# WORLDWIDE PDB

## PROTEIN DATA BANK

# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 15, 2017 – 01:13 am GMT

|  |  |  |
|---|---|---|
| PDB ID | : | 3VK2 |
| Title | : | Crystal Structure of L-Methionine gamma-Lyase from Pseudomonas putida C116H Mutant. |
| Authors | : | Fukumoto, M.; Kudou, D.; Murano, S.; Shiba, T.; Sato, D.; Tamura, T.; Harada, S.; Inagaki, K. |
| Deposited on | : | 2011-11-07 |
| Resolution | : | 2.30 Å(reported) |

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

|  |  |  |
|---|---|---|
| MolProbity | : | 4.02b-467 |
| Mogul | : | 1.7.2 (RC1), CSD as538be (2017) |
| Xtriage (Phenix) | : | 1.9-1692 |
| EDS | : | trunk28620 |
| Percentile statistics | : | 20161228.v01 (using entries in the PDB archive December 28th 2016) |
| 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) | : | recalc28949 |

# 1    Overall quality at a glance   ⓘ

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

The reported resolution of this entry is 2.30 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 | Percentile Ranks | Value |
|---|---|---|
| Rfree | | 0.228 |
| Clashscore | | 8 |
| Ramachandran outliers | | 0.9% |
| Sidechain outliers | | 10.2% |
| RSRZ outliers | | 8.0% |

Worse        Better

▌ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution
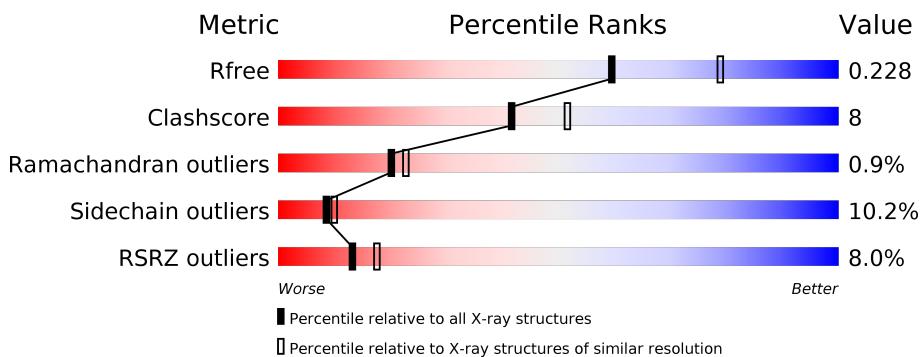
| Metric | Whole archive (#Entries) | Similar resolution (#Entries, resolution range(Å)) |
|---|---|---|
| R$_{free}$ | 100719 | 4130 (2.30-2.30) |
| Clashscore | 112137 | 4751 (2.30-2.30) |
| Ramachandran outliers | 110173 | 4705 (2.30-2.30) |
| Sidechain outliers | 110143 | 4704 (2.30-2.30) |
| RSRZ outliers | 101464 | 4156 (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 | 398 | 8%   81%   15%   · · |
| 1 | B | 398 | 9%   80%   16%   · · |
| 1 | C | 398 | 7%   80%   16%   · · |
| 1 | D | 398 | 8%   77%   18%   · · |
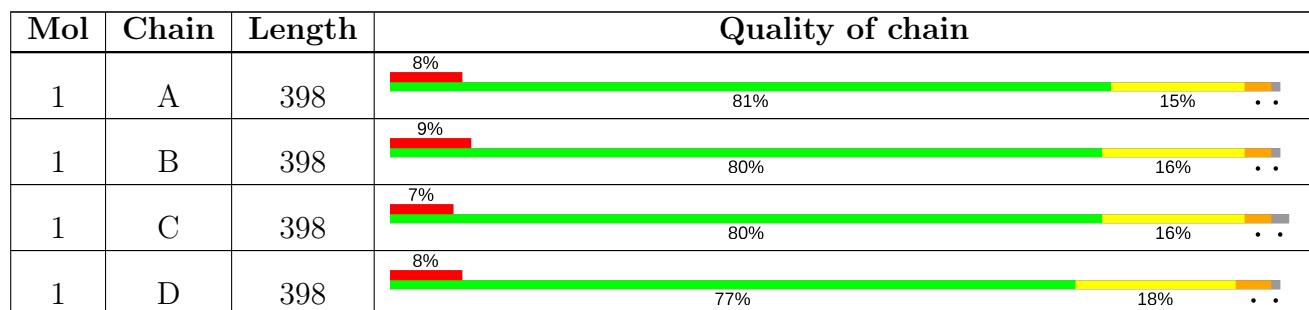
The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit crite-

ria:

| Mol | Type | Chain | Res | Chirality | Geometry | Clashes | Electron density |
|-----|------|-------|-----|-----------|----------|---------|------------------|
| 2 | SO4 | C | 501 | - | - | - | X |

# 2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 12350 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 Methionine gamma-lyase.

| Mol | Chain | Residues | Atoms | | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|----|---------|---------|-------|
| 1 | A | 393 | Total | C | N | O | P | S | 0 | 0 | 0 |
| | | | 2979 | 1880 | 527 | 555 | 1 | 16 | | | |
| 1 | B | 396 | Total | C | N | O | P | S | 0 | 0 | 0 |
| | | | 2997 | 1889 | 531 | 560 | 1 | 16 | | | |
| 1 | C | 392 | Total | C | N | O | P | S | 0 | 0 | 0 |
| | | | 2970 | 1874 | 525 | 554 | 1 | 16 | | | |
| 1 | D | 393 | Total | C | N | O | P | S | 0 | 0 | 0 |
| | | | 2979 | 1880 | 527 | 555 | 1 | 16 | | | |

There are 4 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|---------|-----------|
| A | 116 | HIS | CYS | ENGINEERED MUTATION | UNP P13254 |
| B | 116 | HIS | CYS | ENGINEERED MUTATION | UNP P13254 |
| C | 116 | HIS | CYS | ENGINEERED MUTATION | UNP P13254 |
| D | 116 | HIS | CYS | ENGINEERED MUTATION | UNP P13254 |

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: $O_4S$).

**SO4**

O1

O

O3 O⁻ — S — O⁻ O4

S

O

O2
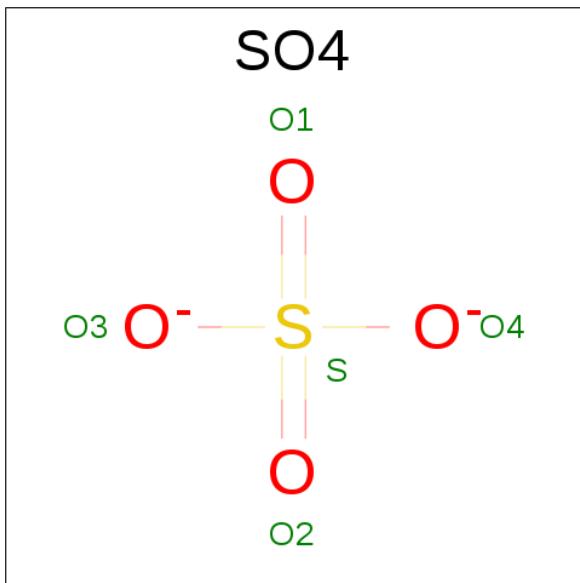
| Mol | Chain | Residues | Atoms | | | ZeroOcc | AltConf |
|-----|-------|----------|-------|---|---|---------|---------|
| 2 | A | 1 | Total 5 | O 4 | S 1 | 0 | 0 |
| 2 | B | 1 | Total 5 | O 4 | S 1 | 0 | 0 |
| 2 | C | 1 | Total 5 | O 4 | S 1 | 0 | 0 |
| 2 | D | 1 | Total 5 | O 4 | S 1 | 0 | 0 |

- Molecule 3 is water.

| Mol | Chain | Residues | Atoms | | ZeroOcc | AltConf |
|-----|-------|----------|-------|---|---------|---------|
| 3 | A | 99 | Total 99 | O 99 | 0 | 0 |
| 3 | B | 115 | Total 115 | O 115 | 0 | 0 |
| 3 | C | 110 | Total 110 | O 110 | 0 | 0 |
| 3 | D | 81 | Total 81 | O 81 | 0 | 0 |

# 3  Residue-property plots ⓘ

These plots are drawn for all protein, RNA and DNA 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: Methionine gamma-lyase

Chain A:

• Molecule 1: Methionine gamma-lyase

Chain B:

• Molecule 1: Methionine gamma-lyase

Chain C:

G321 I322 R326 M329 L334 V339 S340 L341 E345 S346 L347 A348 Q349 S353 S357 S358 Y359 E362 E363 R364 A365 H366 Y367 G368 V374 R375 I383 L386 V390 Q391 A398

• Molecule 1: Methionine gamma-lyase

Chain D:

8%

77%

18%

MET HIS GLY SER ASN K6 L7 P8 L28 V29 P30 P31 V32 Y33 A36 T37 A47 G52 E53 Q54 A55 G56 H57 F58 Y59 S60 R61 I62 S63 T66 E78 L84 I93 T94 S95 T96 L97 W98 T99 L109 H116 L121 H122 K131 H134 L140

Y155 F156 E157 P162 D168 V172 K178 D186 C190 L194 Q195 R196 L200 H207 K211 Y212 L213 L230 I234 R235 L236 K240 T243 G244 A245 D251 L254 L255 N263 L264 Q274 L280 A281 R282 Q283 P284 E287 L288 I289

T301 L302 Q305 I314 K319 I322 R327 L334 V339 S340 L341 E345 S346 L347 H350 P351 A352 S357 S358 Y359 T360 P361 E362 E363 R364 A365 H366 Y367 G368 I369 V374 I383 L386 S397 A398

# 4 Data and refinement statistics (i)

| Property | Value | Source |
|---|---|---|
| Space group | P 21 21 2 | Depositor |
| Cell constants<br>a, b, c, $\alpha$, $\beta$, $\gamma$ | 153.94Å     153.44Å     80.84Å<br>90.00°     90.00°     90.00° | Depositor |
| Resolution (Å) | 30.00    –    2.30<br>29.34    –    2.30 | Depositor<br>EDS |
| % Data completeness<br>(in resolution range) | 99.0 (30.00-2.30)<br>99.0 (29.34-2.30) | Depositor<br>EDS |
| $R_{merge}$ | 0.12 | Depositor |
| $R_{sym}$ | (Not available) | Depositor |
| $< I/\sigma(I) >$ [1] | 2.96 (at 2.31Å) | Xtriage |
| Refinement program | REFMAC 5.5.0102 | Depositor |
| R, $R_{free}$ | 0.189   ,    0.231<br>0.188   ,    0.228 | Depositor<br>DCC |
| $R_{free}$ test set | 4253 reflections (5.28%) | DCC |
| Wilson B-factor (Å$^2$) | 21.8 | Xtriage |
| Anisotropy | 0.021 | Xtriage |
| Bulk solvent $k_{sol}$(e/Å$^3$), $B_{sol}$(Å$^2$) | 0.36 , 38.5 | EDS |
| L-test for twinning[2] | $< \|L\| > = 0.48, < L^2 > = 0.31$ | Xtriage |
| Estimated twinning fraction | 0.014 for k,h,-l | Xtriage |
| $F_o$,$F_c$ correlation | 0.94 | EDS |
| Total number of atoms | 12350 | wwPDB-VP |
| Average B, all atoms (Å$^2$) | 25.0 | wwPDB-VP |

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.65% 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: LLP, SO4

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 | 0.62 | 0/3019 | 0.74 | 2/4097 (0.0%) |
| 1 | B | 0.67 | 0/3037 | 0.74 | 2/4121 (0.0%) |
| 1 | C | 0.62 | 0/3010 | 0.73 | 2/4086 (0.0%) |
| 1 | D | 0.59 | 0/3019 | 0.71 | 1/4097 (0.0%) |
| All | All | 0.62 | 0/12085 | 0.73 | 7/16401 (0.0%) |

There are no bond length outliers.

All (7) bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|-----|-------|-----|------|-------|-----|------|------|
| 1 | A | 230 | LEU | CA-CB-CG | 5.38 | 127.67 | 115.30 |
| 1 | B | 280 | LEU | CA-CB-CG | 5.30 | 127.49 | 115.30 |
| 1 | B | 200 | LEU | CA-CB-CG | 5.20 | 127.25 | 115.30 |
| 1 | D | 251 | ASP | CB-CG-OD2 | 5.19 | 122.97 | 118.30 |
| 1 | A | 233 | ARG | NE-CZ-NH1 | 5.14 | 122.87 | 120.30 |
| 1 | C | 280 | LEU | CA-CB-CG | 5.12 | 127.08 | 115.30 |
| 1 | C | 322 | ILE | CB-CA-C | -5.10 | 101.40 | 111.60 |

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 | 2979 | 0 | 2939 | 45 | 0 |
| 1 | B | 2997 | 0 | 2953 | 53 | 0 |
| 1 | C | 2970 | 0 | 2927 | 51 | 0 |
| 1 | D | 2979 | 0 | 2940 | 55 | 0 |
| 2 | A | 5 | 0 | 0 | 0 | 0 |
| 2 | B | 5 | 0 | 0 | 0 | 0 |
| 2 | C | 5 | 0 | 0 | 0 | 0 |
| 2 | D | 5 | 0 | 0 | 0 | 0 |
| 3 | A | 99 | 0 | 0 | 6 | 0 |
| 3 | B | 115 | 0 | 0 | 7 | 0 |
| 3 | C | 110 | 0 | 0 | 7 | 0 |
| 3 | D | 81 | 0 | 0 | 3 | 0 |
| All | All | 12350 | 0 | 11759 | 190 | 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 8.

All (190) 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:B:362:GLU:O | 1:B:363:GLU:HB2 | 1.51 | 1.09 |
| 1:B:327:ARG:HG2 | 1:B:327:ARG:HH21 | 1.15 | 1.08 |
| 1:B:363:GLU:O | 1:B:364:ARG:HG3 | 1.55 | 1.05 |
| 1:A:93:ILE:HG21 | 3:A:428:HOH:O | 1.57 | 1.02 |
| 1:A:284:PRO:O | 1:A:319:LYS:HE2 | 1.64 | 0.97 |
| 1:B:45:TYR:HB3 | 3:B:449:HOH:O | 1.68 | 0.92 |
| 1:A:57:HIS:HA | 1:A:63:SER:HB2 | 1.54 | 0.89 |
| 1:D:287:GLU:HG2 | 1:D:319:LYS:HG3 | 1.54 | 0.89 |
| 1:D:33:TYR:H | 1:D:66:THR:HG21 | 1.38 | 0.86 |
| 1:B:327:ARG:NH2 | 1:B:327:ARG:HG2 | 1.89 | 0.84 |
| 1:C:33:TYR:H | 1:C:66:THR:CG2 | 1.90 | 0.83 |
| 1:D:33:TYR:H | 1:D:66:THR:CG2 | 1.92 | 0.83 |
| 1:C:7:LEU:HD13 | 1:C:8:PRO:O | 1.79 | 0.83 |
| 1:B:363:GLU:O | 1:B:364:ARG:CG | 2.30 | 0.80 |
| 1:A:33:TYR:H | 1:A:66:THR:HG21 | 1.47 | 0.78 |
| 1:D:99:THR:HG21 | 1:D:234:ILE:HA | 1.66 | 0.78 |
| 1:C:243:THR:HG22 | 1:C:245:ALA:H | 1.49 | 0.77 |
| 1:A:360:THR:HB | 1:A:361:PRO:CD | 2.15 | 0.77 |
| 1:A:360:THR:HB | 1:A:361:PRO:HD2 | 1.66 | 0.77 |
| 1:A:122:HIS:NE2 | 1:A:134:HIS:HE1 | 1.83 | 0.76 |
| 1:B:320:GLY:HA3 | 3:B:414:HOH:O | 1.85 | 0.76 |
| 1:A:236:LEU:O | 1:A:240:LYS:HE3 | 1.86 | 0.75 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:B:325:GLY:HA3 | 1:B:350:HIS:CE1 | 2.19 | 0.75 |
| 1:C:7:LEU:HD13 | 1:C:7:LEU:C | 2.07 | 0.75 |
| 1:C:66:THR:HB | 3:C:469:HOH:O | 1.86 | 0.75 |
| 1:A:284:PRO:HB3 | 3:A:451:HOH:O | 1.87 | 0.74 |
| 1:D:162:PRO:HD2 | 3:D:439:HOH:O | 1.87 | 0.73 |
| 1:A:284:PRO:HD2 | 1:A:285:GLN:OE1 | 1.88 | 0.73 |
| 1:B:58:PHE:HD1 | 1:B:58:PHE:H | 1.36 | 0.73 |
| 1:C:33:TYR:H | 1:C:66:THR:HG21 | 1.52 | 0.73 |
| 1:B:323:GLY:O | 1:B:327:ARG:HD3 | 1.89 | 0.73 |
| 1:A:33:TYR:H | 1:A:66:THR:CG2 | 2.02 | 0.72 |
| 1:C:319:LYS:HA | 3:C:422:HOH:O | 1.89 | 0.71 |
| 1:A:78:GLU:OE2 | 1:A:207:HIS:HE1 | 1.72 | 0.71 |
| 1:D:281:ALA:HA | 1:D:289:ILE:HD11 | 1.70 | 0.71 |
| 1:B:339:VAL:O | 1:B:340:SER:HB2 | 1.90 | 0.70 |
| 1:D:243:THR:HG22 | 1:D:245:ALA:H | 1.56 | 0.70 |
| 1:D:78:GLU:OE2 | 1:D:207:HIS:HE1 | 1.75 | 0.70 |
| 1:A:95:SER:O | 1:A:99:THR:CG2 | 2.41 | 0.69 |
| 1:B:364:ARG:O | 1:B:368:GLY:N | 2.25 | 0.68 |
| 1:C:339:VAL:O | 1:C:340:SER:CB | 2.40 | 0.68 |
| 1:C:116:HIS:CE1 | 1:D:240:LYS:HD2 | 2.27 | 0.68 |
| 1:D:33:TYR:HB2 | 1:D:66:THR:HG23 | 1.75 | 0.68 |
| 1:C:148:THR:HB | 1:C:149:PRO:HD2 | 1.76 | 0.67 |
| 1:D:58:PHE:N | 1:D:63:SER:OG | 2.27 | 0.66 |
| 1:B:211:LLP:HD3 | 1:B:341:LEU:HG | 1.78 | 0.66 |
| 1:A:28:LEU:HD11 | 1:D:345:GLU:HG3 | 1.78 | 0.66 |
| 1:A:99:THR:HG21 | 1:A:234:ILE:HA | 1.78 | 0.65 |
| 1:B:362:GLU:O | 1:B:363:GLU:CB | 2.32 | 0.65 |
| 1:A:243:THR:HG22 | 1:A:245:ALA:H | 1.61 | 0.65 |
| 1:B:58:PHE:N | 1:B:58:PHE:CD1 | 2.65 | 0.65 |
| 1:A:78:GLU:OE2 | 1:A:207:HIS:CE1 | 2.50 | 0.64 |
| 1:D:78:GLU:OE2 | 1:D:207:HIS:CE1 | 2.52 | 0.62 |
| 1:C:339:VAL:O | 1:C:340:SER:HB3 | 1.99 | 0.61 |
| 1:A:95:SER:O | 1:A:99:THR:HG22 | 2.00 | 0.61 |
| 1:C:122:HIS:NE2 | 1:C:134:HIS:HE1 | 1.99 | 0.61 |
| 1:B:327:ARG:HH21 | 1:B:327:ARG:CG | 2.02 | 0.59 |
| 1:D:211:LLP:HD3 | 1:D:341:LEU:HG | 1.85 | 0.59 |
| 1:B:122:HIS:NE2 | 1:B:134:HIS:HE1 | 2.02 | 0.58 |
| 1:C:263:ASN:HD22 | 1:C:263:ASN:H | 1.49 | 0.58 |
| 1:D:95:SER:O | 1:D:99:THR:CG2 | 2.52 | 0.58 |
| 1:D:236:LEU:O | 1:D:240:LYS:HG2 | 2.04 | 0.57 |
| 1:D:95:SER:O | 1:D:99:THR:HG22 | 2.04 | 0.57 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:D:339:VAL:O | 1:D:340:SER:CB | 2.53 | 0.57 |
| 1:A:62:ILE:CG2 | 1:A:235:ARG:HD3 | 2.35 | 0.57 |
| 1:C:7:LEU:CD1 | 1:C:8:PRO:O | 2.53 | 0.56 |
| 1:D:360:THR:HB | 1:D:361:PRO:HD2 | 1.87 | 0.56 |
| 1:A:339:VAL:O | 1:A:340:SER:CB | 2.53 | 0.56 |
| 1:D:93:ILE:HD12 | 1:D:97:LEU:HD22 | 1.88 | 0.56 |
| 1:B:28:LEU:HD11 | 1:C:345:GLU:HG3 | 1.86 | 0.56 |
| 1:B:320:GLY:CA | 3:B:414:HOH:O | 2.49 | 0.56 |
| 1:B:359:TYR:HB2 | 1:B:364:ARG:NH1 | 2.22 | 0.55 |
| 1:A:233:ARG:HD2 | 3:A:441:HOH:O | 2.06 | 0.55 |
| 1:B:49:CYS:HB3 | 3:B:510:HOH:O | 2.07 | 0.55 |
| 1:C:349:GLN:HE21 | 1:C:375:ARG:CZ | 2.21 | 0.54 |
| 1:C:316:PHE:CE1 | 1:C:374:VAL:HG22 | 2.43 | 0.54 |
| 1:C:7:LEU:CD1 | 1:C:7:LEU:C | 2.75 | 0.54 |
| 1:B:363:GLU:C | 1:B:364:ARG:CG | 2.75 | 0.54 |
| 1:C:349:GLN:HE21 | 1:C:375:ARG:NH2 | 2.06 | 0.53 |
| 1:D:62:ILE:HG23 | 1:D:235:ARG:HD3 | 1.89 | 0.53 |
| 1:C:240:LYS:HD2 | 1:D:116:HIS:HE1 | 1.73 | 0.53 |
| 1:A:93:ILE:CG2 | 3:A:428:HOH:O | 2.34 | 0.52 |
| 1:B:243:THR:HG22 | 1:B:245:ALA:H | 1.74 | 0.52 |
| 1:D:122:HIS:NE2 | 1:D:134:HIS:HE1 | 2.08 | 0.52 |
| 1:C:78:GLU:OE2 | 1:C:207:HIS:CE1 | 2.62 | 0.52 |
| 1:A:17:HIS:HD2 | 3:A:453:HOH:O | 1.93 | 0.52 |
| 1:D:334:LEU:HD13 | 1:D:386:LEU:HD23 | 1.91 | 0.52 |
| 1:A:211:LLP:NZ | 1:A:211:LLP:O3 | 2.44 | 0.51 |
| 1:A:57:HIS:HA | 1:A:63:SER:CB | 2.35 | 0.51 |
| 1:B:95:SER:OG | 1:B:243:THR:HG21 | 2.09 | 0.51 |
| 1:B:17:HIS:HD2 | 3:B:461:HOH:O | 1.94 | 0.51 |
| 1:D:157:GLU:HG2 | 1:D:186:ASP:HB3 | 1.93 | 0.51 |
| 1:B:78:GLU:OE2 | 1:B:207:HIS:HE1 | 1.93 | 0.51 |
| 1:A:61:ARG:HG3 | 1:A:246:VAL:CG2 | 2.41 | 0.50 |
| 1:B:363:GLU:C | 1:B:365:ALA:H | 2.14 | 0.50 |
| 1:C:243:THR:CG2 | 1:C:245:ALA:H | 2.23 | 0.50 |
| 1:C:211:LLP:NZ | 1:C:211:LLP:O3 | 2.42 | 0.50 |
| 1:A:238:GLY:O | 1:A:243:THR:HB | 2.12 | 0.50 |
| 1:B:339:VAL:O | 1:B:340:SER:CB | 2.59 | 0.50 |
| 1:C:33:TYR:HB2 | 1:C:66:THR:HG23 | 1.93 | 0.50 |
| 1:B:211:LLP:NZ | 1:B:211:LLP:O3 | 2.45 | 0.50 |
| 1:B:345:GLU:HG2 | 1:C:28:LEU:HD21 | 1.93 | 0.49 |
| 1:C:116:HIS:HE1 | 1:D:240:LYS:HD2 | 1.72 | 0.49 |
| 1:D:339:VAL:O | 1:D:340:SER:HB3 | 2.11 | 0.49 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:D:350:HIS:CE1 | 1:D:352:ALA:HB3 | 2.47 | 0.49 |
| 1:C:191:THR:HB | 1:C:192:PRO:HD2 | 1.93 | 0.49 |
| 1:C:7:LEU:O | 1:C:7:LEU:HD13 | 2.12 | 0.49 |
| 1:A:345:GLU:HG3 | 1:D:28:LEU:HD11 | 1.95 | 0.49 |
| 1:C:326:ARG:HD2 | 3:C:425:HOH:O | 2.12 | 0.49 |
| 1:D:207:HIS:HD2 | 3:D:400:HOH:O | 1.96 | 0.49 |
| 1:B:78:GLU:OE2 | 1:B:207:HIS:CE1 | 2.66 | 0.49 |
| 1:A:243:THR:CG2 | 1:A:245:ALA:H | 2.24 | 0.49 |
| 1:A:95:SER:O | 1:A:99:THR:HG23 | 2.12 | 0.49 |
| 1:B:321:GLY:O | 1:B:322:ILE:C | 2.52 | 0.48 |
| 1:B:327:ARG:NH2 | 1:B:327:ARG:CG | 2.68 | 0.48 |
| 1:A:206:VAL:HG12 | 1:A:224:VAL:HG22 | 1.95 | 0.48 |
| 1:D:284:PRO:O | 1:D:319:LYS:HE3 | 2.12 | 0.48 |
| 1:C:329:MET:HE1 | 1:C:349:GLN:HA | 1.95 | 0.48 |
| 1:C:7:LEU:O | 1:C:7:LEU:CD1 | 2.62 | 0.47 |
| 1:D:36:ALA:O | 1:D:60:SER:HB2 | 2.14 | 0.47 |
| 1:C:240:LYS:HD2 | 1:D:116:HIS:CE1 | 2.49 | 0.47 |
| 1:D:302:LEU:HA | 1:D:305:GLN:HE21 | 1.80 | 0.47 |
| 1:D:59:TYR:O | 1:D:63:SER:N | 2.47 | 0.47 |
| 1:B:329:MET:HE1 | 1:B:349:GLN:HA | 1.96 | 0.47 |
| 1:C:290:HIS:ND1 | 3:C:460:HOH:O | 2.30 | 0.47 |
| 1:B:237:GLN:NE2 | 3:B:430:HOH:O | 2.39 | 0.46 |
| 1:C:238:GLY:O | 1:C:243:THR:HB | 2.15 | 0.46 |
| 1:B:263:ASN:H | 1:B:263:ASN:HD22 | 1.62 | 0.46 |
| 1:B:360:THR:O | 1:B:362:GLU:O | 2.34 | 0.46 |
| 1:D:243:THR:HG22 | 1:D:245:ALA:N | 2.28 | 0.46 |
| 1:D:281:ALA:HA | 1:D:289:ILE:CD1 | 2.43 | 0.46 |
| 1:B:362:GLU:HG3 | 1:B:363:GLU:N | 2.31 | 0.46 |
| 1:C:61:ARG:NE | 1:D:211:LLP:OP3 | 2.49 | 0.46 |
| 1:B:8:PRO:O | 1:B:13:ARG:HD3 | 2.16 | 0.46 |
| 1:B:243:THR:CG2 | 1:B:245:ALA:H | 2.28 | 0.46 |
| 1:D:168:ASP:O | 1:D:172:VAL:HG23 | 2.16 | 0.46 |
| 1:D:66:THR:HB | 3:D:410:HOH:O | 2.15 | 0.46 |
| 1:A:93:ILE:HG13 | 1:A:94:THR:N | 2.30 | 0.46 |
| 1:A:322:ILE:HG13 | 1:A:322:ILE:H | 1.46 | 0.46 |
| 1:B:31:PRO:HB2 | 1:D:31:PRO:HB2 | 1.97 | 0.45 |
| 3:C:450:HOH:O | 1:D:339:VAL:HG22 | 2.15 | 0.45 |
| 1:C:287:GLU:HB2 | 1:C:319:LYS:HG2 | 1.99 | 0.45 |
| 1:A:334:LEU:HD13 | 1:A:386:LEU:HD23 | 1.98 | 0.45 |
| 1:C:334:LEU:HD13 | 1:C:386:LEU:HD23 | 1.98 | 0.45 |
| 1:B:212:TYR:CE1 | 1:B:342:GLY:HA2 | 2.52 | 0.44 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:C:166:MET:HE1 | 1:C:307:MET:SD | 2.57 | 0.44 |
| 1:C:353:SER:O | 1:D:47:ALA:HB2 | 2.16 | 0.44 |
| 1:A:33:TYR:CE2 | 1:C:31:PRO:HG3 | 2.51 | 0.44 |
| 1:B:323:GLY:O | 1:B:327:ARG:CD | 2.63 | 0.44 |
| 1:C:57:HIS:CD2 | 1:C:63:SER:OG | 2.70 | 0.44 |
| 1:C:78:GLU:OE2 | 1:C:207:HIS:HE1 | 2.00 | 0.44 |
| 1:D:93:ILE:HG13 | 1:D:94:THR:N | 2.33 | 0.44 |
| 1:C:386:LEU:O | 1:C:390:VAL:HG13 | 2.19 | 0.43 |
| 1:D:283:GLN:HA | 1:D:284:PRO:HD2 | 1.85 | 0.43 |
| 1:C:236:LEU:O | 1:C:240:LYS:HE3 | 2.18 | 0.43 |
| 1:B:161:ASN:HA | 1:B:162:PRO:HA | 1.83 | 0.43 |
| 1:A:214:SER:HB2 | 1:A:219:ILE:HD11 | 1.99 | 0.43 |
| 1:B:335:PHE:CD1 | 1:B:346:SER:HB3 | 2.54 | 0.43 |
| 1:C:59:TYR:HE1 | 1:D:340:SER:HB2 | 1.84 | 0.43 |
| 1:D:57:HIS:HB2 | 1:D:63:SER:O | 2.19 | 0.42 |
| 1:D:33:TYR:N | 1:D:66:THR:HG21 | 2.20 | 0.42 |
| 1:D:327:ARG:NH2 | 1:D:397:SER:O | 2.51 | 0.42 |
| 1:A:327:ARG:HB3 | 1:A:397:SER:HA | 2.02 | 0.42 |
| 1:B:152:ARG:NH2 | 1:B:180:GLY:O | 2.53 | 0.42 |
| 1:A:330:ASN:OD1 | 1:B:43:VAL:HG22 | 2.19 | 0.42 |
| 1:D:7:LEU:N | 1:D:8:PRO:HD3 | 2.34 | 0.42 |
| 1:A:111:ASN:HD22 | 1:A:134:HIS:HB3 | 1.84 | 0.42 |
| 1:B:347:LEU:HB2 | 1:B:377:SER:HB3 | 2.01 | 0.42 |
| 1:B:350:HIS:NE2 | 1:B:352:ALA:HB3 | 2.35 | 0.41 |
| 1:C:289:ILE:H | 1:C:289:ILE:HD12 | 1.84 | 0.41 |
| 1:C:161:ASN:HA | 1:C:161:ASN:HD22 | 1.56 | 0.41 |
| 1:C:320:GLY:N | 3:C:422:HOH:O | 2.35 | 0.41 |
| 1:A:383:ILE:HG13 | 3:A:417:HOH:O | 2.20 | 0.41 |
| 1:C:202:ALA:O | 3:C:506:HOH:O | 2.22 | 0.41 |
| 1:D:109:LEU:HA | 1:D:155:TYR:O | 2.19 | 0.41 |
| 1:D:29:VAL:HA | 1:D:30:PRO:HD3 | 1.92 | 0.41 |
| 1:B:316:PHE:CE1 | 1:B:374:VAL:HG22 | 2.55 | 0.41 |
| 1:A:111:ASN:HA | 1:A:111:ASN:HD22 | 1.73 | 0.41 |
| 1:A:211:LLP:HD3 | 1:A:341:LEU:HG | 2.02 | 0.41 |
| 1:A:61:ARG:HG3 | 1:A:246:VAL:HG22 | 2.02 | 0.41 |
| 1:A:89:GLY:O | 1:A:93:ILE:HG23 | 2.21 | 0.41 |
| 1:B:13:ARG:NH2 | 3:B:435:HOH:O | 2.51 | 0.41 |
| 1:D:190:CYS:O | 1:D:194:LEU:HB2 | 2.21 | 0.41 |
| 1:C:276:LEU:HA | 1:C:276:LEU:HD23 | 1.94 | 0.41 |
| 1:C:84:LEU:HD13 | 1:C:86:LEU:HD11 | 2.02 | 0.41 |
| 1:B:191:THR:HG21 | 1:B:262:LEU:HD11 | 2.03 | 0.41 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:B:110:GLY:O | 1:B:134:HIS:HD2 | 2.04 | 0.40 |
| 1:A:327:ARG:NH2 | 1:A:397:SER:O | 2.54 | 0.40 |
| 1:D:196:ARG:NH1 | 1:D:196:ARG:HG3 | 2.36 | 0.40 |
| 1:D:213:LEU:HB3 | 1:D:255:LEU:HD11 | 2.04 | 0.40 |

There are no symmetry-related clashes.

## 5.3   Torsion angles ⓘ

### 5.3.1   Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|---|---|---|---|---|---|---|---|
| 1 | A | 390/398 (98%) | 375 (96%) | 12 (3%) | 3 (1%) | 22 | 26 |
| 1 | B | 393/398 (99%) | 377 (96%) | 13 (3%) | 3 (1%) | 22 | 26 |
| 1 | C | 389/398 (98%) | 374 (96%) | 14 (4%) | 1 (0%) | 44 | 55 |
| 1 | D | 390/398 (98%) | 371 (95%) | 12 (3%) | 7 (2%) | 10 | 9 |
| All | All | 1562/1592 (98%) | 1497 (96%) | 51 (3%) | 14 (1%) | 20 | 23 |

All (14) Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | B | 340 | SER |
| 1 | D | 7 | LEU |
| 1 | A | 60 | SER |
| 1 | A | 340 | SER |
| 1 | D | 55 | ALA |
| 1 | D | 340 | SER |
| 1 | B | 322 | ILE |
| 1 | D | 287 | GLU |
| 1 | D | 322 | ILE |
| 1 | A | 53 | GLU |
| 1 | B | 363 | GLU |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | C | 340 | SER |
| 1 | D | 62 | ILE |
| 1 | D | 361 | PRO |

## 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 | 302/306 (99%) | 270 (89%) | 32 (11%) | 8 | 9 |
| 1 | B | 304/306 (99%) | 274 (90%) | 30 (10%) | 9 | 11 |
| 1 | C | 301/306 (98%) | 269 (89%) | 32 (11%) | 8 | 9 |
| 1 | D | 302/306 (99%) | 273 (90%) | 29 (10%) | 10 | 11 |
| All | All | 1209/1224 (99%) | 1086 (90%) | 123 (10%) | 8 | 10 |

All (123) residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | A | 7 | LEU |
| 1 | A | 37 | THR |
| 1 | A | 58 | PHE |
| 1 | A | 62 | ILE |
| 1 | A | 66 | THR |
| 1 | A | 84 | LEU |
| 1 | A | 93 | ILE |
| 1 | A | 97 | LEU |
| 1 | A | 99 | THR |
| 1 | A | 111 | ASN |
| 1 | A | 121 | LEU |
| 1 | A | 132 | LEU |
| 1 | A | 141 | GLN |
| 1 | A | 152 | ARG |
| 1 | A | 200 | LEU |
| 1 | A | 213 | LEU |
| 1 | A | 214 | SER |
| 1 | A | 243 | THR |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | A | 263 | ASN |
| 1 | A | 264 | LEU |
| 1 | A | 280 | LEU |
| 1 | A | 289 | ILE |
| 1 | A | 304 | ARG |
| 1 | A | 322 | ILE |
| 1 | A | 334 | LEU |
| 1 | A | 341 | LEU |
| 1 | A | 347 | LEU |
| 1 | A | 359 | TYR |
| 1 | A | 366 | HIS |
| 1 | A | 374 | VAL |
| 1 | A | 383 | ILE |
| 1 | A | 391 | GLN |
| 1 | B | 7 | LEU |
| 1 | B | 22 | GLN |
| 1 | B | 49 | CYS |
| 1 | B | 58 | PHE |
| 1 | B | 84 | LEU |
| 1 | B | 97 | LEU |
| 1 | B | 111 | ASN |
| 1 | B | 121 | LEU |
| 1 | B | 132 | LEU |
| 1 | B | 140 | LEU |
| 1 | B | 166 | MET |
| 1 | B | 178 | LYS |
| 1 | B | 200 | LEU |
| 1 | B | 213 | LEU |
| 1 | B | 230 | LEU |
| 1 | B | 243 | THR |
| 1 | B | 254 | LEU |
| 1 | B | 263 | ASN |
| 1 | B | 264 | LEU |
| 1 | B | 268 | ARG |
| 1 | B | 280 | LEU |
| 1 | B | 287 | GLU |
| 1 | B | 301 | THR |
| 1 | B | 304 | ARG |
| 1 | B | 327 | ARG |
| 1 | B | 333 | GLN |
| 1 | B | 334 | LEU |
| 1 | B | 339 | VAL |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | B | 347 | LEU |
| 1 | B | 374 | VAL |
| 1 | C | 37 | THR |
| 1 | C | 58 | PHE |
| 1 | C | 66 | THR |
| 1 | C | 84 | LEU |
| 1 | C | 97 | LEU |
| 1 | C | 111 | ASN |
| 1 | C | 121 | LEU |
| 1 | C | 131 | LYS |
| 1 | C | 132 | LEU |
| 1 | C | 140 | LEU |
| 1 | C | 152 | ARG |
| 1 | C | 174 | LYS |
| 1 | C | 177 | ARG |
| 1 | C | 200 | LEU |
| 1 | C | 213 | LEU |
| 1 | C | 230 | LEU |
| 1 | C | 243 | THR |
| 1 | C | 254 | LEU |
| 1 | C | 263 | ASN |
| 1 | C | 264 | LEU |
| 1 | C | 280 | LEU |
| 1 | C | 289 | ILE |
| 1 | C | 322 | ILE |
| 1 | C | 334 | LEU |
| 1 | C | 341 | LEU |
| 1 | C | 347 | LEU |
| 1 | C | 363 | GLU |
| 1 | C | 366 | HIS |
| 1 | C | 374 | VAL |
| 1 | C | 383 | ILE |
| 1 | C | 390 | VAL |
| 1 | C | 391 | GLN |
| 1 | D | 37 | THR |
| 1 | D | 60 | SER |
| 1 | D | 66 | THR |
| 1 | D | 84 | LEU |
| 1 | D | 93 | ILE |
| 1 | D | 97 | LEU |
| 1 | D | 99 | THR |
| 1 | D | 121 | LEU |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | D | 131 | LYS |
| 1 | D | 140 | LEU |
| 1 | D | 178 | LYS |
| 1 | D | 194 | LEU |
| 1 | D | 200 | LEU |
| 1 | D | 213 | LEU |
| 1 | D | 230 | LEU |
| 1 | D | 254 | LEU |
| 1 | D | 263 | ASN |
| 1 | D | 264 | LEU |
| 1 | D | 274 | GLN |
| 1 | D | 280 | LEU |
| 1 | D | 301 | THR |
| 1 | D | 314 | ILE |
| 1 | D | 322 | ILE |
| 1 | D | 334 | LEU |
| 1 | D | 341 | LEU |
| 1 | D | 347 | LEU |
| 1 | D | 359 | TYR |
| 1 | D | 374 | VAL |
| 1 | D | 383 | ILE |

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (37) such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | A | 17 | HIS |
| 1 | A | 111 | ASN |
| 1 | A | 134 | HIS |
| 1 | A | 207 | HIS |
| 1 | A | 250 | HIS |
| 1 | A | 263 | ASN |
| 1 | A | 333 | GLN |
| 1 | B | 5 | ASN |
| 1 | B | 17 | HIS |
| 1 | B | 68 | ASN |
| 1 | B | 111 | ASN |
| 1 | B | 116 | HIS |
| 1 | B | 134 | HIS |
| 1 | B | 207 | HIS |
| 1 | B | 250 | HIS |
| 1 | B | 274 | GLN |
| 1 | B | 391 | GLN |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | C | 111 | ASN |
| 1 | C | 116 | HIS |
| 1 | C | 134 | HIS |
| 1 | C | 161 | ASN |
| 1 | C | 207 | HIS |
| 1 | C | 250 | HIS |
| 1 | C | 263 | ASN |
| 1 | C | 274 | GLN |
| 1 | C | 305 | GLN |
| 1 | C | 349 | GLN |
| 1 | D | 22 | GLN |
| 1 | D | 54 | GLN |
| 1 | D | 116 | HIS |
| 1 | D | 134 | HIS |
| 1 | D | 161 | ASN |
| 1 | D | 207 | HIS |
| 1 | D | 250 | HIS |
| 1 | D | 305 | GLN |
| 1 | D | 309 | GLN |
| 1 | D | 356 | HIS |

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

4 non-standard protein/DNA/RNA residues 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 | #$|Z| > 2$ |
| 1 | LLP | A | 211 | 1 | 24,24,25 | 2.24 | 6 (25%) | 28,32,34 | 1.77 | 7 (25%) |
| 1 | LLP | B | 211 | 1 | 24,24,25 | 2.60 | 8 (33%) | 28,32,34 | 1.79 | 7 (25%) |
| 1 | LLP | C | 211 | 1 | 24,24,25 | 2.36 | 5 (20%) | 28,32,34 | 1.82 | 6 (21%) |

| Mol | Type | Chain | Res | Link | Bond lengths | | | Bond angles | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | Counts | RMSZ | #\|Z\| > 2 | Counts | RMSZ | #\|Z\| > 2 |
| 1 | LLP | D | 211 | 1 | 24,24,25 | 2.43 | 9 (37%) | 28,32,34 | 1.79 | 6 (21%) |

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 |
|---|---|---|---|---|---|---|---|
| 1 | LLP | A | 211 | 1 | - | 0/15/17/19 | 0/1/1/1 |
| 1 | LLP | B | 211 | 1 | - | 0/15/17/19 | 0/1/1/1 |
| 1 | LLP | C | 211 | 1 | - | 0/15/17/19 | 0/1/1/1 |
| 1 | LLP | D | 211 | 1 | - | 0/15/17/19 | 0/1/1/1 |

All (28) bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|---|---|---|---|---|---|---|---|
| 1 | B | 211 | LLP | C2'-C2 | -5.62 | 1.40 | 1.50 |
| 1 | C | 211 | LLP | C2'-C2 | -4.52 | 1.42 | 1.50 |
| 1 | A | 211 | LLP | C2'-C2 | -4.27 | 1.42 | 1.50 |
| 1 | D | 211 | LLP | C2'-C2 | -3.93 | 1.43 | 1.50 |
| 1 | B | 211 | LLP | C4-C4' | -3.77 | 1.39 | 1.46 |
| 1 | B | 211 | LLP | C5'-C5 | -3.59 | 1.41 | 1.50 |
| 1 | C | 211 | LLP | C5'-C5 | -3.06 | 1.42 | 1.50 |
| 1 | D | 211 | LLP | C5'-C5 | -2.95 | 1.42 | 1.50 |
| 1 | D | 211 | LLP | C4-C4' | -2.82 | 1.41 | 1.46 |
| 1 | A | 211 | LLP | C5'-C5 | -2.67 | 1.43 | 1.50 |
| 1 | B | 211 | LLP | C3-C2 | -2.40 | 1.39 | 1.40 |
| 1 | D | 211 | LLP | P-OP3 | -2.18 | 1.45 | 1.54 |
| 1 | A | 211 | LLP | P-OP2 | -2.18 | 1.45 | 1.54 |
| 1 | B | 211 | LLP | P-OP2 | -2.14 | 1.46 | 1.54 |
| 1 | D | 211 | LLP | P-OP2 | -2.11 | 1.46 | 1.54 |
| 1 | B | 211 | LLP | C6-N1 | 2.39 | 1.39 | 1.34 |
| 1 | D | 211 | LLP | CB-CA | 2.68 | 1.57 | 1.53 |
| 1 | A | 211 | LLP | CA-C | 3.01 | 1.54 | 1.50 |
| 1 | A | 211 | LLP | C6-N1 | 3.03 | 1.40 | 1.34 |
| 1 | D | 211 | LLP | CA-C | 3.05 | 1.54 | 1.50 |
| 1 | C | 211 | LLP | C6-N1 | 3.77 | 1.42 | 1.34 |
| 1 | D | 211 | LLP | C6-N1 | 3.87 | 1.42 | 1.34 |
| 1 | C | 211 | LLP | CA-C | 4.29 | 1.55 | 1.50 |
| 1 | B | 211 | LLP | CA-C | 4.63 | 1.56 | 1.50 |
| 1 | B | 211 | LLP | C4'-NZ | 7.13 | 1.47 | 1.27 |
| 1 | C | 211 | LLP | C4'-NZ | 7.41 | 1.48 | 1.27 |

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| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|-----|-------|-----|------|--------|------|-------------|----------|
| 1 | D | 211 | LLP | C4'-NZ | 7.41 | 1.48 | 1.27 |
| 1 | A | 211 | LLP | C4'-NZ | 7.60 | 1.49 | 1.27 |

All (26) bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|-----|-------|-----|------|--------|------|------------|---------|
| 1 | B | 211 | LLP | OP2-P-OP4 | -3.22 | 98.18 | 106.73 |
| 1 | A | 211 | LLP | OP4-P-OP1 | -3.14 | 97.66 | 106.47 |
| 1 | D | 211 | LLP | C4-C4'-NZ | -3.00 | 110.11 | 124.66 |
| 1 | B | 211 | LLP | CE-NZ-C4' | -2.95 | 110.47 | 119.03 |
| 1 | C | 211 | LLP | CE-NZ-C4' | -2.93 | 110.52 | 119.03 |
| 1 | D | 211 | LLP | OP2-P-OP4 | -2.89 | 99.04 | 106.73 |
| 1 | A | 211 | LLP | CE-NZ-C4' | -2.76 | 111.02 | 119.03 |
| 1 | A | 211 | LLP | C3-C2-N1 | -2.57 | 117.37 | 120.75 |
| 1 | B | 211 | LLP | O-C-CA | -2.49 | 118.14 | 125.02 |
| 1 | C | 211 | LLP | C3-C2-N1 | -2.47 | 117.50 | 120.75 |
| 1 | A | 211 | LLP | O-C-CA | -2.47 | 118.20 | 125.02 |
| 1 | C | 211 | LLP | OP2-P-OP4 | -2.32 | 100.56 | 106.73 |
| 1 | B | 211 | LLP | C3-C2-N1 | -2.32 | 117.71 | 120.75 |
| 1 | B | 211 | LLP | C4-C4'-NZ | -2.30 | 113.47 | 124.66 |
| 1 | C | 211 | LLP | O-C-CA | -2.30 | 118.68 | 125.02 |
| 1 | D | 211 | LLP | O-C-CA | -2.22 | 118.88 | 125.02 |
| 1 | A | 211 | LLP | C4-C4'-NZ | -2.12 | 114.36 | 124.66 |
| 1 | C | 211 | LLP | C4-C4'-NZ | -2.09 | 114.53 | 124.66 |
| 1 | D | 211 | LLP | C2'-C2-N1 | 2.25 | 122.38 | 117.89 |
| 1 | D | 211 | LLP | OP3-P-OP2 | 2.26 | 116.73 | 107.61 |
| 1 | A | 211 | LLP | C5'-C5-C4 | 2.43 | 125.90 | 121.66 |
| 1 | B | 211 | LLP | OP3-P-OP2 | 2.46 | 117.54 | 107.61 |
| 1 | B | 211 | LLP | C4-C3-C2 | 4.70 | 123.05 | 120.15 |
| 1 | A | 211 | LLP | C4-C3-C2 | 5.02 | 123.24 | 120.15 |
| 1 | D | 211 | LLP | C4-C3-C2 | 5.65 | 123.63 | 120.15 |
| 1 | C | 211 | LLP | C4-C3-C2 | 5.88 | 123.77 | 120.15 |

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 7 short contacts:

| Mol | Chain | Res | Type | Clashes | Symm-Clashes |
|-----|-------|-----|------|---------|--------------|
| 1 | A | 211 | LLP | 2 | 0 |
| 1 | B | 211 | LLP | 2 | 0 |

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| Mol | Chain | Res | Type | Clashes | Symm-Clashes |
|-----|-------|-----|------|---------|--------------|
| 1 | C | 211 | LLP | 1 | 0 |
| 1 | D | 211 | LLP | 2 | 0 |

## 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 | SO4 | A | 501 | - | 4,4,4 | 0.17 | 0 | 6,6,6 | 0.12 | 0 |
| 2 | SO4 | B | 501 | - | 4,4,4 | 0.18 | 0 | 6,6,6 | 0.08 | 0 |
| 2 | SO4 | C | 501 | - | 4,4,4 | 0.17 | 0 | 6,6,6 | 0.11 | 0 |
| 2 | SO4 | D | 501 | - | 4,4,4 | 0.18 | 0 | 6,6,6 | 0.19 | 0 |

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 | SO4 | A | 501 | - | - | 0/0/0/0 | 0/0/0/0 |
| 2 | SO4 | B | 501 | - | - | 0/0/0/0 | 0/0/0/0 |
| 2 | SO4 | C | 501 | - | - | 0/0/0/0 | 0/0/0/0 |
| 2 | SO4 | D | 501 | - | - | 0/0/0/0 | 0/0/0/0 |

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 | 392/398 (98%) | 0.04 | 30 (7%) | 14 | 19 | 7, 20, 67, 88 | 0 |
| 1 | B | 395/398 (99%) | 0.07 | 37 (9%) | 9 | 12 | 6, 17, 73, 84 | 0 |
| 1 | C | 391/398 (98%) | -0.05 | 28 (7%) | 16 | 22 | 6, 18, 62, 91 | 0 |
| 1 | D | 392/398 (98%) | 0.22 | 30 (7%) | 14 | 19 | 9, 26, 72, 90 | 0 |
| All | All | 1570/1592 (98%) | 0.07 | 125 (7%) | 13 | 17 | 6, 20, 68, 91 | 0 |

All (125) RSRZ outliers are listed below:

| Mol | Chain | Res | Type | RSRZ |
|-----|-------|-----|------|------|
| 1 | D | 59 | TYR | 14.2 |
| 1 | A | 62 | ILE | 9.2 |
| 1 | B | 366 | HIS | 9.2 |
| 1 | D | 62 | ILE | 9.1 |
| 1 | A | 54 | GLN | 9.1 |
| 1 | D | 358 | SER | 9.0 |
| 1 | C | 52 | GLY | 8.9 |
| 1 | B | 51 | ALA | 8.8 |
| 1 | D | 52 | GLY | 8.4 |
| 1 | C | 53 | GLU | 8.4 |
| 1 | B | 55 | ALA | 8.2 |
| 1 | B | 368 | GLY | 8.2 |
| 1 | C | 55 | ALA | 8.2 |
| 1 | C | 51 | ALA | 8.1 |
| 1 | B | 54 | GLN | 7.5 |
| 1 | A | 52 | GLY | 7.4 |
| 1 | D | 61 | ARG | 7.1 |
| 1 | C | 54 | GLN | 6.9 |
| 1 | B | 58 | PHE | 6.8 |
| 1 | D | 365 | ALA | 6.7 |
| 1 | A | 58 | PHE | 6.7 |

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| Mol | Chain | Res | Type | RSRZ |
|-----|-------|-----|------|------|
| 1 | A | 55 | ALA | 6.6 |
| 1 | B | 367 | TYR | 6.4 |
| 1 | C | 58 | PHE | 6.4 |
| 1 | D | 54 | GLN | 6.3 |
| 1 | A | 51 | ALA | 6.3 |
| 1 | D | 55 | ALA | 6.2 |
| 1 | D | 359 | TYR | 6.1 |
| 1 | D | 58 | PHE | 6.1 |
| 1 | D | 60 | SER | 6.0 |
| 1 | B | 360 | THR | 5.9 |
| 1 | B | 48 | ALA | 5.8 |
| 1 | B | 358 | SER | 5.7 |
| 1 | A | 53 | GLU | 5.6 |
| 1 | A | 47 | ALA | 5.5 |
| 1 | A | 59 | TYR | 5.3 |
| 1 | D | 6 | LYS | 5.2 |
| 1 | D | 367 | TYR | 5.2 |
| 1 | A | 60 | SER | 5.2 |
| 1 | D | 57 | HIS | 5.2 |
| 1 | C | 48 | ALA | 5.2 |
| 1 | D | 366 | HIS | 5.1 |
| 1 | D | 368 | GLY | 5.1 |
| 1 | B | 45 | TYR | 5.1 |
| 1 | A | 56 | GLY | 5.0 |
| 1 | C | 45 | TYR | 5.0 |
| 1 | C | 60 | SER | 5.0 |
| 1 | B | 63 | SER | 4.9 |
| 1 | A | 57 | HIS | 4.9 |
| 1 | A | 61 | ARG | 4.9 |
| 1 | D | 360 | THR | 4.8 |
| 1 | B | 59 | TYR | 4.8 |
| 1 | D | 56 | GLY | 4.6 |
| 1 | B | 62 | ILE | 4.6 |
| 1 | C | 359 | TYR | 4.6 |
| 1 | D | 53 | GLU | 4.5 |
| 1 | D | 363 | GLU | 4.5 |
| 1 | A | 367 | TYR | 4.5 |
| 1 | A | 50 | PHE | 4.5 |
| 1 | A | 6 | LYS | 4.5 |
| 1 | D | 362 | GLU | 4.5 |
| 1 | B | 362 | GLU | 4.4 |
| 1 | B | 56 | GLY | 4.3 |

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| Mol | Chain | Res | Type | RSRZ |
|-----|-------|-----|------|------|
| 1 | A | 359 | TYR | 4.3 |
| 1 | B | 49 | CYS | 4.3 |
| 1 | C | 57 | HIS | 4.2 |
| 1 | B | 47 | ALA | 4.2 |
| 1 | A | 48 | ALA | 4.2 |
| 1 | A | 398 | ALA | 4.1 |
| 1 | A | 366 | HIS | 4.0 |
| 1 | C | 63 | SER | 4.0 |
| 1 | D | 357 | SER | 3.9 |
| 1 | C | 366 | HIS | 3.9 |
| 1 | C | 59 | TYR | 3.9 |
| 1 | C | 367 | TYR | 3.8 |
| 1 | B | 359 | TYR | 3.8 |
| 1 | B | 361 | PRO | 3.7 |
| 1 | B | 52 | GLY | 3.7 |
| 1 | B | 398 | ALA | 3.6 |
| 1 | C | 358 | SER | 3.6 |
| 1 | B | 50 | PHE | 3.5 |
| 1 | A | 365 | ALA | 3.4 |
| 1 | A | 360 | THR | 3.4 |
| 1 | B | 320 | GLY | 3.3 |
| 1 | C | 50 | PHE | 3.3 |
| 1 | A | 45 | TYR | 3.3 |
| 1 | A | 362 | GLU | 3.2 |
| 1 | A | 358 | SER | 3.2 |
| 1 | C | 365 | ALA | 3.1 |
| 1 | C | 362 | GLU | 3.1 |
| 1 | C | 368 | GLY | 3.1 |
| 1 | D | 398 | ALA | 3.1 |
| 1 | D | 287 | GLU | 3.0 |
| 1 | B | 44 | GLU | 2.9 |
| 1 | C | 47 | ALA | 2.9 |
| 1 | B | 322 | ILE | 2.9 |
| 1 | B | 6 | LYS | 2.8 |
| 1 | A | 7 | LEU | 2.8 |
| 1 | B | 53 | GLU | 2.8 |
| 1 | B | 57 | HIS | 2.7 |
| 1 | B | 365 | ALA | 2.7 |
| 1 | A | 22 | GLN | 2.7 |
| 1 | C | 62 | ILE | 2.6 |
| 1 | C | 7 | LEU | 2.6 |
| 1 | B | 41 | PRO | 2.6 |

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| Mol | Chain | Res | Type | RSRZ |
|-----|-------|-----|------|------|
| 1 | D | 288 | LEU | 2.6 |
| 1 | B | 371 | GLU | 2.5 |
| 1 | C | 61 | ARG | 2.5 |
| 1 | D | 63 | SER | 2.5 |
| 1 | C | 44 | GLU | 2.5 |
| 1 | C | 149 | PRO | 2.5 |
| 1 | D | 361 | PRO | 2.4 |
| 1 | B | 321 | GLY | 2.4 |
| 1 | D | 7 | LEU | 2.4 |
| 1 | A | 361 | PRO | 2.3 |
| 1 | B | 364 | ARG | 2.3 |
| 1 | D | 364 | ARG | 2.3 |
| 1 | A | 363 | GLU | 2.2 |
| 1 | C | 56 | GLY | 2.2 |
| 1 | B | 43 | VAL | 2.2 |
| 1 | B | 357 | SER | 2.2 |
| 1 | C | 357 | SER | 2.1 |
| 1 | A | 63 | SER | 2.1 |
| 1 | D | 369 | ILE | 2.0 |
| 1 | B | 5 | ASN | 2.0 |

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

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($\text{Å}^2$) | Q<0.9 |
|-----|------|-------|-----|-------|------|-----|------|-------------------------|-------|
| 1 | LLP | C | 211 | 24/25 | 0.97 | 0.13 | - | 9,14,15,17 | 0 |
| 1 | LLP | D | 211 | 24/25 | 0.97 | 0.12 | - | 12,19,21,22 | 0 |
| 1 | LLP | A | 211 | 24/25 | 0.98 | 0.14 | - | 9,15,19,20 | 0 |
| 1 | LLP | B | 211 | 24/25 | 0.97 | 0.11 | - | 8,11,14,15 | 0 |

## 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands (i)

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(Å²) | Q<0.9 |
|-----|------|-------|-----|-------|------|-----|------|---------------|-------|
| 2 | SO4 | C | 501 | 5/5 | 0.81 | 0.31 | 4.58 | 90,90,91,91 | 0 |
| 2 | SO4 | B | 501 | 5/5 | 0.84 | 0.21 | 0.99 | 94,94,94,94 | 0 |
| 2 | SO4 | D | 501 | 5/5 | 0.87 | 0.21 | 0.31 | 90,90,90,91 | 0 |
| 2 | SO4 | A | 501 | 5/5 | 0.91 | 0.15 | -0.13 | 74,74,75,75 | 0 |

## 6.5 Other polymers (i)

There are no such residues in this entry.