# Full wwPDB X-ray Structure Validation Report

Sep 26, 2016 – 05:28 PM EDT

| | | |
|---|---|---|
| PDB ID | : | 5DQO |
| Title | : | Crystal structure of Y347F mutant of human primase p58 iron-sulfur cluster domain |
| Authors | : | Salay, L.E.; Thompson, M.K.; Chazin, W.J. |
| Deposited on | : | 2015-09-15 |
| Resolution | : | 2.30 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
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

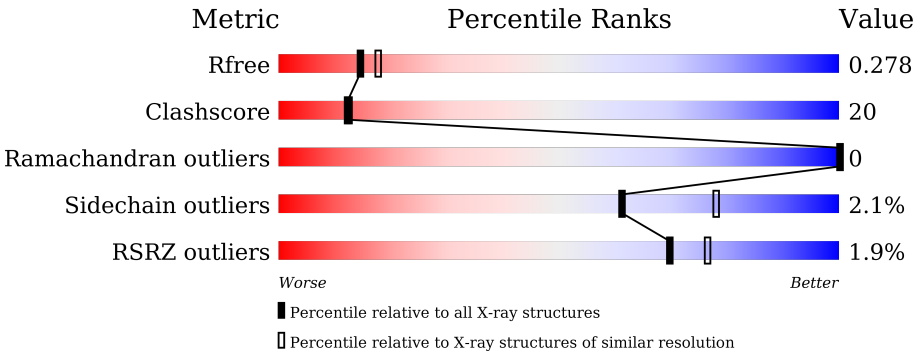
| | | |
|---|---|---|
| MolProbity | : | 4.02b-467 |
| Mogul | : | 1.7.1 (RC1), CSD as537be (2016) |
| Xtriage (Phenix) | : | 1.9-1692 |
| EDS | : | rb-20027939 |
| Percentile statistics | : | 20151230.v01 (using entries in the PDB archive December 30th 2015) |
| Refmac | : | 5.8.0135 |
| CCP4 | : | 6.5.0 |
| Ideal geometry (proteins) | : | Engh & Huber (2001) |
| Ideal geometry (DNA, RNA) | : | Parkinson et al. (1996) |
| Validation Pipeline (wwPDB-VP) | : | rb-20027939 |

# 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 2.30 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.




| Metric | Whole archive (#Entries) | Similar resolution (#Entries, resolution range(Å)) |
|---|---|---|
| $R_{free}$ | 91344 | 3852 (2.30-2.30) |
| Clashscore | 102246 | 4452 (2.30-2.30) |
| Ramachandran outliers | 100387 | 4410 (2.30-2.30) |
| Sidechain outliers | 100360 | 4409 (2.30-2.30) |
| RSRZ outliers | 91569 | 3857 (2.30-2.30) |

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 on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. 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 | 197 | 50% 29% • 20% |
| 1 | B | 197 | 2% 53% 24% • 22% |
| 1 | C | 197 | 56% 23% • 20% |
| 1 | D | 197 | 4% 51% 28% • 19% |

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4911 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

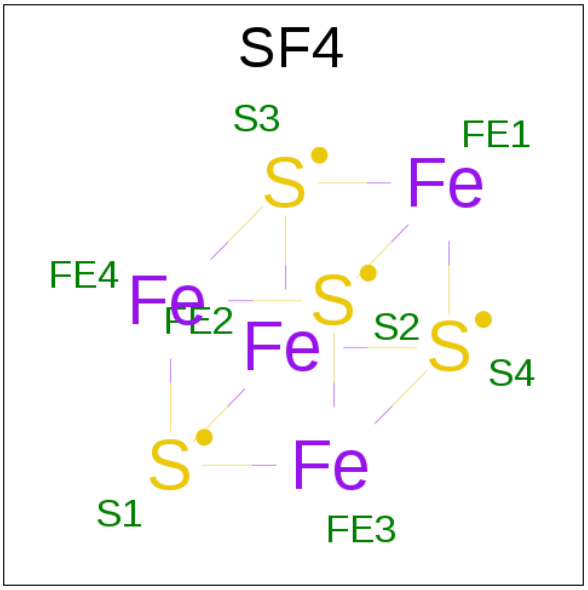
- Molecule 1 is a protein called DNA primase large subunit.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| 1 | A | 158 | Total | C | N | O | S | 0 | 1 | 0 |
| | | | 1229 | 786 | 219 | 215 | 9 | | | |
| 1 | B | 154 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1193 | 752 | 215 | 217 | 9 | | | |
| 1 | C | 158 | Total | C | N | O | S | 0 | 1 | 0 |
| | | | 1236 | 790 | 218 | 219 | 9 | | | |
| 1 | D | 159 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1207 | 762 | 216 | 220 | 9 | | | |

There are 20 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|---|---|---|---|---|---|
| A | 268 | GLY | - | expression tag | UNP P49643 |
| A | 269 | SER | - | expression tag | UNP P49643 |
| A | 270 | PRO | - | expression tag | UNP P49643 |
| A | 271 | ASN | - | expression tag | UNP P49643 |
| A | 347 | PHE | TYR | engineered mutation | UNP P49643 |
| B | 268 | GLY | - | expression tag | UNP P49643 |
| B | 269 | SER | - | expression tag | UNP P49643 |
| B | 270 | PRO | - | expression tag | UNP P49643 |
| B | 271 | ASN | - | expression tag | UNP P49643 |
| B | 347 | PHE | TYR | engineered mutation | UNP P49643 |
| C | 268 | GLY | - | expression tag | UNP P49643 |
| C | 269 | SER | - | expression tag | UNP P49643 |
| C | 270 | PRO | - | expression tag | UNP P49643 |
| C | 271 | ASN | - | expression tag | UNP P49643 |
| C | 347 | PHE | TYR | engineered mutation | UNP P49643 |
| D | 268 | GLY | - | expression tag | UNP P49643 |
| D | 269 | SER | - | expression tag | UNP P49643 |
| D | 270 | PRO | - | expression tag | UNP P49643 |
| D | 271 | ASN | - | expression tag | UNP P49643 |
| D | 347 | PHE | TYR | engineered mutation | UNP P49643 |

- Molecule 2 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: $Fe_4S_4$).




| Mol | Chain | Residues | Atoms | ZeroOcc | AltConf |
|---|---|---|---|---|---|
| 2 | A | 1 | Total Fe S<br>8 4 4 | 0 | 0 |
| 2 | B | 1 | Total Fe S<br>8 4 4 | 0 | 0 |
| 2 | C | 1 | Total Fe S<br>8 4 4 | 0 | 0 |
| 2 | D | 1 | Total Fe S<br>8 4 4 | 0 | 0 |

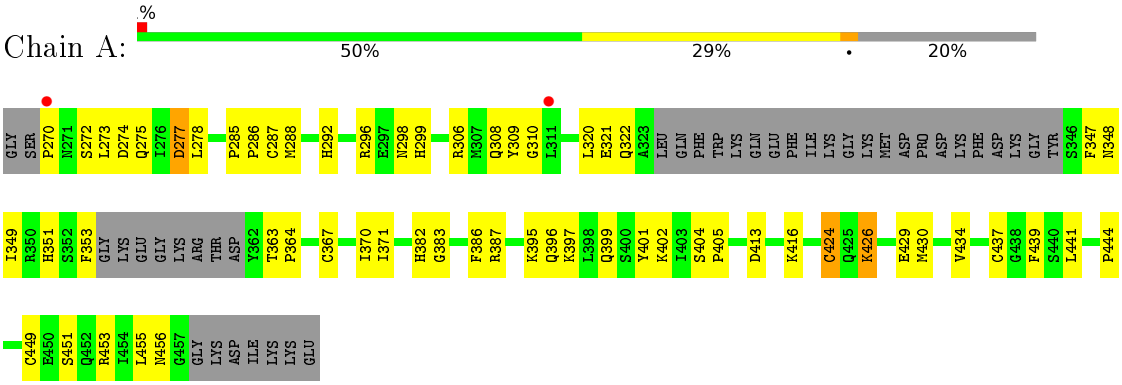
- Molecule 3 is water.

| Mol | Chain | Residues | Atoms | ZeroOcc | AltConf |
|---|---|---|---|---|---|
| 3 | A | 4 | Total O<br>4 4 | 0 | 0 |
| 3 | B | 3 | Total O<br>3 3 | 0 | 0 |
| 3 | C | 5 | Total O<br>5 5 | 0 | 0 |
| 3 | D | 2 | Total O<br>2 2 | 0 | 0 |

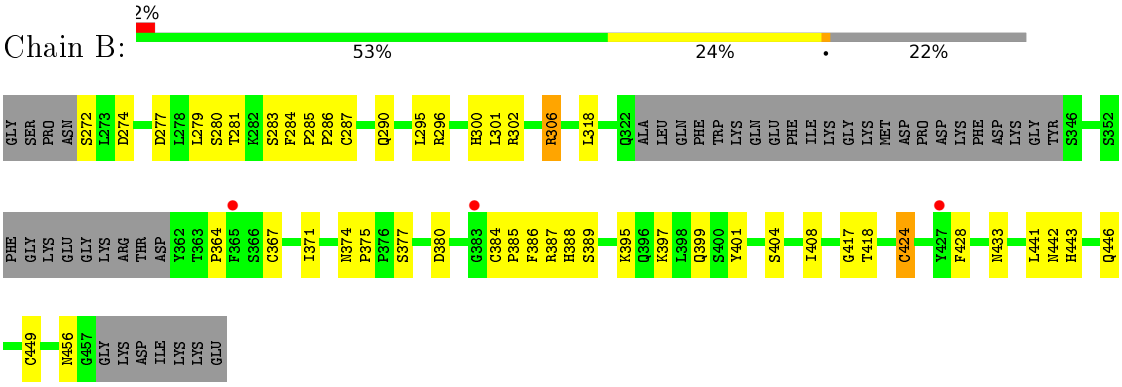
# 3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

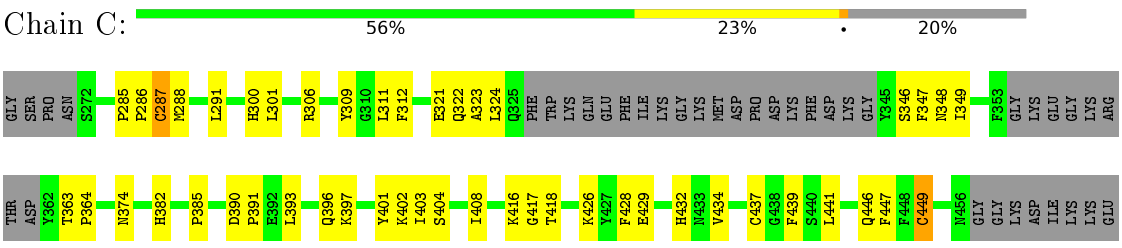
- Molecule 1: DNA primase large subunit




- Molecule 1: DNA primase large subunit

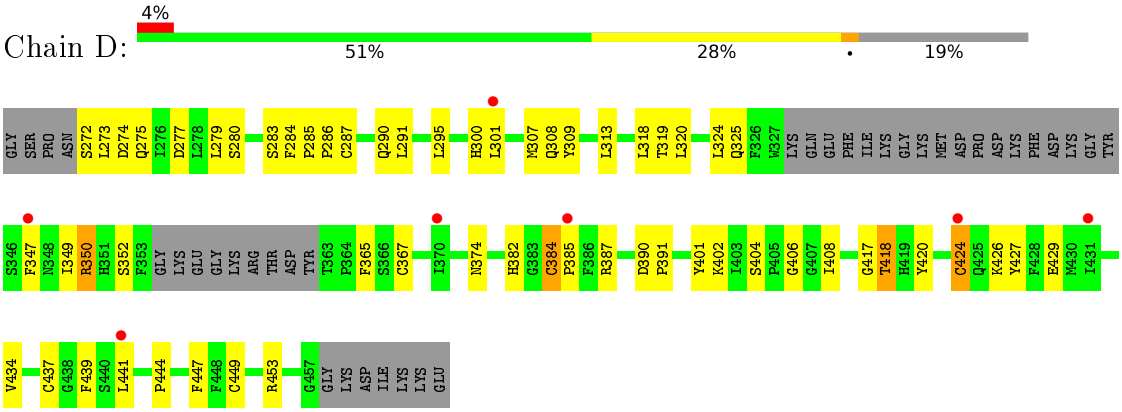



- Molecule 1: DNA primase large subunit




- Molecule 1: DNA primase large subunit

Chain D:


4%
51%
28%
19%
GLY SER PRO ASN S272 L273 D274 Q275 I276 D277 L278 L279 S280 S283 F284 P285 P286 C287 Q290 L291 L295 H300 L301 M307 Q308 Y309 L313 L318 T319 L320 L324 Q325 P326 W327 LYS GLN GLU PHE ILE LYS GLY LYS MET ASP PRO ASP LYS PHE ASP LYS GLY TYR
S346 F347 N348 I349 R350 H351 S352 F353 GLY LYS GLU GLY LYS ARG THR ASP TYR T363 P364 F365 S366 C367 I370 N374 H382 G383 C384 P385 F386 R387 D390 P391 Y401 K402 I403 S404 P405 G406 G407 I408 G417 T418 H419 Y420 C424 Q425 K426 Y427 F428 E429 M430 I431
V434 C437 G438 F439 S440 L441 P444 F447 F448 C449 R453 G457 GLY LYS ASP ILE LYS LYS GLU

# 4 Data and refinement statistics (i)

| Property | Value | Source |
|---|---|---|
| Space group | P 31 | Depositor |
| Cell constants<br>a, b, c, $\alpha$, $\beta$, $\gamma$ | 60.40Å 60.40Å 246.73Å<br>90.00° 90.00° 120.00° | Depositor |
| Resolution (Å) | 44.14 – 2.30<br>44.14 – 2.30 | Depositor<br>EDS |
| % Data completeness<br>(in resolution range) | 95.3 (44.14-2.30)<br>95.3 (44.14-2.30) | Depositor<br>EDS |
| $R_{merge}$ | 0.06 | Depositor |
| $R_{sym}$ | (Not available) | Depositor |
| $< I/\sigma(I) >$ [1] | 1.19 (at 2.29Å) | Xtriage |
| Refinement program | REFMAC 5.8.0135 | Depositor |
| R, $R_{free}$ | 0.251 , 0.275<br>0.253 , 0.278 | Depositor<br>DCC |
| $R_{free}$ test set | 2045 reflections (5.03%) | DCC |
| Wilson B-factor (Å$^2$) | 58.1 | Xtriage |
| Anisotropy | 0.066 | Xtriage |
| Bulk solvent $k_{sol}$(e/Å$^3$), $B_{sol}$(Å$^2$) | 0.37 , 47.1 | EDS |
| L-test for twinning[2] | $< \|L\| > = 0.49$, $< L^2 > = 0.33$ | Xtriage |
| Estimated twinning fraction | 0.026 for -h,-k,l<br>0.300 for h,-h-k,-l<br>0.037 for -k,-h,-l | Xtriage |
| Reported twinning fraction | 0.365 for H, K, L<br>0.232 for -K, -H, -L<br>0.221 for -H, -K, L<br>0.182 for K, H, -L | Depositor |
| Outliers | 0 of 42683 reflections | Xtriage |
| $F_o$,$F_c$ correlation | 0.93 | EDS |
| Total number of atoms | 4911 | wwPDB-VP |
| Average B, all atoms (Å$^2$) | 54.0 | wwPDB-VP |

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.22% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

# 5 Model quality

## 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SF4

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 | 1.41 | 0/1267 | 0.97 | 0/1711 |
| 1 | B | 1.27 | 0/1223 | 1.00 | 3/1653 (0.2%) |
| 1 | C | 1.38 | 0/1273 | 1.09 | 4/1717 (0.2%) |
| 1 | D | 1.21 | 0/1238 | 1.00 | 2/1675 (0.1%) |
| All | All | 1.32 | 0/5001 | 1.02 | 9/6756 (0.1%) |

There are no bond length outliers.

All (9) bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 1 | C | 324 | LEU | N-CA-C | 11.80 | 142.85 | 111.00 |
| 1 | C | 323 | ALA | CB-CA-C | -10.58 | 94.23 | 110.10 |
| 1 | C | 324 | LEU | CB-CA-C | -9.40 | 92.34 | 110.20 |
| 1 | D | 424 | CYS | CA-CB-SG | 8.46 | 129.22 | 114.00 |
| 1 | B | 424 | CYS | CA-CB-SG | 6.99 | 126.58 | 114.00 |
| 1 | D | 350 | ARG | CB-CA-C | 6.78 | 123.96 | 110.40 |
| 1 | B | 306 | ARG | NE-CZ-NH2 | -5.48 | 117.56 | 120.30 |
| 1 | C | 287 | CYS | CA-CB-SG | 5.46 | 123.82 | 114.00 |
| 1 | B | 283 | SER | N-CA-C | 5.18 | 124.99 | 111.00 |

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 | 1229 | 0 | 1164 | 54 | 0 |
| 1 | B | 1193 | 0 | 1101 | 44 | 0 |
| 1 | C | 1236 | 0 | 1173 | 42 | 0 |
| 1 | D | 1207 | 0 | 1088 | 56 | 0 |
| 2 | A | 8 | 0 | 0 | 1 | 0 |
| 2 | B | 8 | 0 | 0 | 1 | 0 |
| 2 | C | 8 | 0 | 0 | 0 | 0 |
| 2 | D | 8 | 0 | 0 | 0 | 0 |
| 3 | A | 4 | 0 | 0 | 1 | 0 |
| 3 | B | 3 | 0 | 0 | 0 | 0 |
| 3 | C | 5 | 0 | 0 | 0 | 0 |
| 3 | D | 2 | 0 | 0 | 0 | 0 |
| All | All | 4911 | 0 | 4526 | 186 | 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 20.

All (186) 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:449:CYS:SG | 1:B:449:CYS:SG | 1.35 | 1.33 |
| 1:B:301:LEU:O | 1:B:306:ARG:NH1 | 1.76 | 1.17 |
| 1:D:295:LEU:HD13 | 1:D:301:LEU:HD12 | 1.35 | 1.03 |
| 1:B:367:CYS:O | 1:B:371:ILE:HD12 | 1.59 | 0.99 |
| 1:B:286:PRO:HD2 | 2:B:501:SF4:S3 | 2.07 | 0.94 |
| 1:A:274:ASP:HA | 1:A:277:ASP:OD1 | 1.68 | 0.93 |
| 1:B:286:PRO:O | 1:B:290:GLN:HG2 | 1.68 | 0.92 |
| 1:C:321:GLU:HG3 | 1:C:322:GLN:H | 1.34 | 0.92 |
| 1:C:286:PRO:HB2 | 1:C:385:PRO:HG2 | 1.51 | 0.92 |
| 1:D:273:LEU:HD21 | 1:D:295:LEU:HD23 | 1.53 | 0.89 |
| 1:D:417:GLY:O | 1:D:418:THR:HG23 | 1.77 | 0.84 |
| 1:D:274:ASP:HA | 1:D:277:ASP:OD2 | 1.81 | 0.80 |
| 1:D:424:CYS:SG | 1:D:441:LEU:CD2 | 2.70 | 0.79 |
| 1:D:417:GLY:C | 1:D:418:THR:HG23 | 2.02 | 0.79 |
| 1:A:286:PRO:HG2 | 1:A:386:PHE:CE2 | 2.18 | 0.78 |
| 1:C:321:GLU:HG3 | 1:C:322:GLN:N | 1.99 | 0.77 |
| 1:C:426:LYS:HD3 | 1:C:429:GLU:OE1 | 1.85 | 0.76 |
| 1:C:322:GLN:HB2 | 1:C:346:SER:O | 1.86 | 0.75 |
| 1:D:309:TYR:O | 1:D:313:LEU:HG | 1.87 | 0.75 |
| 1:B:274:ASP:HB3 | 1:B:296:ARG:NH2 | 2.03 | 0.74 |
| 1:A:277:ASP:OD1 | 1:A:296:ARG:NE | 2.20 | 0.74 |
| 1:C:437:CYS:HB2 | 1:C:439:PHE:CE1 | 2.25 | 0.72 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:A:453:ARG:HD2 | 1:B:446:GLN:CD | 2.08 | 0.72 |
| 1:D:439:PHE:HE2 | 1:D:441:LEU:HB2 | 1.55 | 0.71 |
| 1:A:449:CYS:SG | 1:B:449:CYS:CB | 2.77 | 0.71 |
| 1:B:274:ASP:HB3 | 1:B:296:ARG:CZ | 2.22 | 0.70 |
| 1:C:397:LYS:HE3 | 1:C:401:TYR:CZ | 2.26 | 0.70 |
| 1:D:424:CYS:SG | 1:D:441:LEU:HD21 | 2.32 | 0.69 |
| 1:B:395:LYS:HG2 | 1:B:399:GLN:OE1 | 1.93 | 0.68 |
| 1:C:346:SER:O | 1:C:347:PHE:CD1 | 2.46 | 0.68 |
| 1:C:390:ASP:HB3 | 1:C:393:LEU:HD12 | 1.75 | 0.67 |
| 1:C:404:SER:O | 1:C:408:ILE:HG13 | 1.95 | 0.67 |
| 1:D:324:LEU:HD12 | 1:D:325:GLN:O | 1.94 | 0.67 |
| 1:D:387:ARG:HD2 | 1:D:387:ARG:O | 1.95 | 0.66 |
| 1:A:285:PRO:HD2 | 1:A:288:MET:HB2 | 1.78 | 0.66 |
| 1:B:418:THR:HG22 | 1:B:418:THR:O | 1.97 | 0.64 |
| 1:D:309:TYR:CE2 | 1:D:313:LEU:HD11 | 2.32 | 0.64 |
| 1:A:285:PRO:HG2 | 1:A:288:MET:HG2 | 1.79 | 0.64 |
| 1:D:295:LEU:HD13 | 1:D:301:LEU:CD1 | 2.22 | 0.64 |
| 1:D:309:TYR:CZ | 1:D:313:LEU:HD21 | 2.32 | 0.63 |
| 1:D:287:CYS:O | 1:D:290:GLN:HG2 | 1.99 | 0.62 |
| 1:D:439:PHE:CE2 | 1:D:441:LEU:HB2 | 2.35 | 0.62 |
| 1:C:322:GLN:CB | 1:C:346:SER:O | 2.48 | 0.61 |
| 1:D:300:HIS:CG | 1:D:301:LEU:N | 2.68 | 0.61 |
| 1:C:321:GLU:O | 1:C:348:ASN:N | 2.34 | 0.61 |
| 1:A:286:PRO:HG2 | 1:A:386:PHE:HE2 | 1.62 | 0.60 |
| 1:B:377:SER:O | 1:B:380:ASP:HB2 | 2.02 | 0.60 |
| 1:A:321:GLU:N | 1:A:348:ASN:O | 2.31 | 0.60 |
| 1:B:300:HIS:CG | 1:B:301:LEU:N | 2.71 | 0.58 |
| 1:B:280:SER:HA | 1:B:284:PHE:CG | 2.39 | 0.58 |
| 1:B:300:HIS:O | 1:B:301:LEU:HD23 | 2.04 | 0.58 |
| 1:A:429:GLU:HA | 1:A:434:VAL:CG2 | 2.35 | 0.57 |
| 1:A:396:GLN:HA | 1:A:399:GLN:OE1 | 2.05 | 0.56 |
| 1:D:300:HIS:CD2 | 1:D:301:LEU:H | 2.23 | 0.56 |
| 1:D:324:LEU:HD12 | 1:D:324:LEU:O | 2.06 | 0.56 |
| 1:A:401:TYR:O | 1:A:402:LYS:CB | 2.51 | 0.56 |
| 1:A:306:ARG:O | 1:A:310:GLY:N | 2.33 | 0.55 |
| 1:B:302:ARG:O | 1:B:306:ARG:HG3 | 2.07 | 0.54 |
| 1:A:351:HIS:CE1 | 1:B:318:LEU:HD21 | 2.42 | 0.54 |
| 1:C:285:PRO:HD2 | 1:C:288:MET:HB2 | 1.89 | 0.54 |
| 1:C:417:GLY:O | 1:C:418:THR:OG1 | 2.22 | 0.54 |
| 1:D:324:LEU:HD12 | 1:D:324:LEU:C | 2.27 | 0.54 |
| 1:A:426:LYS:O | 1:A:430:MET:HG2 | 2.07 | 0.54 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:B:272:SER:HB2 | 1:B:274:ASP:OD1 | 2.07 | 0.54 |
| 1:A:322:GLN:CB | 1:A:347:PHE:CE1 | 2.91 | 0.54 |
| 1:C:374:ASN:O | 1:C:382:HIS:NE2 | 2.39 | 0.54 |
| 1:A:286:PRO:HD2 | 2:A:501:SF4:S2 | 2.48 | 0.54 |
| 1:D:287:CYS:HB3 | 1:D:384:CYS:HA | 1.90 | 0.54 |
| 1:C:288:MET:HG3 | 1:C:312:PHE:CD2 | 2.43 | 0.53 |
| 1:C:346:SER:O | 1:C:347:PHE:CG | 2.60 | 0.53 |
| 1:D:417:GLY:O | 1:D:418:THR:CG2 | 2.53 | 0.53 |
| 1:D:319:THR:O | 1:D:349:ILE:HA | 2.09 | 0.53 |
| 1:A:386:PHE:CE2 | 1:A:424:CYS:HB2 | 2.44 | 0.53 |
| 1:A:453:ARG:HD2 | 1:B:446:GLN:NE2 | 2.23 | 0.53 |
| 1:A:322:GLN:CB | 1:A:347:PHE:HE1 | 2.22 | 0.53 |
| 1:B:287:CYS:HA | 1:B:290:GLN:NE2 | 2.24 | 0.53 |
| 1:A:395:LYS:O | 1:A:399:GLN:OE1 | 2.27 | 0.52 |
| 1:C:321:GLU:O | 1:C:347:PHE:HA | 2.09 | 0.51 |
| 1:A:453:ARG:NH2 | 3:A:601:HOH:O | 2.42 | 0.51 |
| 1:C:311:LEU:HD13 | 1:C:363:THR:O | 2.10 | 0.51 |
| 1:A:404:SER:HB2 | 1:A:405:PRO:HD2 | 1.92 | 0.51 |
| 1:D:300:HIS:CG | 1:D:301:LEU:H | 2.29 | 0.51 |
| 1:D:286:PRO:HG3 | 1:D:427:TYR:CE2 | 2.46 | 0.50 |
| 1:D:444:PRO:O | 1:D:447:PHE:HB3 | 2.12 | 0.50 |
| 1:D:309:TYR:CE1 | 1:D:313:LEU:HD21 | 2.46 | 0.50 |
| 1:C:437:CYS:HB2 | 1:C:439:PHE:HE1 | 1.74 | 0.50 |
| 1:D:284:PHE:CD1 | 1:D:284:PHE:N | 2.79 | 0.50 |
| 1:C:441:LEU:CD1 | 1:C:447:PHE:HD2 | 2.24 | 0.49 |
| 1:C:288:MET:HG3 | 1:C:312:PHE:CG | 2.47 | 0.49 |
| 1:D:287:CYS:HB3 | 1:D:385:PRO:HD3 | 1.95 | 0.49 |
| 1:A:353:PHE:HB3 | 1:B:279:LEU:HD13 | 1.94 | 0.48 |
| 1:D:290:GLN:OE1 | 1:D:385:PRO:HG3 | 2.13 | 0.48 |
| 1:A:320:LEU:HA | 1:A:348:ASN:O | 2.14 | 0.48 |
| 1:A:273:LEU:HD11 | 1:A:320:LEU:CD1 | 2.44 | 0.48 |
| 1:A:273:LEU:HD12 | 1:A:349:ILE:HG12 | 1.96 | 0.48 |
| 1:A:298:ASN:O | 1:A:299:HIS:HB2 | 2.14 | 0.48 |
| 1:A:287:CYS:HB2 | 1:A:308:GLN:NE2 | 2.29 | 0.48 |
| 1:C:403:ILE:HG22 | 1:C:404:SER:N | 2.29 | 0.47 |
| 1:B:285:PRO:HB2 | 1:B:287:CYS:SG | 2.54 | 0.47 |
| 1:D:284:PHE:HD1 | 1:D:284:PHE:N | 2.12 | 0.47 |
| 1:D:273:LEU:HD13 | 1:D:347:PHE:HB3 | 1.96 | 0.47 |
| 1:A:285:PRO:HG3 | 1:A:444:PRO:HB3 | 1.96 | 0.47 |
| 1:B:277:ASP:O | 1:B:281:THR:HG23 | 2.14 | 0.47 |
| 1:D:272:SER:O | 1:D:275:GLN:CB | 2.62 | 0.47 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:D:374:ASN:O | 1:D:382:HIS:NE2 | 2.43 | 0.47 |
| 1:B:387:ARG:HG3 | 1:B:388:HIS:N | 2.29 | 0.47 |
| 1:C:346:SER:C | 1:C:347:PHE:CD1 | 2.87 | 0.47 |
| 1:D:318:LEU:C | 1:D:352:SER:OG | 2.53 | 0.47 |
| 1:A:272:SER:O | 1:A:275:GLN:CB | 2.63 | 0.47 |
| 1:B:417:GLY:O | 1:B:418:THR:HB | 2.15 | 0.47 |
| 1:A:367:CYS:SG | 1:A:444:PRO:HD3 | 2.55 | 0.46 |
| 1:C:390:ASP:CG | 1:C:391:PRO:HD2 | 2.36 | 0.46 |
| 1:C:441:LEU:HD11 | 1:C:447:PHE:HD2 | 1.80 | 0.46 |
| 1:A:429:GLU:HA | 1:A:434:VAL:HG23 | 1.96 | 0.46 |
| 1:A:439:PHE:N | 1:A:439:PHE:CD1 | 2.84 | 0.46 |
| 1:A:277:ASP:CG | 1:A:296:ARG:HE | 2.13 | 0.46 |
| 1:D:324:LEU:CD1 | 1:D:325:GLN:O | 2.63 | 0.46 |
| 1:D:367:CYS:N | 1:D:444:PRO:HD3 | 2.30 | 0.46 |
| 1:A:397:LYS:HA | 1:A:397:LYS:HD3 | 1.72 | 0.46 |
| 1:A:371:ILE:HG23 | 1:A:387:ARG:HG2 | 1.98 | 0.45 |
| 1:B:295:LEU:HD12 | 1:B:295:LEU:O | 2.17 | 0.45 |
| 1:C:390:ASP:HB3 | 1:C:393:LEU:CD1 | 2.42 | 0.45 |
| 1:B:300:HIS:CD2 | 1:B:301:LEU:H | 2.34 | 0.45 |
| 1:D:273:LEU:HD11 | 1:D:320:LEU:CD1 | 2.47 | 0.45 |
| 1:D:291:LEU:HD11 | 1:D:308:GLN:NE2 | 2.31 | 0.44 |
| 1:B:433:ASN:O | 1:B:433:ASN:CG | 2.56 | 0.44 |
| 1:A:292:HIS:ND1 | 1:A:309:TYR:OH | 2.34 | 0.44 |
| 1:C:397:LYS:HE3 | 1:C:401:TYR:OH | 2.17 | 0.44 |
| 1:A:387:ARG:HD2 | 1:A:387:ARG:O | 2.17 | 0.44 |
| 1:B:364:PRO:HB2 | 1:B:443:HIS:CE1 | 2.53 | 0.44 |
| 1:A:451:SER:O | 1:A:455:LEU:HG | 2.18 | 0.44 |
| 1:D:404:SER:O | 1:D:408:ILE:HG13 | 2.18 | 0.44 |
| 1:D:426:LYS:HA | 1:D:429:GLU:HB2 | 1.99 | 0.44 |
| 1:A:353:PHE:CD1 | 1:A:353:PHE:C | 2.91 | 0.44 |
| 1:C:301:LEU:O | 1:C:306:ARG:NH1 | 2.51 | 0.44 |
| 1:A:308:GLN:OE1 | 1:A:382:HIS:HB2 | 2.18 | 0.43 |
| 1:C:397:LYS:HE3 | 1:C:401:TYR:CE1 | 2.53 | 0.43 |
| 1:A:413:ASP:O | 1:A:416:LYS:HB2 | 2.17 | 0.43 |
| 1:A:455:LEU:N | 1:A:455:LEU:HD23 | 2.32 | 0.43 |
| 1:B:286:PRO:HB2 | 1:B:385:PRO:CD | 2.49 | 0.43 |
| 1:D:387:ARG:HD3 | 1:D:420:TYR:CZ | 2.54 | 0.43 |
| 1:C:390:ASP:OD2 | 1:C:391:PRO:HD2 | 2.19 | 0.43 |
| 1:A:270:PRO:HB2 | 1:A:348:ASN:CB | 2.49 | 0.43 |
| 1:A:453:ARG:NE | 1:B:442:ASN:OD1 | 2.50 | 0.43 |
| 1:C:428:PHE:CD1 | 1:C:428:PHE:C | 2.93 | 0.43 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:B:428:PHE:C | 1:B:428:PHE:CD1 | 2.93 | 0.42 |
| 1:D:318:LEU:HD23 | 1:D:350:ARG:O | 2.19 | 0.42 |
| 1:D:307:MET:HB3 | 1:D:365:PHE:HZ | 1.83 | 0.42 |
| 1:B:385:PRO:O | 1:B:389:SER:HB2 | 2.20 | 0.42 |
| 1:C:349:ILE:O | 1:C:349:ILE:HG13 | 2.19 | 0.42 |
| 1:D:285:PRO:HG3 | 1:D:447:PHE:CG | 2.54 | 0.42 |
| 1:D:434:VAL:HG23 | 1:D:434:VAL:O | 2.18 | 0.42 |
| 1:B:287:CYS:HA | 1:B:290:GLN:HE21 | 1.83 | 0.42 |
| 1:C:393:LEU:O | 1:C:396:GLN:HB2 | 2.19 | 0.42 |
| 1:D:404:SER:C | 1:D:406:GLY:H | 2.22 | 0.42 |
| 1:A:370:ILE:HG23 | 1:A:383:GLY:HA2 | 2.00 | 0.42 |
| 1:A:429:GLU:HG3 | 1:A:437:CYS:HB3 | 2.02 | 0.42 |
| 1:C:311:LEU:HB3 | 1:C:364:PRO:HA | 2.01 | 0.42 |
| 1:C:449:CYS:SG | 1:D:449:CYS:C | 2.98 | 0.42 |
| 1:A:363:THR:HA | 1:A:364:PRO:HD3 | 1.98 | 0.42 |
| 1:B:286:PRO:CB | 1:B:385:PRO:HG2 | 2.50 | 0.42 |
| 1:D:390:ASP:OD1 | 1:D:391:PRO:HD2 | 2.19 | 0.42 |
| 1:B:274:ASP:OD1 | 1:B:274:ASP:N | 2.53 | 0.41 |
| 1:D:401:TYR:O | 1:D:402:LYS:HB2 | 2.20 | 0.41 |
| 1:A:278:LEU:HG | 1:A:278:LEU:O | 2.21 | 0.41 |
| 1:C:432:HIS:O | 1:C:434:VAL:HG13 | 2.20 | 0.41 |
| 1:D:307:MET:HB3 | 1:D:365:PHE:CZ | 2.55 | 0.41 |
| 1:B:367:CYS:O | 1:B:371:ILE:CD1 | 2.48 | 0.41 |
| 1:B:404:SER:O | 1:B:408:ILE:HG13 | 2.21 | 0.41 |
| 1:C:291:LEU:HD13 | 1:C:309:TYR:HB2 | 2.03 | 0.41 |
| 1:A:273:LEU:C | 1:A:275:GLN:H | 2.23 | 0.41 |
| 1:A:424:CYS:SG | 1:A:441:LEU:HD22 | 2.61 | 0.41 |
| 1:A:456:ASN:HB3 | 1:B:443:HIS:NE2 | 2.35 | 0.41 |
| 1:B:397:LYS:HG3 | 1:B:401:TYR:CZ | 2.55 | 0.41 |
| 1:C:401:TYR:O | 1:C:402:LYS:HB2 | 2.20 | 0.41 |
| 1:B:286:PRO:HG2 | 1:B:386:PHE:CE2 | 2.56 | 0.41 |
| 1:D:287:CYS:HA | 1:D:385:PRO:HD3 | 2.02 | 0.41 |
| 1:C:446:GLN:HB2 | 1:D:453:ARG:NH1 | 2.36 | 0.40 |
| 1:D:277:ASP:O | 1:D:280:SER:OG | 2.26 | 0.40 |
| 1:D:417:GLY:O | 1:D:418:THR:CB | 2.66 | 0.40 |
| 1:B:374:ASN:HA | 1:B:375:PRO:HD2 | 1.76 | 0.40 |
| 1:C:300:HIS:CG | 1:C:301:LEU:N | 2.90 | 0.40 |
| 1:C:322:GLN:HA | 1:C:347:PHE:HA | 2.03 | 0.40 |
| 1:B:280:SER:O | 1:B:284:PHE:HB2 | 2.22 | 0.40 |
| 1:B:424:CYS:SG | 1:B:441:LEU:HD21 | 2.61 | 0.40 |
| 1:D:279:LEU:O | 1:D:283:SER:N | 2.43 | 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 | 153/197 (78%) | 147 (96%) | 6 (4%) | 0 | 100 | 100 |
| 1 | B | 148/197 (75%) | 140 (95%) | 8 (5%) | 0 | 100 | 100 |
| 1 | C | 153/197 (78%) | 148 (97%) | 5 (3%) | 0 | 100 | 100 |
| 1 | D | 153/197 (78%) | 145 (95%) | 8 (5%) | 0 | 100 | 100 |
| All | All | 607/788 (77%) | 580 (96%) | 27 (4%) | 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 | 131/176 (74%) | 128 (98%) | 3 (2%) | 58 | 75 |
| 1 | B | 127/176 (72%) | 125 (98%) | 2 (2%) | 70 | 84 |
| 1 | C | 133/176 (76%) | 130 (98%) | 3 (2%) | 58 | 75 |
| 1 | D | 124/176 (70%) | 121 (98%) | 3 (2%) | 57 | 74 |
| All | All | 515/704 (73%) | 504 (98%) | 11 (2%) | 61 | 78 |

All (11) residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | A | 277 | ASP |
| 1 | A | 424 | CYS |
| 1 | A | 426 | LYS |
| 1 | B | 384 | CYS |
| 1 | B | 456 | ASN |
| 1 | C | 287 | CYS |
| 1 | C | 416 | LYS |
| 1 | C | 449 | CYS |
| 1 | D | 384 | CYS |
| 1 | D | 418 | THR |
| 1 | D | 437 | CYS |

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | C | 322 | GLN |
| 1 | D | 300 | 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 carbohydrates in this entry.

### 5.6 Ligand geometry (i)

4 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected

value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

| Mol | Type | Chain | Res | Link | Bond lengths | | | Bond angles | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | Counts | RMSZ | $\#\|Z\|>2$ | Counts | RMSZ | $\#\|Z\|>2$ |
| 2 | SF4 | A | 501 | 1 | 0,12,12 | 0.00 | - | 0,24,24 | 0.00 | - |
| 2 | SF4 | B | 501 | 1 | 0,12,12 | 0.00 | - | 0,24,24 | 0.00 | - |
| 2 | SF4 | C | 501 | 1 | 0,12,12 | 0.00 | - | 0,24,24 | 0.00 | - |
| 2 | SF4 | D | 501 | 1 | 0,12,12 | 0.00 | - | 0,24,24 | 0.00 | - |

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

| Mol | Type | Chain | Res | Link | Chirals | Torsions | Rings |
|---|---|---|---|---|---|---|---|
| 2 | SF4 | A | 501 | 1 | - | 0/0/48/48 | 0/6/5/5 |
| 2 | SF4 | B | 501 | 1 | - | 0/0/48/48 | 0/6/5/5 |
| 2 | SF4 | C | 501 | 1 | - | 0/0/48/48 | 0/6/5/5 |
| 2 | SF4 | D | 501 | 1 | - | 0/0/48/48 | 0/6/5/5 |

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.

2 monomers are involved in 2 short contacts:

| Mol | Chain | Res | Type | Clashes | Symm-Clashes |
|---|---|---|---|---|---|
| 2 | A | 501 | SF4 | 1 | 0 |
| 2 | B | 501 | SF4 | 1 | 0 |

## 5.7 Other polymers (i)

There are no such residues in this entry.

## 5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

# 6 Fit of model and data

## 6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, $95^{th}$ percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

| Mol | Chain | Analysed | <RSRZ> | #RSRZ>2 | OWAB(Å$^2$) | Q<0.9 |
|---|---|---|---|---|---|---|
| 1 | A | 158/197 (80%) | 0.36 | 2 (1%) 79 84 | 35, 50, 65, 83 | 5 (3%) |
| 1 | B | 154/197 (78%) | 0.33 | 3 (1%) 70 76 | 36, 55, 73, 81 | 4 (2%) |
| 1 | C | 158/197 (80%) | 0.24 | 0 100 100 | 32, 53, 69, 83 | 3 (1%) |
| 1 | D | 159/197 (80%) | 0.37 | 7 (4%) 38 47 | 33, 56, 71, 92 | 3 (1%) |
| All | All | 629/788 (79%) | 0.33 | 12 (1%) 70 76 | 32, 54, 72, 92 | 15 (2%) |

All (12) RSRZ outliers are listed below:

| Mol | Chain | Res | Type | RSRZ |
|---|---|---|---|---|
| 1 | D | 347 | PHE | 3.1 |
| 1 | B | 383 | GLY | 2.9 |
| 1 | D | 424 | CYS | 2.9 |
| 1 | B | 365 | PHE | 2.9 |
| 1 | A | 270 | PRO | 2.8 |
| 1 | D | 431 | ILE | 2.6 |
| 1 | D | 370 | ILE | 2.4 |
| 1 | D | 301 | LEU | 2.3 |
| 1 | D | 385 | PRO | 2.3 |
| 1 | B | 427 | TYR | 2.2 |
| 1 | A | 311 | LEU | 2.2 |
| 1 | D | 441 | LEU | 2.2 |

## 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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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 | LLDF | B-factors(Å$^2$) | Q<0.9 |
|---|---|---|---|---|---|---|---|---|---|
| 2 | SF4 | A | 501 | 8/8 | 0.96 | 0.18 | 0.91 | 51,57,67,77 | 0 |
| 2 | SF4 | C | 501 | 8/8 | 0.96 | 0.18 | 0.28 | 44,57,58,60 | 0 |
| 2 | SF4 | D | 501 | 8/8 | 0.96 | 0.17 | -0.40 | 53,58,64,67 | 0 |
| 2 | SF4 | B | 501 | 8/8 | 0.91 | 0.16 | -0.50 | 51,59,63,63 | 0 |

## 6.5 Other polymers

There are no such residues in this entry.