outliers are listed below:

| Mol | Chain | Res | Type | RSRZ |
|-----|-------|-----|------|------|
| 1 | D | 386 | ILE | 4.4 |
| 1 | C | 366 | PHE | 3.8 |
| 1 | D | 460 | HIS | 3.7 |
| 1 | C | 295 | TYR | 3.6 |
| 1 | A | 365 | LEU | 3.5 |

## 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 ⓘ

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($\text{Å}^2$) | Q<0.9 |
|-----|------|-------|-----|-------|------|-----|------------------------|-------|
| 5 | CA | A | 505 | 1/1 | 0.28 | 0.50 | 160,160,160,160 | 0 |
| 5 | CA | B | 503 | 1/1 | 0.81 | 0.61 | 121,121,121,121 | 0 |
| 5 | CA | A | 504 | 1/1 | 0.82 | 0.39 | 132,132,132,132 | 0 |
| 5 | CA | C | 502 | 1/1 | 0.84 | 0.65 | 145,145,145,145 | 0 |
| 5 | CA | D | 502 | 1/1 | 0.88 | 0.98 | 145,145,145,145 | 0 |
| 5 | CA | E | 101 | 1/1 | 0.92 | 0.47 | 118,118,118,118 | 0 |
| 5 | CA | B | 502 | 1/1 | 0.95 | 0.66 | 125,125,125,125 | 0 |
| 4 | ZN | A | 502 | 1/1 | 0.96 | 0.14 | 87,87,87,87 | 0 |
| 4 | ZN | C | 501 | 1/1 | 0.97 | 0.08 | 144,144,144,144 | 0 |
| 4 | ZN | D | 501 | 1/1 | 0.99 | 0.12 | 116,116,116,116 | 0 |
| 4 | ZN | A | 503 | 1/1 | 0.99 | 0.13 | 110,110,110,110 | 0 |
| 4 | ZN | B | 501 | 1/1 | 1.00 | 0.15 | 94,94,94,94 | 0 |
| 4 | ZN | A | 501 | 1/1 | 1.00 | 0.10 | 106,106,106,106 | 0 |

## 6.5 Other polymers ⓘ

There are no such residues in this entry.