# Full wwPDB X-ray Structure Validation Report ⓘ

Nov 12, 2024 – 11:39 AM EST

| | | |
|---|---|---|
| PDB ID | : | 3PNW |
| Title | : | Crystal Structure of the tudor domain of human TDRD3 in complex with an anti-TDRD3 FAB |
| Authors | : | Loppnau, P.; Tempel, W.; Wernimont, A.K.; Lam, R.; Ravichandran, M.; Adams-Cioaba, M.A.; Persson, H.; Sidhu, S.S.; Arrowsmith, C.H.; Edwards, A.M.; Bountra, C.; Weigelt, J.; Cossar, D.; Structural Genomics Consortium (SGC) |
| Deposited on | : | 2010-11-19 |
| Resolution | : | 2.05 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:

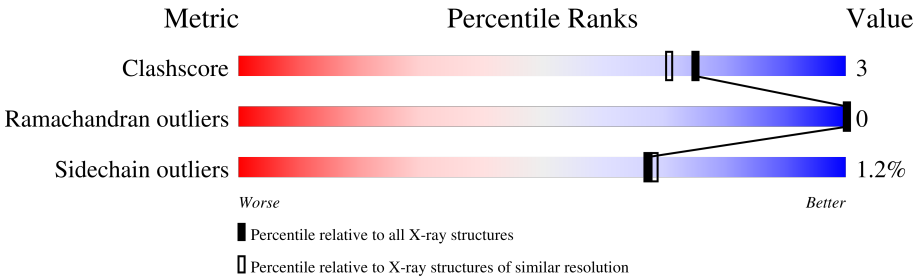
| | | |
|---|---|---|
| MolProbity | : | 4.02b-467 |
| Xtriage (Phenix) | : | 1.20.1 |
| EDS | : | FAILED |
| Percentile statistics | : | 20231227.v01 (using entries in the PDB archive December 27th 2023) |
| Ideal geometry (proteins) | : | Engh & Huber (2001) |
| Ideal geometry (DNA, RNA) | : | Parkinson et al. (1996) |
| Validation Pipeline (wwPDB-VP) | : | 2.39 |

# 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 2.05 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)) |
|---|---|---|
| Clashscore | 180529 | 2229 (2.04-2.04) |
| Ramachandran outliers | 177936 | 2217 (2.04-2.04) |
| Sidechain outliers | 177891 | 2217 (2.04-2.04) |

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.

Note EDS failed to run properly.

| Mol | Chain | Length | Quality of chain |
|---|---|---|---|
| 1 | A | 228 | 82% 10% • 7% |
| 1 | D | 228 | 87% 7% 7% |
| 1 | G | 228 | 89% • 7% |
| 1 | J | 228 | 86% 7% 7% |
| 1 | M | 228 | 80% 14% 6% |
| 1 | P | 228 | 88% 5% 7% |
| 1 | S | 228 | 85% 9% 6% |

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| Mol | Chain | Length | Quality of chain |
|---|---|---|---|
| 1 | V | 228 | 86% 7% 7% |
| 2 | B | 246 | 87% 9% |
| 2 | E | 246 | 85% 7% 8% |
| 2 | H | 246 | 84% 11% |
| 2 | K | 246 | 85% 11% |
| 2 | N | 246 | 85% 7% 8% |
| 2 | Q | 246 | 81% 7% 11% |
| 2 | T | 246 | 85% 6% 9% |
| 2 | W | 246 | 83% 7% 11% |
| 3 | C | 77 | 78% 22% |
| 3 | F | 77 | 66% 31% |
| 3 | I | 77 | 65% 6% 29% |
| 3 | L | 77 | 70% 30% |
| 3 | O | 77 | 73% 6% 21% |
| 3 | R | 77 | 75% 21% |
| 3 | U | 77 | 61% 9% 30% |
| 3 | X | 77 | 53% 14% 31% |

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 |
|---|---|---|---|---|---|---|---|
| 4 | UNX | E | 1814 | - | - | X | - |
| 4 | UNX | G | 1820 | - | - | X | - |

## 2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 31176 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 FAB light chain.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| 1 | A | 213 | Total | C | N | O | S | 0 | 4 | 0 |
| | | | 1639 | 1045 | 269 | 320 | 5 | | | |
| 1 | D | 213 | Total | C | N | O | S | 0 | 2 | 0 |
| | | | 1619 | 1028 | 267 | 319 | 5 | | | |
| 1 | G | 213 | Total | C | N | O | S | 0 | 4 | 0 |
| | | | 1639 | 1039 | 271 | 324 | 5 | | | |
| 1 | J | 213 | Total | C | N | O | S | 0 | 2 | 0 |
| | | | 1632 | 1033 | 269 | 325 | 5 | | | |
| 1 | M | 214 | Total | C | N | O | S | 0 | 4 | 0 |
| | | | 1648 | 1049 | 272 | 322 | 5 | | | |
| 1 | P | 213 | Total | C | N | O | S | 0 | 4 | 0 |
| | | | 1645 | 1042 | 271 | 327 | 5 | | | |
| 1 | S | 214 | Total | C | N | O | S | 0 | 3 | 0 |
| | | | 1633 | 1041 | 266 | 321 | 5 | | | |
| 1 | V | 212 | Total | C | N | O | S | 0 | 1 | 0 |
| | | | 1602 | 1021 | 259 | 317 | 5 | | | |

- Molecule 2 is a protein called FAB heavy chain.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| 2 | B | 225 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1650 | 1040 | 275 | 328 | 7 | | | |
| 2 | E | 226 | Total | C | N | O | S | 0 | 2 | 0 |
| | | | 1676 | 1057 | 281 | 331 | 7 | | | |
| 2 | H | 218 | Total | C | N | O | S | 0 | 3 | 0 |
| | | | 1624 | 1029 | 267 | 319 | 9 | | | |
| 2 | K | 218 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1610 | 1020 | 267 | 316 | 7 | | | |
| 2 | N | 226 | Total | C | N | O | S | 0 | 2 | 0 |
| | | | 1663 | 1048 | 278 | 330 | 7 | | | |
| 2 | Q | 218 | Total | C | N | O | S | 0 | 2 | 0 |
| | | | 1618 | 1026 | 268 | 317 | 7 | | | |

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| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| 2 | T | 225 | Total | C | N | O | S | 0 | 2 | 0 |
| | | | 1654 | 1047 | 273 | 327 | 7 | | | |
| 2 | W | 220 | Total | C | N | O | S | 0 | 1 | 0 |
| | | | 1624 | 1029 | 267 | 321 | 7 | | | |

- Molecule 3 is a protein called Tudor domain-containing protein 3.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| 3 | C | 60 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 482 | 316 | 71 | 92 | 3 | | | |
| 3 | F | 53 | Total | C | N | O | S | 0 | 1 | 0 |
| | | | 434 | 285 | 64 | 83 | 2 | | | |
| 3 | I | 55 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 436 | 286 | 64 | 84 | 2 | | | |
| 3 | L | 54 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 423 | 275 | 63 | 83 | 2 | | | |
| 3 | O | 61 | Total | C | N | O | S | 0 | 1 | 0 |
| | | | 482 | 315 | 70 | 95 | 2 | | | |
| 3 | R | 61 | Total | C | N | O | S | 0 | 1 | 0 |
| | | | 488 | 321 | 70 | 93 | 4 | | | |
| 3 | U | 54 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 433 | 284 | 66 | 81 | 2 | | | |
| 3 | X | 53 | Total | C | N | O | S | 0 | 1 | 0 |
| | | | 404 | 266 | 61 | 75 | 2 | | | |

There are 8 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|---|---|---|---|---|---|
| C | 539 | GLY | - | expression tag | UNP Q9H7E2 |
| F | 539 | GLY | - | expression tag | UNP Q9H7E2 |
| I | 539 | GLY | - | expression tag | UNP Q9H7E2 |
| L | 539 | GLY | - | expression tag | UNP Q9H7E2 |
| O | 539 | GLY | - | expression tag | UNP Q9H7E2 |
| R | 539 | GLY | - | expression tag | UNP Q9H7E2 |
| U | 539 | GLY | - | expression tag | UNP Q9H7E2 |
| X | 539 | GLY | - | expression tag | UNP Q9H7E2 |

- Molecule 4 is UNKNOWN ATOM OR ION (three-letter code: UNX) (formula: X).

| Mol | Chain | Residues | Atoms | | ZeroOcc | AltConf |
|---|---|---|---|---|---|---|
| 4 | A | 7 | Total | X | 0 | 0 |
| | | | 7 | 7 | | |

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| Mol | Chain | Residues | Atoms | ZeroOcc | AltConf |
|---|---|---|---|---|---|
| 4 | B | 12 | Total X<br>12 12 | 0 | 0 |
| 4 | C | 2 | Total X<br>2 2 | 0 | 0 |
| 4 | D | 5 | Total X<br>5 5 | 0 | 0 |
| 4 | E | 11 | Total X<br>11 11 | 0 | 0 |
| 4 | F | 1 | Total X<br>1 1 | 0 | 0 |
| 4 | G | 9 | Total X<br>9 9 | 0 | 0 |
| 4 | H | 16 | Total X<br>16 16 | 0 | 0 |
| 4 | I | 1 | Total X<br>1 1 | 0 | 0 |
| 4 | J | 7 | Total X<br>7 7 | 0 | 0 |
| 4 | K | 6 | Total X<br>6 6 | 0 | 0 |
| 4 | M | 3 | Total X<br>3 3 | 0 | 0 |
| 4 | N | 12 | Total X<br>12 12 | 0 | 0 |
| 4 | P | 11 | Total X<br>11 11 | 0 | 0 |
| 4 | Q | 8 | Total X<br>8 8 | 0 | 0 |
| 4 | R | 1 | Total X<br>1 1 | 0 | 0 |
| 4 | S | 2 | Total X<br>2 2 | 0 | 0 |
| 4 | T | 12 | Total X<br>12 12 | 0 | 0 |
| 4 | V | 7 | Total X<br>7 7 | 0 | 0 |
| 4 | W | 10 | Total X<br>10 10 | 0 | 0 |

- Molecule 5 is water.

| Mol | Chain | Residues | Atoms | ZeroOcc | AltConf |
|---|---|---|---|---|---|
| 5 | A | 69 | Total O<br>69 69 | 0 | 0 |
| 5 | B | 111 | Total O<br>111 111 | 0 | 0 |
| 5 | C | 13 | Total O<br>13 13 | 0 | 0 |
| 5 | D | 51 | Total O<br>51 51 | 0 | 0 |
| 5 | E | 107 | Total O<br>107 107 | 0 | 0 |
| 5 | F | 2 | Total O<br>2 2 | 0 | 0 |
| 5 | G | 52 | Total O<br>52 52 | 0 | 0 |
| 5 | H | 82 | Total O<br>82 82 | 0 | 0 |
| 5 | I | 8 | Total O<br>8 8 | 0 | 0 |
| 5 | J | 60 | Total O<br>60 60 | 0 | 0 |
| 5 | K | 89 | Total O<br>89 89 | 0 | 0 |
| 5 | L | 2 | Total O<br>2 2 | 0 | 0 |
| 5 | M | 55 | Total O<br>55 55 | 0 | 0 |
| 5 | N | 104 | Total O<br>104 104 | 0 | 0 |
| 5 | O | 7 | Total O<br>7 7 | 0 | 0 |
| 5 | P | 60 | Total O<br>60 60 | 0 | 0 |
| 5 | Q | 106 | Total O<br>106 106 | 0 | 0 |
| 5 | R | 14 | Total O<br>14 14 | 0 | 0 |
| 5 | S | 45 | Total O<br>45 45 | 0 | 0 |
| 5 | T | 108 | Total O<br>108 108 | 0 | 0 |
| 5 | U | 6 | Total O<br>6 6 | 0 | 0 |
| 5 | V | 42 | Total O<br>42 42 | 0 | 0 |

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| Mol | Chain | Residues | Atoms | ZeroOcc | AltConf |
|---|---|---|---|---|---|
| 5 | W | 81 | Total O<br>81 81 | 0 | 0 |
| 5 | X | 1 | Total O<br>1 1 | 0 | 0 |

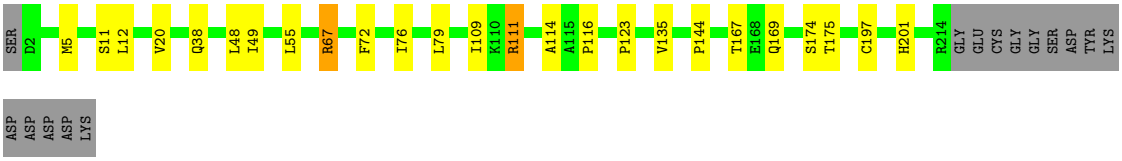
# 3 Residue-property plots (i)

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.

Note EDS failed to run properly.

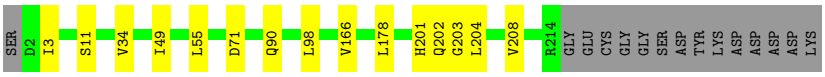
• Molecule 1: FAB light chain

Chain A:


• Molecule 1: FAB light chain

Chain D:

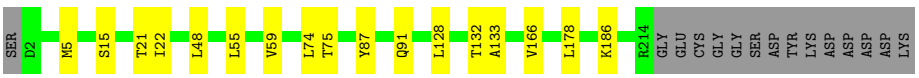

• Molecule 1: FAB light chain

Chain G:



• Molecule 1: FAB light chain

Chain J:


• Molecule 1: FAB light chain

Chain M:



• Molecule 1: FAB light chain

Chain P:



• Molecule 1: FAB light chain

Chain S:



• Molecule 1: FAB light chain

Chain V:



• Molecule 2: FAB heavy chain

Chain B:



• Molecule 2: FAB heavy chain

Chain E:



• Molecule 2: FAB heavy chain

Chain H:



• Molecule 2: FAB heavy chain

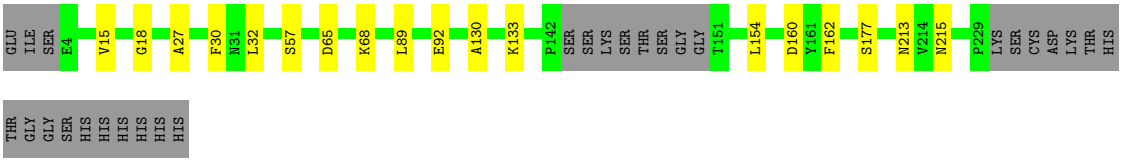
Chain K:

• Molecule 2: FAB heavy chain

Chain N:


• Molecule 2: FAB heavy chain

Chain Q:

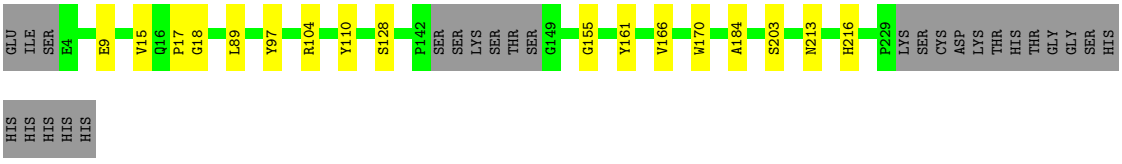



• Molecule 2: FAB heavy chain

Chain T:

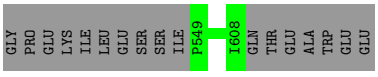

• Molecule 2: FAB heavy chain

Chain W:

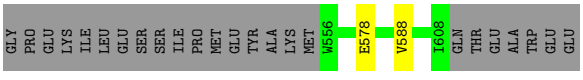
• Molecule 3: Tudor domain-containing protein 3

Chain C:

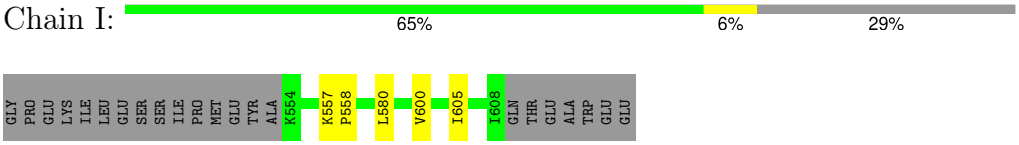
• Molecule 3: Tudor domain-containing protein 3

Chain F:

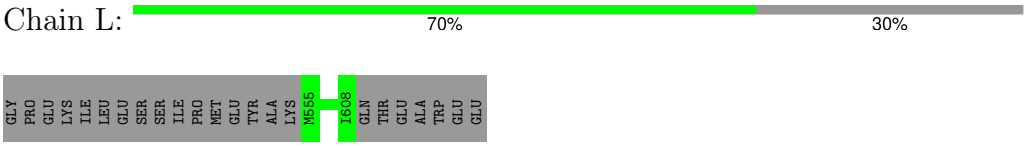
• Molecule 3: Tudor domain-containing protein 3

Chain I:



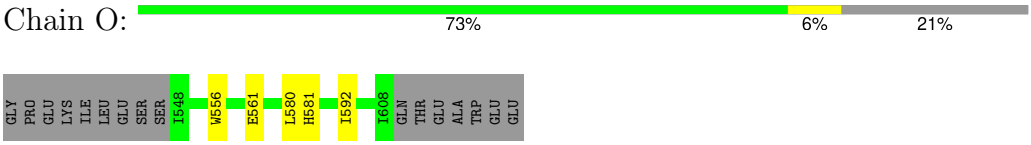

• Molecule 3: Tudor domain-containing protein 3

Chain L:



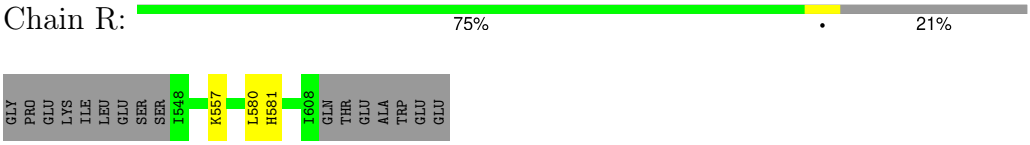

• Molecule 3: Tudor domain-containing protein 3

Chain O:



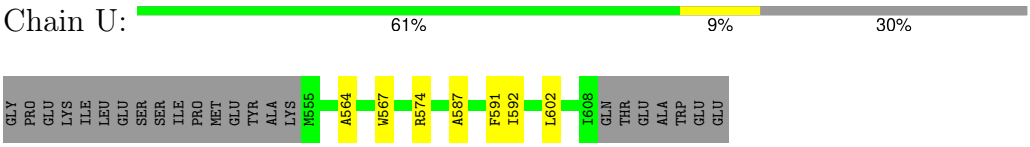

• Molecule 3: Tudor domain-containing protein 3

Chain R:



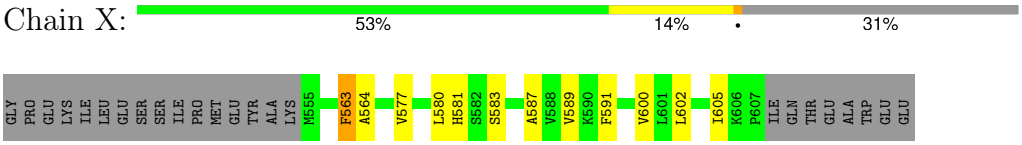

• Molecule 3: Tudor domain-containing protein 3

Chain U:




• Molecule 3: Tudor domain-containing protein 3

Chain X:



# 4 Data and refinement statistics (i)

EDS failed to run properly - this section is therefore incomplete.

| Property | Value | Source |
|---|---|---|
| Space group | P 1 | Depositor |
| Cell constants<br>a, b, c, $\alpha$, $\beta$, $\gamma$ | 76.71Å 93.73Å 159.93Å<br>80.96° 82.82° 90.06° | Depositor |
| Resolution (Å) | 30.00 – 2.05 | Depositor |
| % Data completeness<br>(in resolution range) | 97.2 (30.00-2.05) | Depositor |
| $R_{merge}$ | 0.09 | Depositor |
| $R_{sym}$ | (Not available) | Depositor |
| $< I/\sigma(I) >$ [1] | 1.98 (at 2.05Å) | Xtriage |
| Refinement program | REFMAC 5.5.0109 | Depositor |
| R, $R_{free}$ | 0.223 , 0.264 | Depositor |
| Wilson B-factor (Å$^2$) | 29.3 | Xtriage |
| Anisotropy | 0.122 | Xtriage |
| L-test for twinning[2] | $< \|L\| > = 0.47$, $< L^2 > = 0.30$ | Xtriage |
| Estimated twinning fraction | No twinning to report. | Xtriage |
| Total number of atoms | 31176 | wwPDB-VP |
| Average B, all atoms (Å$^2$) | 55.0 | wwPDB-VP |

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 58.12 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.1425e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[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: UNX

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 | 0.63 | 0/1690 | 0.61 | 0/2305 |
| 1 | D | 0.63 | 0/1667 | 0.61 | 0/2274 |
| 1 | G | 0.63 | 0/1693 | 0.60 | 0/2307 |
| 1 | J | 0.59 | 0/1679 | 0.60 | 0/2288 |
| 1 | M | 0.63 | 0/1702 | 0.61 | 0/2320 |
| 1 | P | 0.62 | 0/1698 | 0.61 | 0/2315 |
| 1 | S | 0.61 | 0/1684 | 0.57 | 0/2297 |
| 1 | V | 0.62 | 0/1646 | 0.60 | 0/2246 |
| 2 | B | 0.73 | 0/1692 | 0.69 | 0/2312 |
| 2 | E | 0.72 | 0/1724 | 0.66 | 0/2352 |
| 2 | H | 0.74 | 0/1674 | 0.70 | 0/2286 |
| 2 | K | 0.67 | 0/1651 | 0.66 | 0/2256 |
| 2 | N | 0.75 | 0/1711 | 0.68 | 0/2338 |
| 2 | Q | 0.75 | 0/1665 | 0.70 | 0/2275 |
| 2 | T | 0.71 | 0/1702 | 0.66 | 0/2326 |
| 2 | W | 0.76 | 0/1668 | 0.66 | 0/2278 |
| 3 | C | 0.62 | 0/497 | 0.56 | 0/675 |
| 3 | F | 0.56 | 0/450 | 0.50 | 0/612 |
| 3 | I | 0.61 | 0/449 | 0.55 | 0/612 |
| 3 | L | 0.52 | 0/435 | 0.49 | 0/594 |
| 3 | O | 0.59 | 0/500 | 0.51 | 0/683 |
| 3 | R | 0.61 | 0/506 | 0.54 | 0/689 |
| 3 | U | 0.55 | 0/446 | 0.51 | 0/607 |
| 3 | X | 0.61 | 0/419 | 0.53 | 0/573 |
| All | All | 0.67 | 0/30648 | 0.63 | 0/41820 |

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 | 1639 | 0 | 1543 | 17 | 0 |
| 1 | D | 1619 | 0 | 1509 | 6 | 0 |
| 1 | G | 1639 | 0 | 1559 | 7 | 0 |
| 1 | J | 1632 | 0 | 1551 | 11 | 0 |
| 1 | M | 1648 | 0 | 1574 | 20 | 0 |
| 1 | P | 1645 | 0 | 1559 | 7 | 0 |
| 1 | S | 1633 | 0 | 1534 | 13 | 0 |
| 1 | V | 1602 | 0 | 1499 | 8 | 0 |
| 2 | B | 1650 | 0 | 1573 | 6 | 0 |
| 2 | E | 1676 | 0 | 1617 | 12 | 0 |
| 2 | H | 1624 | 0 | 1554 | 6 | 0 |
| 2 | K | 1610 | 0 | 1537 | 5 | 0 |
| 2 | N | 1663 | 0 | 1587 | 9 | 0 |
| 2 | Q | 1618 | 0 | 1552 | 9 | 0 |
| 2 | T | 1654 | 0 | 1578 | 9 | 0 |
| 2 | W | 1624 | 0 | 1550 | 8 | 0 |
| 3 | C | 482 | 0 | 442 | 0 | 0 |
| 3 | F | 434 | 0 | 400 | 1 | 0 |
| 3 | I | 436 | 0 | 389 | 4 | 0 |
| 3 | L | 423 | 0 | 376 | 0 | 0 |
| 3 | O | 482 | 0 | 417 | 3 | 0 |
| 3 | R | 488 | 0 | 438 | 3 | 0 |
| 3 | U | 433 | 0 | 394 | 4 | 0 |
| 3 | X | 404 | 0 | 352 | 9 | 0 |
| 4 | A | 7 | 0 | 0 | 0 | 0 |
| 4 | B | 12 | 0 | 0 | 0 | 0 |
| 4 | C | 2 | 0 | 0 | 0 | 0 |
| 4 | D | 5 | 0 | 0 | 0 | 0 |
| 4 | E | 11 | 0 | 0 | 2 | 0 |
| 4 | F | 1 | 0 | 0 | 0 | 0 |
| 4 | G | 9 | 0 | 0 | 2 | 0 |
| 4 | H | 16 | 0 | 0 | 0 | 0 |
| 4 | I | 1 | 0 | 0 | 0 | 0 |
| 4 | J | 7 | 0 | 0 | 0 | 0 |
| 4 | K | 6 | 0 | 0 | 0 | 0 |
| 4 | M | 3 | 0 | 0 | 0 | 0 |
| 4 | N | 12 | 0 | 0 | 0 | 0 |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|---|---|---|---|---|---|---|
| 4 | P | 11 | 0 | 0 | 0 | 0 |
| 4 | Q | 8 | 0 | 0 | 0 | 0 |
| 4 | R | 1 | 0 | 0 | 0 | 0 |
| 4 | S | 2 | 0 | 0 | 0 | 0 |
| 4 | T | 12 | 0 | 0 | 0 | 0 |
| 4 | V | 7 | 0 | 0 | 0 | 0 |
| 4 | W | 10 | 0 | 0 | 0 | 0 |
| 5 | A | 69 | 0 | 0 | 0 | 0 |
| 5 | B | 111 | 0 | 0 | 1 | 0 |
| 5 | C | 13 | 0 | 0 | 0 | 0 |
| 5 | D | 51 | 0 | 0 | 0 | 0 |
| 5 | E | 107 | 0 | 0 | 1 | 0 |
| 5 | F | 2 | 0 | 0 | 0 | 0 |
| 5 | G | 52 | 0 | 0 | 0 | 0 |
| 5 | H | 82 | 0 | 0 | 0 | 0 |
| 5 | I | 8 | 0 | 0 | 0 | 0 |
| 5 | J | 60 | 0 | 0 | 0 | 0 |
| 5 | K | 89 | 0 | 0 | 0 | 0 |
| 5 | L | 2 | 0 | 0 | 0 | 0 |
| 5 | M | 55 | 0 | 0 | 0 | 0 |
| 5 | N | 104 | 0 | 0 | 1 | 0 |
| 5 | O | 7 | 0 | 0 | 0 | 0 |
| 5 | P | 60 | 0 | 0 | 0 | 0 |
| 5 | Q | 106 | 0 | 0 | 0 | 0 |
| 5 | R | 14 | 0 | 0 | 0 | 0 |
| 5 | S | 45 | 0 | 0 | 0 | 0 |
| 5 | T | 108 | 0 | 0 | 0 | 0 |
| 5 | U | 6 | 0 | 0 | 0 | 0 |
| 5 | V | 42 | 0 | 0 | 0 | 0 |
| 5 | W | 81 | 0 | 0 | 0 | 0 |
| 5 | X | 1 | 0 | 0 | 0 | 0 |
| All | All | 31176 | 0 | 28084 | 168 | 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 3.

All (168) 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) |
|---|---|---|---|
| 2:E:143:SER:OG | 4:E:1814:UNX:UNK | 1.42 | 0.99 |
| 1:G:64:SER:OG | 4:G:1820:UNX:UNK | 1.48 | 0.93 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:S:29:SER:CB | 1:S:70:THR:HG22 | 2.23 | 0.69 |
| 2:E:143:SER:HG | 4:E:1814:UNX:UNK | 1.35 | 0.68 |
| 1:M:12[B]:LEU:HD23 | 1:M:107:VAL:HG13 | 1.74 | 0.67 |
| 1:D:204:LEU:HD13 | 1:D:208:VAL:HG23 | 1.76 | 0.66 |
| 1:A:76:ILE:HG21 | 1:A:79:LEU:HD12 | 1.80 | 0.63 |
| 1:J:166:VAL:HG22 | 1:J:178:LEU:HD12 | 1.81 | 0.63 |
| 1:J:22:ILE:HD12 | 1:J:74:LEU:HD23 | 1.81 | 0.62 |
| 3:I:600:VAL:CG2 | 3:I:605:ILE:HD11 | 2.31 | 0.61 |
| 1:M:123:PRO:HD3 | 1:M:135:VAL:HG22 | 1.83 | 0.60 |
| 2:Q:15:VAL:HG11 | 2:Q:89:LEU:HD13 | 1.83 | 0.60 |
| 2:N:161:TYR:CE1 | 2:N:166:VAL:HG13 | 2.36 | 0.59 |
| 1:G:111:ARG:HD2 | 1:G:174:SER:HB2 | 1.84 | 0.59 |
| 1:S:166:VAL:HG22 | 1:S:178:LEU:HD12 | 1.85 | 0.59 |
| 3:X:587:ALA:HB2 | 3:X:602:LEU:HD21 | 1.83 | 0.59 |
| 1:G:111:ARG:HH12 | 1:G:114:ALA:HB2 | 1.69 | 0.58 |
| 1:M:20:VAL:HG13 | 1:M:76[A]:ILE:HB | 1.86 | 0.58 |
| 3:U:574:ARG:HG2 | 3:U:592:ILE:HD12 | 1.85 | 0.58 |
| 2:K:169:SER:HB3 | 2:K:213:ASN:HB2 | 1.85 | 0.58 |
| 1:V:38:GLN:HB2 | 1:V:48:LEU:HD11 | 1.85 | 0.57 |
| 1:D:49:ILE:HD13 | 1:D:55:LEU:HA | 1.86 | 0.57 |
| 3:U:587:ALA:HB2 | 3:U:602:LEU:HD21 | 1.86 | 0.56 |
| 2:E:22:ARG:NH1 | 5:E:790:HOH:O | 2.37 | 0.56 |
| 1:M:20:VAL:HG13 | 1:M:76[B]:ILE:HB | 1.87 | 0.56 |
| 2:T:137:VAL:HG21 | 2:T:214:VAL:HG21 | 1.88 | 0.56 |
| 1:A:38:GLN:HB2 | 1:A:48:LEU:HD11 | 1.88 | 0.55 |
| 1:D:201[B]:HIS:CD2 | 1:D:203:GLY:H | 2.24 | 0.55 |
| 1:J:128:LEU:HD22 | 1:J:186:LYS:HG3 | 1.87 | 0.55 |
| 1:D:166:VAL:HG22 | 1:D:178:LEU:HD12 | 1.89 | 0.55 |
| 2:T:186:LEU:HD13 | 2:T:192:TYR:CZ | 2.42 | 0.55 |
| 1:M:111:ARG:HH12 | 1:M:114:ALA:HB2 | 1.72 | 0.54 |
| 2:H:208:GLN:HG2 | 2:H:210:TYR:CZ | 2.43 | 0.54 |
| 1:M:20:VAL:HG11 | 1:M:79:LEU:HD13 | 1.89 | 0.54 |
| 1:M:29:SER:CB | 1:M:70:THR:HG22 | 2.38 | 0.54 |
| 1:D:34:VAL:HA | 1:D:90:GLN:O | 2.08 | 0.53 |
| 1:M:111:ARG:HD2 | 1:M:174:SER:HB2 | 1.91 | 0.53 |
| 1:A:111:ARG:HH12 | 1:A:114:ALA:HB2 | 1.73 | 0.53 |
| 2:W:15:VAL:HG11 | 2:W:89:LEU:HD13 | 1.91 | 0.52 |
| 1:A:109:ILE:HG22 | 1:A:169:GLN:OE1 | 2.09 | 0.52 |
| 2:T:166:VAL:CG2 | 2:T:194:LEU:HD21 | 2.39 | 0.52 |
| 3:I:600:VAL:HG23 | 3:I:605:ILE:HD11 | 1.92 | 0.51 |
| 1:M:112:THR:HG22 | 1:M:113:VAL:O | 2.10 | 0.51 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:V:3:ILE:HD12 | 1:V:98:LEU:HD12 | 1.93 | 0.51 |
| 1:A:111:ARG:NH1 | 1:A:175:THR:HG22 | 2.25 | 0.51 |
| 2:H:25:CYS:SG | 2:H:99[B]:CYS:HB3 | 2.50 | 0.51 |
| 1:J:5:MET:HE3 | 1:J:91:GLN:HB2 | 1.92 | 0.51 |
| 1:M:20:VAL:CG1 | 1:M:79:LEU:HD13 | 2.40 | 0.51 |
| 3:X:577:VAL:HG11 | 3:X:580:LEU:HD11 | 1.92 | 0.51 |
| 2:H:25:CYS:SG | 2:H:99[B]:CYS:CB | 2.99 | 0.50 |
| 2:B:161:TYR:CE2 | 2:B:166:VAL:HG13 | 2.46 | 0.50 |
| 1:A:111:ARG:HD2 | 1:A:174:SER:HB2 | 1.92 | 0.50 |
| 1:J:5:MET:CE | 1:J:91:GLN:HB2 | 2.41 | 0.50 |
| 3:I:557:LYS:HA | 3:I:580:LEU:HD11 | 1.94 | 0.49 |
| 1:A:49:ILE:HD13 | 1:A:55:LEU:HA | 1.94 | 0.49 |
| 2:E:54:ILE:HD12 | 2:E:61:THR:HG22 | 1.95 | 0.49 |
| 1:P:111:ARG:HD2 | 1:P:174:SER:HB2 | 1.94 | 0.48 |
| 3:O:561:GLU:OE1 | 3:O:592:ILE:HD11 | 2.13 | 0.48 |
| 2:E:161:TYR:CE1 | 2:E:166:VAL:HG13 | 2.49 | 0.48 |
| 1:P:31:SER:O | 1:P:67:ARG:NH1 | 2.46 | 0.48 |
| 3:F:578:GLU:HB3 | 3:F:588:VAL:HG12 | 1.96 | 0.48 |
| 2:T:9:GLU:OE1 | 2:T:97:TYR:O | 2.32 | 0.48 |
| 3:O:556:TRP:O | 3:O:580:LEU:HD11 | 2.14 | 0.48 |
| 3:X:564:ALA:HB3 | 3:X:591:PHE:CE1 | 2.49 | 0.48 |
| 3:X:577:VAL:HA | 3:X:589:VAL:HG12 | 1.96 | 0.48 |
| 2:B:69:GLY:O | 5:B:1101:HOH:O | 2.20 | 0.47 |
| 3:R:557:LYS:HA | 3:R:580:LEU:HD11 | 1.96 | 0.47 |
| 2:W:17:PRO:HD3 | 2:W:128:SER:C | 2.34 | 0.47 |
| 1:D:3:ILE:HD12 | 1:D:98:LEU:HD12 | 1.95 | 0.47 |
| 1:A:123:PRO:HD3 | 1:A:135:VAL:HG22 | 1.96 | 0.47 |
| 2:E:39:TRP:HD1 | 2:E:73:ILE:HD12 | 1.79 | 0.47 |
| 1:M:38:GLN:HB2 | 1:M:48:LEU:HD11 | 1.97 | 0.47 |
| 1:A:109:ILE:HG22 | 1:A:169:GLN:CD | 2.35 | 0.47 |
| 1:M:36:TRP:CZ3 | 1:M:89:CYS:HB3 | 2.49 | 0.47 |
| 1:G:166:VAL:HG22 | 1:G:178:LEU:HD12 | 1.96 | 0.47 |
| 2:K:15:VAL:HG11 | 2:K:89:LEU:HD13 | 1.96 | 0.46 |
| 3:X:600:VAL:HG21 | 3:X:605:ILE:CG2 | 2.45 | 0.46 |
| 1:S:201[B]:HIS:CD2 | 1:S:203:GLY:H | 2.34 | 0.46 |
| 3:X:563:PHE:O | 3:X:605:ILE:HA | 2.15 | 0.46 |
| 1:S:48:LEU:HD11 | 1:S:87:TYR:CE2 | 2.50 | 0.46 |
| 1:S:127:GLN:NE2 | 1:S:132:THR:HG22 | 2.31 | 0.46 |
| 1:V:113:VAL:HG22 | 1:V:144:PRO:HD3 | 1.98 | 0.46 |
| 1:A:111:ARG:HH12 | 1:A:114:ALA:CB | 2.29 | 0.46 |
| 3:U:564:ALA:HB3 | 3:U:591:PHE:CE1 | 2.50 | 0.46 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:V:5:MET:CE | 1:V:91:GLN:HB2 | 2.46 | 0.46 |
| 1:J:48:LEU:HD11 | 1:J:87:TYR:HE2 | 1.81 | 0.45 |
| 2:Q:65:ASP:HA | 2:Q:68:LYS:HE3 | 1.97 | 0.45 |
| 2:N:212:CYS:SG | 2:N:225:LYS:HB3 | 2.56 | 0.45 |
| 2:Q:57:SER:HB3 | 3:R:581:HIS:NE2 | 2.31 | 0.45 |
| 3:X:580:LEU:N | 3:X:580:LEU:HD12 | 2.32 | 0.45 |
| 2:N:68:LYS:NZ | 5:N:842:HOH:O | 2.48 | 0.45 |
| 2:T:109:PRO:HB3 | 3:U:567:TRP:CE2 | 2.51 | 0.45 |
| 1:A:67:ARG:HB3 | 1:A:72:PHE:CD2 | 2.51 | 0.45 |
| 2:H:15:VAL:HG11 | 2:H:89:LEU:HD13 | 1.98 | 0.45 |
| 2:E:20:SER:HA | 2:E:86:MET:O | 2.17 | 0.45 |
| 2:B:15:VAL:HG11 | 2:B:89:LEU:HD13 | 1.98 | 0.45 |
| 2:B:23:LEU:HD21 | 2:B:86:MET:HE1 | 1.98 | 0.45 |
| 1:J:55:LEU:HD11 | 1:J:59:VAL:HG12 | 1.99 | 0.45 |
| 2:E:54:ILE:HD12 | 2:E:61:THR:CG2 | 2.47 | 0.44 |
| 1:S:5:MET:HE1 | 1:S:91:GLN:HB2 | 1.98 | 0.44 |
| 1:J:48:LEU:HA | 1:J:59:VAL:HG21 | 1.99 | 0.44 |
| 2:N:144[B]:SER:OG | 2:N:152:ALA:HB2 | 2.17 | 0.44 |
| 2:N:172:SER:O | 2:Q:92:GLU:HB3 | 2.17 | 0.44 |
| 1:A:12:LEU:CD2 | 1:A:20:VAL:HG13 | 2.47 | 0.44 |
| 1:V:55:LEU:HD11 | 1:V:59:VAL:CG1 | 2.47 | 0.44 |
| 1:A:116:PRO:HD3 | 1:A:201[B]:HIS:CD2 | 2.52 | 0.44 |
| 1:M:109:ILE:HG22 | 1:M:169:GLN:OE1 | 2.17 | 0.44 |
| 1:G:64:SER:HG | 4:G:1820:UNX:UNK | 1.59 | 0.44 |
| 3:I:558:PRO:HD3 | 3:I:580:LEU:HD12 | 1.99 | 0.44 |
| 2:E:186:LEU:HD13 | 2:E:192:TYR:CZ | 2.53 | 0.44 |
| 2:N:186:LEU:HD13 | 2:N:192:TYR:CZ | 2.53 | 0.44 |
| 2:Q:57:SER:HB3 | 3:R:581:HIS:CD2 | 2.53 | 0.44 |
| 1:A:111:ARG:HH11 | 1:A:175:THR:HG22 | 1.83 | 0.43 |
| 3:X:587:ALA:HB2 | 3:X:602:LEU:CD2 | 2.48 | 0.43 |
| 2:E:217:LYS:N | 2:E:218:PRO:CD | 2.82 | 0.43 |
| 1:P:111:ARG:HH12 | 1:P:114:ALA:CB | 2.30 | 0.43 |
| 2:T:147:THR:HG21 | 1:V:157:LEU:HD11 | 1.99 | 0.43 |
| 2:Q:18:GLY:HA3 | 2:W:18:GLY:HA3 | 2.00 | 0.43 |
| 1:V:55:LEU:HD11 | 1:V:59:VAL:HG12 | 2.00 | 0.43 |
| 2:N:27:ALA:HB2 | 2:N:32:LEU:HD13 | 2.00 | 0.43 |
| 1:P:111:ARG:NH1 | 1:P:175:THR:HG22 | 2.33 | 0.43 |
| 2:K:161:TYR:OH | 2:K:184:ALA:HB2 | 2.19 | 0.43 |
| 1:M:116:PRO:HD3 | 1:M:201[B]:HIS:CD2 | 2.54 | 0.43 |
| 1:S:60:PRO:HB2 | 1:S:62:ARG:HG2 | 1.99 | 0.43 |
| 1:P:49:ILE:HD13 | 1:P:55:LEU:HA | 2.01 | 0.43 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 2:W:166:VAL:HG12 | 2:W:216:HIS:CD2 | 2.54 | 0.43 |
| 2:Q:130:ALA:HB3 | 2:Q:162:PHE:CE2 | 2.54 | 0.42 |
| 2:W:9:GLU:OE1 | 2:W:97:TYR:O | 2.38 | 0.42 |
| 2:K:194:LEU:C | 2:K:194:LEU:HD12 | 2.40 | 0.42 |
| 1:A:167:THR:HG23 | 2:B:182:PHE:CE1 | 2.55 | 0.42 |
| 1:M:34:VAL:HA | 1:M:90:GLN:O | 2.20 | 0.42 |
| 1:J:21:THR:HG22 | 1:J:75:THR:HG23 | 2.02 | 0.42 |
| 2:N:57:SER:HB3 | 3:O:581:HIS:NE2 | 2.35 | 0.42 |
| 2:Q:133:LYS:NZ | 2:Q:160:ASP:O | 2.43 | 0.42 |
| 1:G:111:ARG:NH1 | 1:G:112:THR:O | 2.53 | 0.41 |
| 1:J:48:LEU:HD11 | 1:J:87:TYR:CE2 | 2.56 | 0.41 |
| 1:P:51:SER:O | 1:P:52:ALA:HB3 | 2.20 | 0.41 |
| 2:T:161:TYR:CE1 | 2:T:166:VAL:HG13 | 2.55 | 0.41 |
| 2:E:15:VAL:HG11 | 2:E:89:LEU:HD13 | 2.02 | 0.41 |
| 2:N:43:ALA:HB3 | 2:N:46:LYS:HG3 | 2.02 | 0.41 |
| 1:P:111:ARG:HH11 | 1:P:175:THR:HG22 | 1.85 | 0.41 |
| 2:H:101:ARG:CZ | 2:H:103:VAL:HG11 | 2.50 | 0.41 |
| 1:S:97[A]:TRP:CH2 | 2:T:36:TYR:CE2 | 3.09 | 0.41 |
| 2:H:102:THR:HG21 | 2:H:114:TRP:HA | 2.02 | 0.41 |
| 2:W:104:ARG:HG3 | 2:W:110:TYR:HB3 | 2.02 | 0.41 |
| 2:W:155:GLY:HA2 | 2:W:170:TRP:CZ2 | 2.55 | 0.41 |
| 1:A:12:LEU:HD21 | 1:A:20:VAL:HG13 | 2.03 | 0.41 |
| 2:B:160:ASP:HB3 | 2:B:191:LEU:HD13 | 2.03 | 0.41 |
| 1:G:55:LEU:HD11 | 1:G:59:VAL:HG12 | 2.02 | 0.41 |
| 1:M:5:MET:SD | 1:M:26:ALA:HB2 | 2.61 | 0.41 |
| 3:X:581:HIS:ND1 | 3:X:583:SER:HB3 | 2.36 | 0.41 |
| 1:M:123:PRO:HG3 | 1:M:133:ALA:HB1 | 2.04 | 0.40 |
| 2:Q:27:ALA:HB1 | 2:Q:30:PHE:CE1 | 2.56 | 0.40 |
| 1:S:5:MET:HE1 | 1:S:91:GLN:CB | 2.51 | 0.40 |
| 1:V:183:THR:O | 1:V:184:LEU:HD23 | 2.21 | 0.40 |
| 2:E:23:LEU:HD21 | 2:E:86:MET:HE1 | 2.03 | 0.40 |
| 1:S:164:GLU:HA | 1:S:179:SER:O | 2.20 | 0.40 |
| 2:K:100:ALA:HB1 | 2:K:116:MET:HB3 | 2.03 | 0.40 |
| 1:M:55:LEU:HD11 | 1:M:59:VAL:HG12 | 2.03 | 0.40 |
| 2:T:163:PRO:HD2 | 2:T:218:PRO:HB2 | 2.03 | 0.40 |
| 1:A:144:PRO:O | 1:A:201[B]:HIS:HE1 | 2.05 | 0.40 |
| 1:J:132:THR:HG22 | 1:J:133:ALA:N | 2.37 | 0.40 |
| 1:M:51:SER:O | 1:M:52:ALA:HB3 | 2.22 | 0.40 |
| 1:S:34:VAL:HA | 1:S:90:GLN:O | 2.22 | 0.40 |
| 2:W:161:TYR:OH | 2:W:184:ALA:HB2 | 2.21 | 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 | 215/228 (94%) | 209 (97%) | 6 (3%) | 0 | 100 | 100 |
| 1 | D | 213/228 (93%) | 204 (96%) | 9 (4%) | 0 | 100 | 100 |
| 1 | G | 215/228 (94%) | 204 (95%) | 11 (5%) | 0 | 100 | 100 |
| 1 | J | 213/228 (93%) | 204 (96%) | 9 (4%) | 0 | 100 | 100 |
| 1 | M | 216/228 (95%) | 208 (96%) | 8 (4%) | 0 | 100 | 100 |
| 1 | P | 215/228 (94%) | 205 (95%) | 10 (5%) | 0 | 100 | 100 |
| 1 | S | 215/228 (94%) | 203 (94%) | 12 (6%) | 0 | 100 | 100 |
| 1 | V | 211/228 (92%) | 201 (95%) | 10 (5%) | 0 | 100 | 100 |
| 2 | B | 223/246 (91%) | 220 (99%) | 3 (1%) | 0 | 100 | 100 |
| 2 | E | 226/246 (92%) | 222 (98%) | 4 (2%) | 0 | 100 | 100 |
| 2 | H | 217/246 (88%) | 212 (98%) | 5 (2%) | 0 | 100 | 100 |
| 2 | K | 214/246 (87%) | 209 (98%) | 5 (2%) | 0 | 100 | 100 |
| 2 | N | 226/246 (92%) | 223 (99%) | 3 (1%) | 0 | 100 | 100 |
| 2 | Q | 216/246 (88%) | 213 (99%) | 3 (1%) | 0 | 100 | 100 |
| 2 | T | 225/246 (92%) | 222 (99%) | 3 (1%) | 0 | 100 | 100 |
| 2 | W | 217/246 (88%) | 212 (98%) | 5 (2%) | 0 | 100 | 100 |
| 3 | C | 58/77 (75%) | 58 (100%) | 0 | 0 | 100 | 100 |
| 3 | F | 52/77 (68%) | 52 (100%) | 0 | 0 | 100 | 100 |
| 3 | I | 53/77 (69%) | 53 (100%) | 0 | 0 | 100 | 100 |
| 3 | L | 52/77 (68%) | 52 (100%) | 0 | 0 | 100 | 100 |
| 3 | O | 60/77 (78%) | 59 (98%) | 1 (2%) | 0 | 100 | 100 |
| 3 | R | 60/77 (78%) | 60 (100%) | 0 | 0 | 100 | 100 |
| 3 | U | 52/77 (68%) | 52 (100%) | 0 | 0 | 100 | 100 |
| 3 | X | 52/77 (68%) | 50 (96%) | 2 (4%) | 0 | 100 | 100 |
| All | All | 3916/4408 (89%) | 3807 (97%) | 109 (3%) | 0 | 100 | 100 |

There are no Ramachandran outliers to report.

### 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 | 175/200 (88%) | 170 (97%) | 5 (3%) | 37 | 32 |
| 1 | D | 173/200 (86%) | 170 (98%) | 3 (2%) | 56 | 55 |
| 1 | G | 182/200 (91%) | 181 (100%) | 1 (0%) | 86 | 88 |
| 1 | J | 182/200 (91%) | 181 (100%) | 1 (0%) | 86 | 88 |
| 1 | M | 181/200 (90%) | 179 (99%) | 2 (1%) | 70 | 71 |
| 1 | P | 182/200 (91%) | 178 (98%) | 4 (2%) | 47 | 43 |
| 1 | S | 174/200 (87%) | 173 (99%) | 1 (1%) | 84 | 86 |
| 1 | V | 171/200 (86%) | 169 (99%) | 2 (1%) | 67 | 68 |
| 2 | B | 180/205 (88%) | 179 (99%) | 1 (1%) | 84 | 86 |
| 2 | E | 184/205 (90%) | 183 (100%) | 1 (0%) | 86 | 88 |
| 2 | H | 178/205 (87%) | 176 (99%) | 2 (1%) | 70 | 71 |
| 2 | K | 174/205 (85%) | 172 (99%) | 2 (1%) | 70 | 71 |
| 2 | N | 181/205 (88%) | 179 (99%) | 2 (1%) | 70 | 71 |
| 2 | Q | 176/205 (86%) | 171 (97%) | 5 (3%) | 38 | 34 |
| 2 | T | 178/205 (87%) | 175 (98%) | 3 (2%) | 56 | 55 |
| 2 | W | 175/205 (85%) | 173 (99%) | 2 (1%) | 70 | 71 |
| 3 | C | 49/67 (73%) | 49 (100%) | 0 | 100 | 100 |
| 3 | F | 45/67 (67%) | 45 (100%) | 0 | 100 | 100 |
| 3 | I | 43/67 (64%) | 43 (100%) | 0 | 100 | 100 |
| 3 | L | 42/67 (63%) | 42 (100%) | 0 | 100 | 100 |
| 3 | O | 46/67 (69%) | 46 (100%) | 0 | 100 | 100 |
| 3 | R | 48/67 (72%) | 48 (100%) | 0 | 100 | 100 |
| 3 | U | 43/67 (64%) | 43 (100%) | 0 | 100 | 100 |
| 3 | X | 37/67 (55%) | 36 (97%) | 1 (3%) | 40 | 35 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles |
|---|---|---|---|---|---|
| All | All | 3199/3776 (85%) | 3161 (99%) | 38 (1%) | 67 68 |

All (38) residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | A | 5 | MET |
| 1 | A | 11 | SER |
| 1 | A | 67 | ARG |
| 1 | A | 111 | ARG |
| 1 | A | 197 | CYS |
| 2 | B | 154 | LEU |
| 1 | D | 11 | SER |
| 1 | D | 71 | ASP |
| 1 | D | 202 | GLN |
| 2 | E | 202 | SER |
| 1 | G | 13 | SER |
| 2 | H | 208 | GLN |
| 2 | H | 213 | ASN |
| 1 | J | 15 | SER |
| 2 | K | 208 | GLN |
| 2 | K | 213 | ASN |
| 1 | M | 20 | VAL |
| 1 | M | 61 | SER |
| 2 | N | 154 | LEU |
| 2 | N | 194 | LEU |
| 1 | P | 111 | ARG |
| 1 | P | 132 | THR |
| 1 | P | 150 | GLN |
| 1 | P | 155 | ASN |
| 2 | Q | 32 | LEU |
| 2 | Q | 154 | LEU |
| 2 | Q | 177 | SER |
| 2 | Q | 213 | ASN |
| 2 | Q | 215 | ASN |
| 1 | S | 11 | SER |
| 2 | T | 33 | SER |
| 2 | T | 147 | THR |
| 2 | T | 154 | LEU |
| 1 | V | 66 | SER |
| 1 | V | 211 | SER |
| 2 | W | 203 | SER |
| 2 | W | 213 | ASN |

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| Mol | Chain | Res | Type |
|---|---|---|---|
| 3 | X | 563 | PHE |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 2 | B | 215 | ASN |
| 2 | E | 85 | GLN |
| 2 | E | 87 | ASN |
| 2 | K | 180 | HIS |

#### 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 oligosaccharides in this entry.

### 5.6 Ligand geometry (i)

Of 143 ligands modelled in this entry, 143 are unknown - 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 (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

EDS failed to run properly - this section is therefore empty.

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

EDS failed to run properly - this section is therefore empty.

## 6.3 Carbohydrates

EDS failed to run properly - this section is therefore empty.

## 6.4 Ligands

EDS failed to run properly - this section is therefore empty.

## 6.5 Other polymers

EDS failed to run properly - this section is therefore empty.