# WORLDWIDE PDB

## PROTEIN DATA BANK

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

Apr 20, 2024 – 09:05 am BST

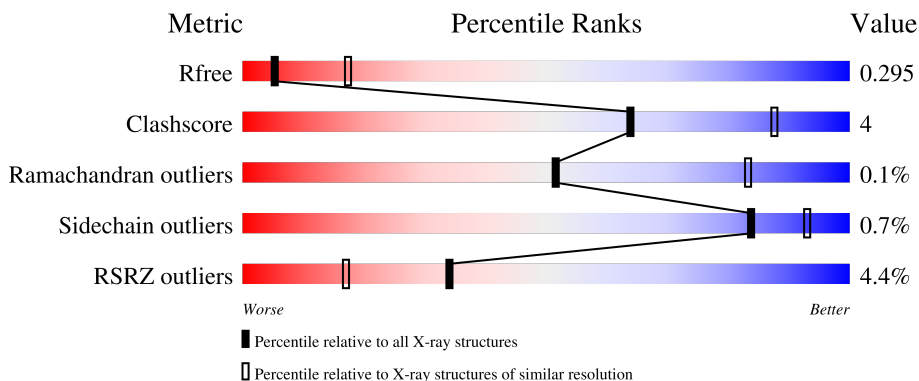|  |  |  |
|---|---|---|
| PDB ID | : | 8RKS |
| Title | : | Structure of VPS29-VPS35 bound to the LFa motif R21 of Fam21. |
| Authors | : | Romano-Moreno, M.; Astorga-Simon, E.N.; Rojas, A.L.; Hierro, A. |
| Deposited on | : | 2023-12-30 |
| Resolution | : | 3.10 Å(reported) |

# 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 3.10 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.
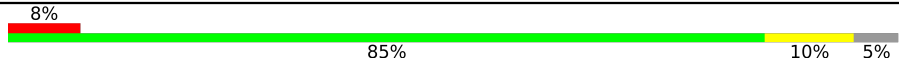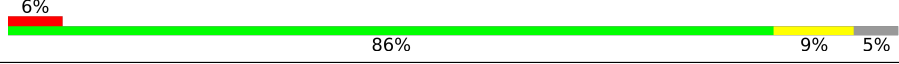
| Metric | Percentile Ranks | Value |
|---|---|---|
| Rfree | | 0.295 |
| Clashscore | | 4 |
| Ramachandran outliers | | 0.1% |
| Sidechain outliers | | 0.7% |
| RSRZ outliers | | 4.4% |

*Worse*　　　　　　　　　　　　　　　　　　　*Better*

▌ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution
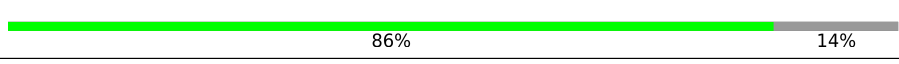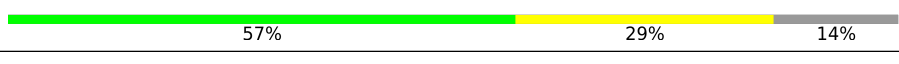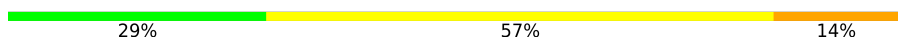
| Metric | Whole archive (#Entries) | Similar resolution (#Entries, resolution range(Å)) |
|---|---|---|
| $R_{free}$ | 130704 | 1094 (3.10-3.10) |
| Clashscore | 141614 | 1184 (3.10-3.10) |
| Ramachandran outliers | 138981 | 1141 (3.10-3.10) |
| Sidechain outliers | 138945 | 1141 (3.10-3.10) |
| RSRZ outliers | 127900 | 1067 (3.10-3.10) |

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 | 182 | .% 90% 10% |
| 1 | C | 182 | .% 90% 10% |
| 1 | E | 182 | 2% 87% 13% |
| 1 | G | 182 | .% 91% 9% |
| 2 | B | 311 | 5% 82% 13% 5% |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 2 | D | 311 | 8% ... 85% ... 10% ... 5% |
| 2 | F | 311 | 6% ... 86% ... 10% ... · |
| 2 | H | 311 | 6% ... 86% ... 9% ... 5% |
| 3 | I | 7 | 86% ... 14% |
| 3 | J | 7 | 57% ... 29% ... 14% |
| 3 | K | 7 | 57% ... 29% ... 14% |
| 3 | L | 7 | 29% ... 57% ... 14% |

## 2 Entry composition ⓘ

There are 3 unique types of molecules in this entry. The entry contains 15571 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 Vacuolar protein sorting-associated protein 29.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| 1 | A | 182 | Total | C | N | O | S | 0 | 0 | 0 |
|   |   |     | 1447 | 936 | 242 | 263 | 6 |   |   |   |
| 1 | C | 182 | Total | C | N | O | S | 0 | 0 | 0 |
|   |   |     | 1447 | 936 | 242 | 263 | 6 |   |   |   |
| 1 | E | 182 | Total | C | N | O | S | 0 | 0 | 0 |
|   |   |     | 1447 | 936 | 242 | 263 | 6 |   |   |   |
| 1 | G | 182 | Total | C | N | O | S | 0 | 0 | 0 |
|   |   |     | 1446 | 936 | 242 | 262 | 6 |   |   |   |

- Molecule 2 is a protein called Vacuolar protein sorting-associated protein 35.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| 2 | B | 297 | Total | C | N | O | S | 0 | 0 | 0 |
|   |   |     | 2405 | 1527 | 418 | 450 | 10 |   |   |   |
| 2 | D | 296 | Total | C | N | O | S | 0 | 0 | 0 |
|   |   |     | 2394 | 1521 | 414 | 449 | 10 |   |   |   |
| 2 | F | 298 | Total | C | N | O | S | 0 | 0 | 0 |
|   |   |     | 2413 | 1533 | 419 | 451 | 10 |   |   |   |
| 2 | H | 295 | Total | C | N | O | S | 0 | 0 | 0 |
|   |   |     | 2385 | 1515 | 416 | 444 | 10 |   |   |   |

- Molecule 3 is a protein called WASH complex subunit 2A.

| Mol | Chain | Residues | Atoms | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 3 | K | 6 | Total | C | N | O | 0 | 0 | 0 |
|   |   |   | 44 | 26 | 7 | 11 |   |   |   |
| 3 | I | 6 | Total | C | N | O | 0 | 0 | 0 |
|   |   |   | 44 | 26 | 7 | 11 |   |   |   |
| 3 | J | 6 | Total | C | N | O | 0 | 0 | 0 |
|   |   |   | 44 | 26 | 7 | 11 |   |   |   |
| 3 | L | 7 | Total | C | N | O | 0 | 0 | 0 |
|   |   |   | 55 | 35 | 8 | 12 |   |   |   |

# 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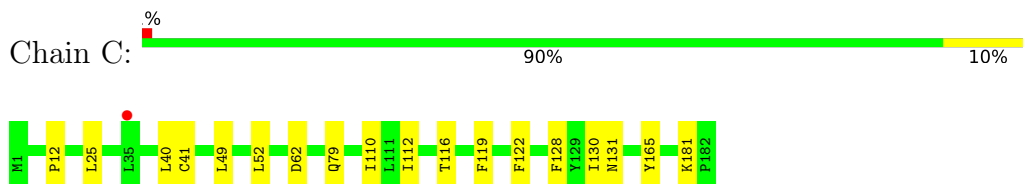 = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Vacuolar protein sorting-associated protein 29

Chain A:

- Molecule 1: Vacuolar protein sorting-associated protein 29

Chain C:
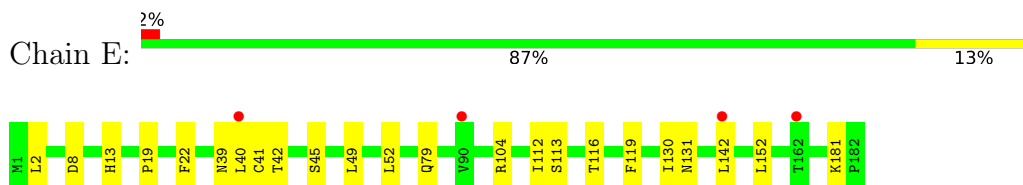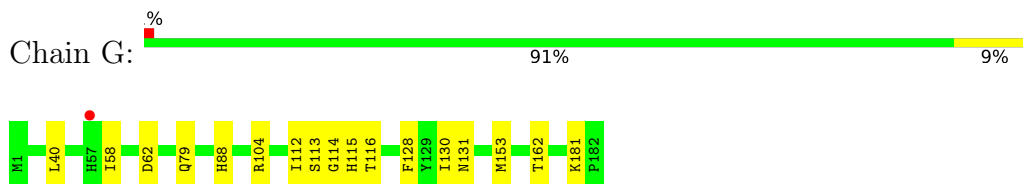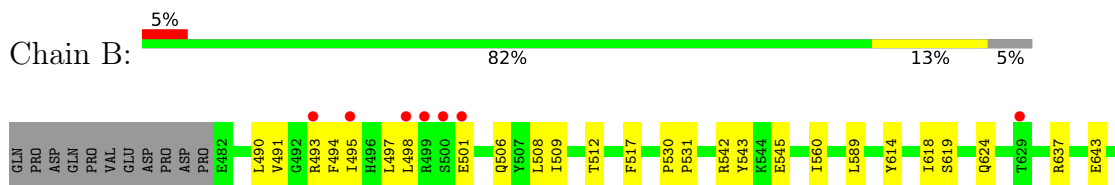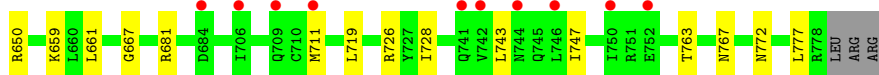
- Molecule 1: Vacuolar protein sorting-associated protein 29

Chain E:

- Molecule 1: Vacuolar protein sorting-associated protein 29

Chain G:

- Molecule 2: Vacuolar protein sorting-associated protein 35

Chain B:

R650 K659 L660 L661 G667 R681 D684 I706 Q709 C710 M711 L719 R726 Y727 I728 Q741 V742 L743 N744 Q745 L746 I747 I750 R751 E752 T763 N767 N772 L777 R778 LEU ARG ARG

• Molecule 2: Vacuolar protein sorting-associated protein 35

Chain D:

8%
85% 10% 5%

GLN PRO ASP GLN PRO VAL GLU ASP PRO ASP PRO E482 A485 Q488 F494 I495 S500 E501 D502 P503 Q506 Y507 L508 I509 T512 A513 H516 A535 R542 Y543 K555 K556 C557 I560 R582 S608 Y614 I618 S619 D620 A623 E643

R650 G667 T672 R681 N686 L700 A703 I706 C710 M711 L719 R726 Y727 F730 Y731 A737 L743 L746 I747 Q748 K749 I750 L754 E758 S759 S760 E761 T762 T763 N767 L777 ARG LEU ARG ARG

• Molecule 2: Vacuolar protein sorting-associated protein 35

Chain F:

6%
86% 10% ·

GLN PRO ASP GLN PRO VAL GLU ASP PRO ASP PRO E482 D483 Q488 R493 F494 I495 S500 E501 D502 Q505 L508 P531 A535 Y543 K552 K555 K556 C557 I560 H565 L583 F584 L585 Q586 L589 E605 F606 M607 S608 Y614 I618

E643 E647 R650 L655 S679 G680 R681 N682 N686 L690 L715 Q718 N725 R726 Y727 F730 L743 L746 I747 I750 L754 L757 T763 N767 N772 L779 ARG ARG

• Molecule 2: Vacuolar protein sorting-associated protein 35

Chain H:

6%
86% 9% 5%

GLN PRO ASP GLN PRO VAL GLU ASP PRO ASP PRO GLU ASP PHE A485 S489 R493 F494 I495 H496 L497 L498 R499 S500 E501 D504 Y507 L508 I509 L510 N511 T512 K515 G520 L532 Y543 K556 I560 I568 R582 Y614 I618 S621 K622

A626 E643 R650 S679 G680 R681 C710 M711 L715 N725 R726 Y727 I728 L743 I747 T763 I766 N767 L777 R778 L779 ARG ARG

• Molecule 3: WASH complex subunit 2A

Chain K:

57% 29% 14%

D140 D141 P142 L143 N144 A145 PHE

• Molecule 3: WASH complex subunit 2A

Chain I:

86% 14%

D140 A145 PHE

• Molecule 3: WASH complex subunit 2A

Chain J:

57% 29% 14%

D140 D141 N144 A145 PHE

• Molecule 3: WASH complex subunit 2A

Chain L:

29% 57% 14%

D140 D141 P142 L143 N144 A145 F146
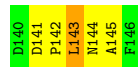
# 4 Data and refinement statistics ⓘ

| Property | Value | Source |
|---|---|---|
| Space group | P 1 21 1 | Depositor |
| Cell constants<br>a, b, c, $\alpha$, $\beta$, $\gamma$ | 59.27Å   139.09Å   146.15Å<br>90.00°   90.00°   90.00° | Depositor |
| Resolution (Å) | 146.15   –   3.10<br>146.15   –   2.96 | Depositor<br>EDS |
| % Data completeness<br>(in resolution range) | 73.6 (146.15-3.10)<br>64.5 (146.15-2.96) | Depositor<br>EDS |
| $R_{merge}$ | 0.17 | Depositor |
| $R_{sym}$ | (Not available) | Depositor |
| $< I/\sigma(I) >$ [1] | 1.23 (at 2.96Å) | Xtriage |
| Refinement program | PHENIX 1.19.1 | Depositor |
| R, $R_{free}$ | 0.251   ,   0.288<br>0.256   ,   0.295 | Depositor<br>DCC |
| $R_{free}$ test set | 1613 reflections (5.05%) | wwPDB-VP |
| Wilson B-factor (Å$^2$) | 91.5 | Xtriage |
| Anisotropy | 0.037 | Xtriage |
| Bulk solvent $k_{sol}$(e/Å$^3$), $B_{sol}$(Å$^2$) | 0.33 , 50.4 | EDS |
| L-test for twinning[2] | $< |L| > = 0.49$, $< L^2 > = 0.33$ | Xtriage |
| Estimated twinning fraction | 0.000 for -h,l,k<br>0.004 for -h,-l,-k<br>0.378 for h,-k,-l | Xtriage |
| $F_o$,$F_c$ correlation | 0.90 | EDS |
| Total number of atoms | 15571 | wwPDB-VP |
| Average B, all atoms (Å$^2$) | 96.0 | wwPDB-VP |

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.84% 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 (i)

## 5.1 Standard geometry (i)

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 | 0/1481 | 0.47 | 0/2008 |
| 1 | C | 0.24 | 0/1481 | 0.48 | 0/2008 |
| 1 | E | 0.24 | 0/1481 | 0.48 | 0/2008 |
| 1 | G | 0.24 | 0/1480 | 0.50 | 0/2007 |
| 2 | B | 0.24 | 0/2452 | 0.44 | 0/3302 |
| 2 | D | 0.24 | 0/2441 | 0.44 | 0/3288 |
| 2 | F | 0.24 | 0/2460 | 0.44 | 0/3313 |
| 2 | H | 0.24 | 0/2431 | 0.44 | 0/3274 |
| 3 | I | 0.21 | 0/44 | 0.34 | 0/60 |
| 3 | J | 0.20 | 0/44 | 0.33 | 0/60 |
| 3 | K | 0.23 | 0/44 | 0.51 | 0/60 |
| 3 | L | 0.29 | 0/56 | 0.52 | 0/76 |
| All | All | 0.24 | 0/15895 | 0.46 | 0/21464 |

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 1 | A | 1447 | 0 | 1459 | 12 | 0 |
| 1 | C | 1447 | 0 | 1459 | 14 | 0 |
| 1 | E | 1447 | 0 | 1459 | 19 | 0 |
| 1 | G | 1446 | 0 | 1456 | 11 | 0 |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 2 | B | 2405 | 0 | 2383 | 30 | 0 |
| 2 | D | 2394 | 0 | 2370 | 21 | 0 |
| 2 | F | 2413 | 0 | 2394 | 27 | 0 |
| 2 | H | 2385 | 0 | 2375 | 16 | 0 |
| 3 | I | 44 | 0 | 36 | 0 | 0 |
| 3 | J | 44 | 0 | 36 | 1 | 0 |
| 3 | K | 44 | 0 | 36 | 3 | 0 |
| 3 | L | 55 | 0 | 45 | 7 | 0 |
| All | All | 15571 | 0 | 15508 | 130 | 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 4.

The worst 5 of 130 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:122:PHE:HB2 | 2:H:778:ARG:HG2 | 1.52 | 0.89 |
| 2:B:509:ILE:HG12 | 2:D:516:HIS:NE2 | 2.05 | 0.72 |
| 1:G:116:THR:OG1 | 1:G:131:ASN:ND2 | 2.28 | 0.67 |
| 1:G:104:ARG:NH1 | 2:H:725:ASN:OD1 | 2.29 | 0.66 |
| 1:A:25:LEU:HB3 | 3:K:143:LEU:HD13 | 1.78 | 0.65 |

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 | 180/182 (99%) | 175 (97%) | 5 (3%) | 0 | 100 | 100 |
| 1 | C | 180/182 (99%) | 172 (96%) | 8 (4%) | 0 | 100 | 100 |
| 1 | E | 180/182 (99%) | 174 (97%) | 6 (3%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|----------|----------|---------|----------|-----|-----|
| 1 | G | 180/182 (99%) | 175 (97%) | 4 (2%) | 1 (1%) | 25 | 59 |
| 2 | B | 295/311 (95%) | 283 (96%) | 12 (4%) | 0 | 100 | 100 |
| 2 | D | 294/311 (94%) | 285 (97%) | 9 (3%) | 0 | 100 | 100 |
| 2 | F | 296/311 (95%) | 288 (97%) | 8 (3%) | 0 | 100 | 100 |
| 2 | H | 293/311 (94%) | 284 (97%) | 9 (3%) | 0 | 100 | 100 |
| 3 | I | 4/7 (57%) | 3 (75%) | 1 (25%) | 0 | 100 | 100 |
| 3 | J | 4/7 (57%) | 3 (75%) | 1 (25%) | 0 | 100 | 100 |
| 3 | K | 4/7 (57%) | 3 (75%) | 1 (25%) | 0 | 100 | 100 |
| 3 | L | 5/7 (71%) | 4 (80%) | 0 | 1 (20%) | 0 | 0 |
| All | All | 1915/2000 (96%) | 1849 (97%) | 64 (3%) | 2 (0%) | 51 | 83 |

All (2) Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 3 | L | 142 | PRO |
| 1 | G | 114 | GLY |

### 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 | 160/160 (100%) | 158 (99%) | 2 (1%) | 69 | 87 |
| 1 | C | 160/160 (100%) | 160 (100%) | 0 | 100 | 100 |
| 1 | E | 160/160 (100%) | 160 (100%) | 0 | 100 | 100 |
| 1 | G | 159/160 (99%) | 159 (100%) | 0 | 100 | 100 |
| 2 | B | 258/272 (95%) | 256 (99%) | 2 (1%) | 81 | 92 |
| 2 | D | 257/272 (94%) | 254 (99%) | 3 (1%) | 71 | 88 |
| 2 | F | 259/272 (95%) | 258 (100%) | 1 (0%) | 91 | 96 |
| 2 | H | 256/272 (94%) | 254 (99%) | 2 (1%) | 81 | 92 |
| 3 | I | 5/6 (83%) | 5 (100%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|----------|-----------|----------|:-----------:|:---:|
| 3 | J | 5/6 (83%) | 5 (100%) | 0 | 100 | 100 |
| 3 | K | 5/6 (83%) | 5 (100%) | 0 | 100 | 100 |
| 3 | L | 6/6 (100%) | 5 (83%) | 1 (17%) | 2 | 9 |
| All | All | 1690/1752 (96%) | 1679 (99%) | 11 (1%) | 84 | 93 |

5 of 11 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 2 | F | 681 | ARG |
| 2 | H | 681 | ARG |
| 3 | L | 143 | LEU |
| 2 | H | 726 | ARG |
| 2 | D | 542 | ARG |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | E | 10 | HIS |
| 1 | G | 124 | HIS |
| 1 | E | 124 | HIS |
| 2 | H | 744 | ASN |
| 2 | F | 511 | 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 ⓘ

There are no ligands in this entry.

## 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 | 182/182 (100%) | -0.03 | 1 (0%) | 91 | 81 | 59, 85, 117, 135 | 0 |
| 1 | C | 182/182 (100%) | -0.02 | 1 (0%) | 91 | 81 | 43, 87, 121, 148 | 0 |
| 1 | E | 182/182 (100%) | 0.03 | 4 (2%) | 62 | 41 | 56, 87, 128, 159 | 0 |
| 1 | G | 182/182 (100%) | -0.05 | 1 (0%) | 91 | 81 | 51, 88, 120, 151 | 0 |
| 2 | B | 297/311 (95%) | 0.26 | 17 (5%) | 23 | 11 | 55, 91, 147, 180 | 0 |
| 2 | D | 296/311 (95%) | 0.47 | 24 (8%) | 12 | 5 | 51, 98, 157, 206 | 0 |
| 2 | F | 298/311 (95%) | 0.28 | 18 (6%) | 21 | 10 | 63, 96, 139, 189 | 0 |
| 2 | H | 295/311 (94%) | 0.31 | 20 (6%) | 17 | 7 | 52, 96, 151, 182 | 0 |
| 3 | I | 6/7 (85%) | -0.60 | 0 | 100 | 100 | 86, 89, 117, 119 | 0 |
| 3 | J | 6/7 (85%) | -0.24 | 0 | 100 | 100 | 104, 123, 136, 157 | 0 |
| 3 | K | 6/7 (85%) | -0.34 | 0 | 100 | 100 | 92, 113, 131, 131 | 0 |
| 3 | L | 7/7 (100%) | -0.77 | 0 | 100 | 100 | 96, 104, 111, 112 | 0 |
| All | All | 1939/2000 (96%) | 0.19 | 86 (4%) | 34 | 17 | 43, 92, 144, 206 | 0 |

The worst 5 of 86 RSRZ outliers are listed below:

| Mol | Chain | Res | Type | RSRZ |
|-----|-------|-----|------|------|
| 2 | D | 759 | SER | 13.5 |
| 2 | D | 750 | ILE | 8.9 |
| 2 | H | 501 | GLU | 8.4 |
| 2 | D | 500 | SER | 8.4 |
| 2 | B | 498 | LEU | 8.3 |

## 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 ⓘ

There are no ligands in this entry.

## 6.5 Other polymers ⓘ

There are no such residues in this entry.