# Full wwPDB X-ray Structure Validation Report ⓘ

May 26, 2020 – 08:00 pm BST

| | | |
|---|---|---|
| PDB ID | : | 2XVN |
| Title | : | A. fumigatus chitinase A1 phenyl-methylguanylurea complex |
| Authors | : | Rush, C.L.; Schuttelkopf, A.W.; Hurtado-Guerrero, R.; Blair, D.E.; Ibrahim, A.F.M.; Desvergnes, S.; Eggleston, I.M.; van Aalten, D.M.F. |
| Deposited on | : | 2010-10-26 |
| Resolution | : | 2.35 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 following versions of software and data (see references ①) were used in the production of this report:

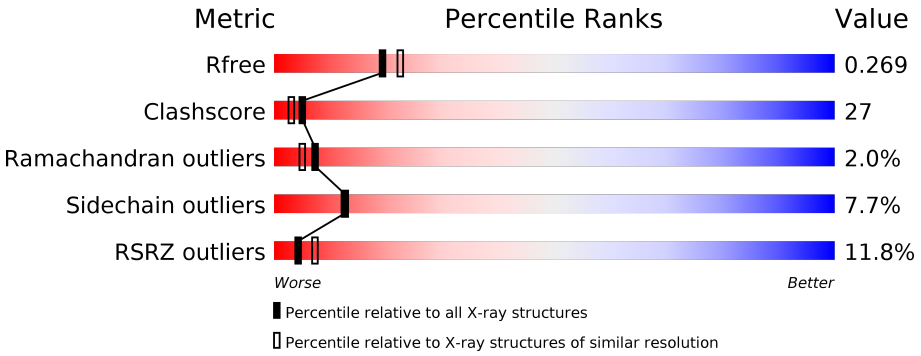
| | | |
|---|---|---|
| MolProbity | : | 4.02b-467 |
| Mogul | : | 1.8.5 (274361), CSD as541be (2020) |
| Xtriage (Phenix) | : | 1.13 |
| EDS | : | 2.11 |
| Percentile statistics | : | 20191225.v01 (using entries in the PDB archive December 25th 2019) |
| Refmac | : | 5.8.0158 |
| CCP4 | : | 7.0.044 (Gargrove) |
| Ideal geometry (proteins) | : | Engh & Huber (2001) |
| Ideal geometry (DNA, RNA) | : | Parkinson et al. (1996) |
| Validation Pipeline (wwPDB-VP) | : | 2.11 |

# 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 2.35 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)) |
|---|---|---|
| $R_{free}$ | 130704 | 1164 (2.36-2.36) |
| Clashscore | 141614 | 1232 (2.36-2.36) |
| Ramachandran outliers | 138981 | 1211 (2.36-2.36) |
| Sidechain outliers | 138945 | 1212 (2.36-2.36) |
| RSRZ outliers | 127900 | 1150 (2.36-2.36) |

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 respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

| Mol | Chain | Length | Quality of chain |
|---|---|---|---|
| 1 | A | 309 | 3% 75% 22% |
| 1 | B | 309 | 2% 72% 25% |
| 1 | C | 309 | 27% 28% 30% 8% 32% |

## 2 Entry composition

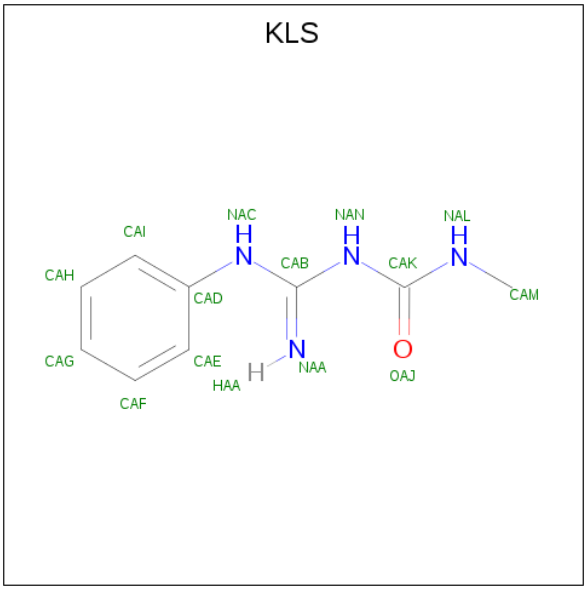
There are 4 unique types of molecules in this entry. The entry contains 6669 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 ASPERGILLUS FUMIGATUS CHITINASE A1.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| 1 | A | 309 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 2396 | 1541 | 382 | 461 | 12 | | | |
| 1 | B | 309 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 2396 | 1541 | 382 | 461 | 12 | | | |
| 1 | C | 210 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1631 | 1062 | 253 | 307 | 9 | | | |

- Molecule 2 is 1-METHYL-3-(N-PHENYLCARBAMIMIDOYL)UREA (three-letter code: KLS) (formula: $C_9H_{12}N_4O$).




| Mol | Chain | Residues | Atoms | | | | ZeroOcc | AltConf |
|---|---|---|---|---|---|---|---|---|
| 2 | A | 1 | Total | C | N | O | 0 | 0 |
| | | | 14 | 9 | 4 | 1 | | |
| 2 | B | 1 | Total | C | N | O | 0 | 0 |
| | | | 14 | 9 | 4 | 1 | | |

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

| Mol | Chain | Residues | Atoms | ZeroOcc | AltConf |
|---|---|---|---|---|---|
| 3 | B | 2 | Total Cl<br>2 2 | 0 | 0 |

- Molecule 4 is water.

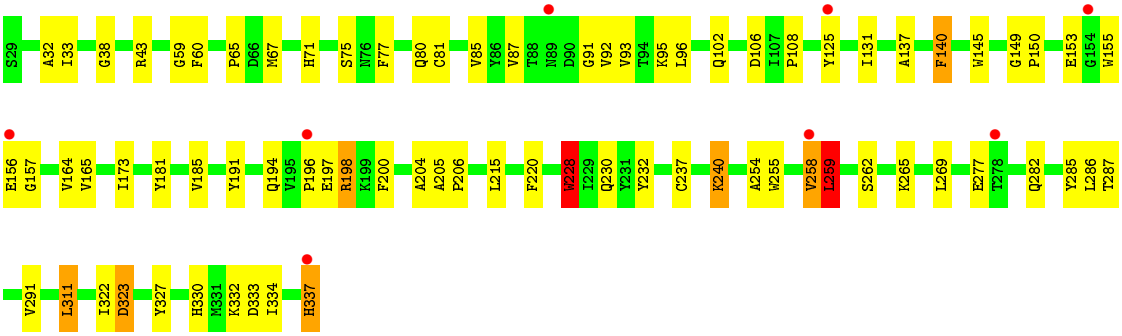
| Mol | Chain | Residues | Atoms | ZeroOcc | AltConf |
|---|---|---|---|---|---|
| 4 | A | 89 | Total O<br>89 89 | 0 | 0 |
| 4 | B | 95 | Total O<br>95 95 | 0 | 0 |
| 4 | C | 32 | Total O<br>32 32 | 0 | 0 |

# 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 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.

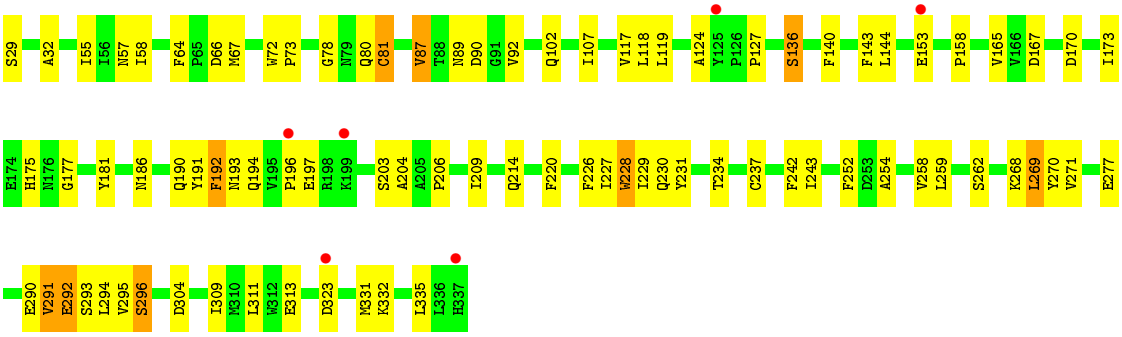
• Molecule 1: ASPERGILLUS FUMIGATUS CHITINASE A1

Chain A:



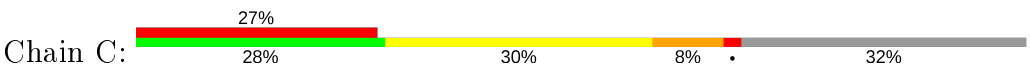

• Molecule 1: ASPERGILLUS FUMIGATUS CHITINASE A1

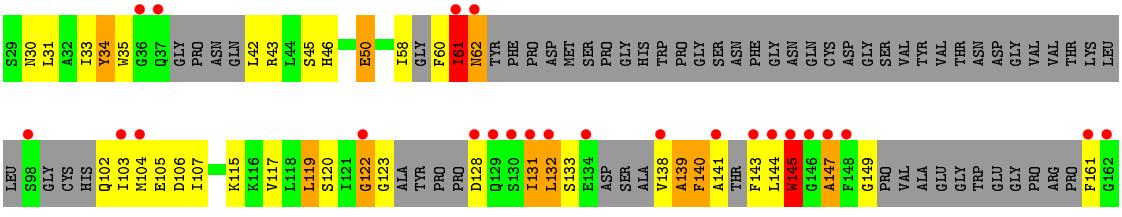
Chain B:

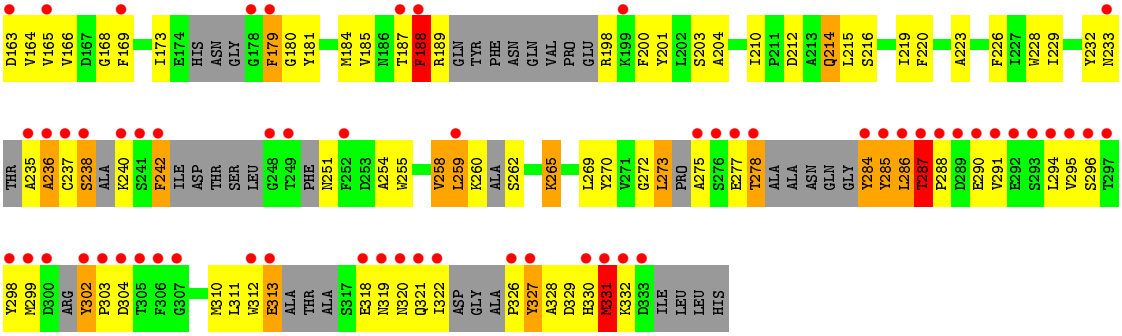



• Molecule 1: ASPERGILLUS FUMIGATUS CHITINASE A1

Chain C:




D163 V164 V165 V166 D167 G168 F169
I173 E174 HIS ASN GLY G178 F179 G180 Y181
M184 V185 N186 T187 F188 R189 GLN TYR PHE ASN GLN VAL PRO GLU R198 K199 F200 Y201 L202 S203 A204
I210 P211 D212 A213 Q214 L215 S216
I219 F220
A223
F226 I227 W228 I229
Y232 N233
THR A235 A236 C237 S238 ALA K240 S241 F242
ILE ASP THR SER LEU G248 T249 PHE N251 F252 D253 A254 W255
V258 L259 K260 ALA S262
K265
L269 Y270 V271 G272 L273 PRO A275 S276 E277 T278
ALA ALA ASN GLN GLY Y284 Y285 L286 T287 P288 D289 E290 V291 E292 S293 L294 V295 S296 T297
Y298 M299 D300 ARG Y302 P303 D304 T305 F306 G307
M310 L311 W312 E313 ALA THR ALA S317 E318 N319 N320 Q321 I322 ASP GLY ALA P326 Y327 A328 D329 H330 M331 K332 D333 ILE LEU LEU HIS

# 4 Data and refinement statistics (i)

| Property | Value | Source |
|---|---|---|
| Space group | P 32 | Depositor |
| Cell constants<br>a, b, c, $\alpha$, $\beta$, $\gamma$ | 99.98Å 99.98Å 111.30Å<br>90.00° 90.00° 120.00° | Depositor |
| Resolution (Å) | 12.00 – 2.35<br>10.00 – 2.40 | Depositor<br>EDS |
| % Data completeness<br>(in resolution range) | 98.4 (12.00-2.35)<br>96.9 (10.00-2.40) | Depositor<br>EDS |
| $R_{merge}$ | 0.11 | Depositor |
| $R_{sym}$ | (Not available) | Depositor |
| $< I/\sigma(I) >$ [1] | 4.10 (at 2.41Å) | Xtriage |
| Refinement program | REFMAC 5.5.0088 | Depositor |
| R, $R_{free}$ | 0.259 , 0.299<br>0.252 , 0.269 | Depositor<br>DCC |
| $R_{free}$ test set | 465 reflections (1.00%) | wwPDB-VP |
| Wilson B-factor (Å$^2$) | 17.5 | Xtriage |
| Anisotropy | 0.068 | Xtriage |
| Bulk solvent $k_{sol}$(e/Å$^3$), $B_{sol}$(Å$^2$) | 0.49 , 27.9 | EDS |
| L-test for twinning[2] | $< \|L\| > = 0.48$, $< L^2 > = 0.31$ | Xtriage |
| Estimated twinning fraction | 0.025 for -h,-k,l<br>0.449 for h,-h-k,-l<br>0.027 for -k,-h,-l | Xtriage |
| Reported twinning fraction | 0.460 for H, K, L<br>0.540 for K, H, -L | Depositor |
| Outliers | 0 of 46543 reflections | Xtriage |
| $F_o$,$F_c$ correlation | 0.86 | EDS |
| Total number of atoms | 6669 | wwPDB-VP |
| Average B, all atoms (Å$^2$) | 15.0 | wwPDB-VP |

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.33% 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: CL, KLS

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 | 1.16 | 5/2468 (0.2%) | 1.04 | 11/3368 (0.3%) |
| 1 | B | 1.10 | 3/2468 (0.1%) | 0.98 | 3/3368 (0.1%) |
| 1 | C | 0.98 | 2/1655 (0.1%) | 0.91 | 1/2218 (0.0%) |
| All | All | 1.09 | 10/6591 (0.2%) | 0.99 | 15/8954 (0.2%) |

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

| Mol | Chain | #Chirality outliers | #Planarity outliers |
|---|---|---|---|
| 1 | C | 0 | 1 |

All (10) bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|---|---|---|---|---|---|---|---|
| 1 | A | 198 | ARG | C-N | -17.89 | 0.93 | 1.34 |
| 1 | B | 291 | VAL | C-N | -10.51 | 1.09 | 1.34 |
| 1 | B | 292 | GLU | C-N | 7.73 | 1.51 | 1.34 |
| 1 | A | 327 | TYR | CD2-CE2 | 7.31 | 1.50 | 1.39 |
| 1 | B | 277 | GLU | C-N | -7.31 | 1.17 | 1.34 |
| 1 | A | 140 | PHE | CE2-CZ | 6.37 | 1.49 | 1.37 |
| 1 | C | 34 | TYR | CD1-CE1 | 6.10 | 1.48 | 1.39 |
| 1 | C | 145 | TRP | CB-CG | -5.95 | 1.39 | 1.50 |
| 1 | A | 32 | ALA | CA-CB | 5.55 | 1.64 | 1.52 |
| 1 | A | 228 | TRP | CB-CG | 5.04 | 1.59 | 1.50 |

All (15) bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 1 | A | 258 | VAL | CB-CA-C | -12.04 | 88.53 | 111.40 |
| 1 | A | 198 | ARG | C-N-CA | 11.74 | 151.04 | 121.70 |
| 1 | A | 43 | ARG | NE-CZ-NH1 | -10.04 | 115.28 | 120.30 |
| 1 | A | 258 | VAL | N-CA-C | -9.64 | 84.97 | 111.00 |
| 1 | A | 259 | LEU | N-CA-C | -8.18 | 88.93 | 111.00 |
| 1 | A | 43 | ARG | NE-CZ-NH2 | 7.34 | 123.97 | 120.30 |
| 1 | A | 198 | ARG | O-C-N | -7.03 | 111.45 | 122.70 |
| 1 | B | 292 | GLU | O-C-N | 6.93 | 133.79 | 122.70 |
| 1 | A | 259 | LEU | N-CA-CB | 6.50 | 123.40 | 110.40 |
| 1 | A | 106 | ASP | CB-CG-OD2 | -5.59 | 113.27 | 118.30 |
| 1 | C | 331 | MET | CB-CG-SD | 5.54 | 129.02 | 112.40 |
| 1 | B | 292 | GLU | CA-C-N | -5.53 | 105.03 | 117.20 |
| 1 | A | 311 | LEU | CB-CG-CD1 | -5.19 | 102.17 | 111.00 |
| 1 | A | 286 | LEU | CA-CB-CG | 5.04 | 126.89 | 115.30 |
| 1 | B | 119 | LEU | CB-CG-CD1 | 5.02 | 119.53 | 111.00 |

There are no chirality outliers.

All (1) planarity outliers are listed below:

| Mol | Chain | Res | Type | Group |
|---|---|---|---|---|
| 1 | C | 302 | TYR | Peptide |

## 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 | 2396 | 0 | 2235 | 51 | 3 |
| 1 | B | 2396 | 0 | 2234 | 56 | 1 |
| 1 | C | 1631 | 0 | 1511 | 228 | 2 |
| 2 | A | 14 | 0 | 11 | 0 | 0 |
| 2 | B | 14 | 0 | 11 | 5 | 0 |
| 3 | B | 2 | 0 | 0 | 0 | 0 |
| 4 | A | 89 | 0 | 0 | 8 | 0 |
| 4 | B | 95 | 0 | 0 | 3 | 0 |
| 4 | C | 32 | 0 | 0 | 20 | 0 |
| All | All | 6669 | 0 | 6002 | 338 | 3 |

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 27.

All (338) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:C:286:LEU:HA | 1:C:287:THR:CG2 | 1.40 | 1.50 |
| 1:C:287:THR:OG1 | 1:C:290:GLU:CB | 1.68 | 1.41 |
| 1:C:133:SER:O | 1:C:138:VAL:CG2 | 1.68 | 1.39 |
| 1:C:132:LEU:HA | 1:C:179:PHE:CZ | 1.60 | 1.35 |
| 1:C:286:LEU:CA | 1:C:287:THR:HG23 | 1.58 | 1.33 |
| 1:C:60:PHE:CB | 1:C:122:GLY:O | 1.76 | 1.32 |
| 1:C:286:LEU:HD22 | 1:C:287:THR:CG2 | 1.63 | 1.29 |
| 1:C:286:LEU:CD2 | 1:C:287:THR:HG21 | 1.64 | 1.27 |
| 1:C:285:TYR:OH | 1:C:288:PRO:HD3 | 1.35 | 1.27 |
| 1:C:238:SER:HB3 | 1:C:284:TYR:OH | 1.14 | 1.25 |
| 1:C:258:VAL:HG12 | 1:C:259:LEU:CD2 | 1.67 | 1.25 |
| 1:A:255:TRP:O | 1:A:258:VAL:O | 1.58 | 1.21 |
| 1:C:286:LEU:HA | 1:C:287:THR:CB | 1.64 | 1.20 |
| 1:C:60:PHE:HB3 | 1:C:122:GLY:O | 1.04 | 1.19 |
| 1:C:285:TYR:CE2 | 1:C:287:THR:HG22 | 1.77 | 1.19 |
| 1:C:132:LEU:CA | 1:C:179:PHE:HZ | 1.50 | 1.17 |
| 1:C:163:ASP:HB2 | 4:C:2010:HOH:O | 1.44 | 1.15 |
| 1:A:277:GLU:OE2 | 4:A:2069:HOH:O | 1.62 | 1.14 |
| 1:C:286:LEU:HD22 | 1:C:287:THR:CB | 1.76 | 1.14 |
| 1:C:238:SER:CB | 1:C:284:TYR:CZ | 2.31 | 1.14 |
| 1:C:238:SER:CB | 1:C:284:TYR:OH | 1.94 | 1.14 |
| 1:C:259:LEU:HD23 | 1:C:259:LEU:N | 1.67 | 1.09 |
| 1:C:240:LYS:CG | 1:C:284:TYR:HB2 | 1.81 | 1.09 |
| 1:C:131:ILE:HD12 | 1:C:131:ILE:H | 1.13 | 1.07 |
| 1:C:133:SER:O | 1:C:138:VAL:HG21 | 1.48 | 1.07 |
| 1:C:296:SER:HA | 4:C:2031:HOH:O | 1.53 | 1.07 |
| 1:C:61:ILE:CD1 | 1:C:119:LEU:HD11 | 1.83 | 1.06 |
| 1:C:286:LEU:HD22 | 1:C:287:THR:HG21 | 1.22 | 1.05 |
| 1:C:61:ILE:HD11 | 1:C:119:LEU:HD11 | 1.34 | 1.05 |
| 1:C:240:LYS:CD | 1:C:284:TYR:HB2 | 1.87 | 1.05 |
| 1:B:196:PRO:HD2 | 1:B:197:GLU:OE1 | 1.57 | 1.04 |
| 1:C:133:SER:O | 1:C:138:VAL:HG22 | 1.52 | 1.04 |
| 1:C:60:PHE:CG | 1:C:122:GLY:O | 2.11 | 1.03 |
| 1:C:258:VAL:HG12 | 1:C:259:LEU:HD21 | 1.36 | 1.03 |
| 1:C:286:LEU:CD2 | 1:C:287:THR:CG2 | 2.30 | 1.02 |
| 1:C:238:SER:HB3 | 1:C:284:TYR:CZ | 1.95 | 1.01 |
| 1:C:140:PHE:CD2 | 1:C:184:MET:HE3 | 1.96 | 1.00 |
| 1:B:243:ILE:HG13 | 1:B:290:GLU:HG2 | 1.43 | 0.99 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:C:240:LYS:HD3 | 1:C:284:TYR:HB2 | 1.43 | 0.99 |
| 1:C:132:LEU:HA | 1:C:179:PHE:HZ | 0.91 | 0.99 |
| 1:C:173:ILE:HG22 | 1:C:214:GLN:HG3 | 1.39 | 0.99 |
| 1:C:286:LEU:N | 1:C:287:THR:HG23 | 1.79 | 0.98 |
| 1:C:145:TRP:HH2 | 1:C:200:PHE:CE2 | 1.81 | 0.97 |
| 1:C:240:LYS:HG2 | 1:C:284:TYR:HB2 | 1.43 | 0.97 |
| 1:C:286:LEU:HA | 1:C:287:THR:HG23 | 0.98 | 0.97 |
| 1:C:35:TRP:O | 1:C:58:ILE:HA | 1.65 | 0.97 |
| 1:C:286:LEU:HD22 | 1:C:287:THR:OG1 | 1.64 | 0.95 |
| 1:C:132:LEU:CA | 1:C:179:PHE:CZ | 2.35 | 0.95 |
| 1:C:299:MET:HB3 | 4:C:2031:HOH:O | 1.66 | 0.95 |
| 1:C:258:VAL:CG1 | 1:C:259:LEU:CD2 | 2.45 | 0.94 |
| 1:C:238:SER:HB2 | 1:C:284:TYR:CZ | 2.02 | 0.92 |
| 1:C:286:LEU:HD23 | 1:C:287:THR:HG21 | 1.48 | 0.92 |
| 1:C:179:PHE:C | 1:C:179:PHE:CD1 | 2.41 | 0.92 |
| 1:A:80:GLN:HE22 | 1:A:102:GLN:NE2 | 1.66 | 0.91 |
| 1:C:287:THR:OG1 | 1:C:290:GLU:HB2 | 0.74 | 0.91 |
| 1:C:285:TYR:CG | 1:C:286:LEU:N | 2.35 | 0.91 |
| 1:C:255:TRP:O | 1:C:259:LEU:CD2 | 2.18 | 0.91 |
| 1:C:258:VAL:HG12 | 1:C:259:LEU:HD23 | 1.53 | 0.90 |
| 1:A:333:ASP:HB3 | 4:A:2089:HOH:O | 1.71 | 0.90 |
| 1:C:285:TYR:CE2 | 1:C:287:THR:CG2 | 2.53 | 0.90 |
| 1:C:60:PHE:O | 1:C:62:ASN:N | 2.04 | 0.89 |
| 1:C:277:GLU:HB2 | 4:C:2027:HOH:O | 1.72 | 0.89 |
| 1:C:140:PHE:CD2 | 1:C:184:MET:CE | 2.56 | 0.88 |
| 1:C:161:PHE:HB2 | 1:C:164:VAL:HB | 1.53 | 0.88 |
| 1:C:145:TRP:CH2 | 1:C:200:PHE:CE2 | 2.61 | 0.88 |
| 1:B:229:ILE:HD11 | 1:B:269:LEU:HD21 | 1.54 | 0.87 |
| 1:C:318:GLU:O | 1:C:321:GLN:NE2 | 2.08 | 0.87 |
| 1:C:258:VAL:C | 1:C:259:LEU:HD23 | 1.96 | 0.86 |
| 1:C:285:TYR:CZ | 1:C:287:THR:HA | 2.10 | 0.85 |
| 1:C:275:ALA:HB3 | 1:C:312:TRP:O | 1.76 | 0.84 |
| 1:C:284:TYR:O | 1:C:284:TYR:HD1 | 1.61 | 0.83 |
| 1:B:78:GLY:HA2 | 4:B:2001:HOH:O | 1.78 | 0.83 |
| 1:C:131:ILE:CD1 | 1:C:131:ILE:H | 1.90 | 0.83 |
| 1:C:251:ASN:N | 4:C:2025:HOH:O | 2.09 | 0.83 |
| 1:C:240:LYS:HG2 | 1:C:284:TYR:CB | 2.08 | 0.83 |
| 1:C:286:LEU:CA | 1:C:287:THR:CG2 | 2.30 | 0.82 |
| 1:A:95:LYS:HE3 | 4:A:2011:HOH:O | 1.79 | 0.82 |
| 1:C:143:PHE:HD2 | 4:C:2009:HOH:O | 1.60 | 0.81 |
| 1:C:50:GLU:O | 1:C:115:LYS:NZ | 2.12 | 0.81 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:C:179:PHE:HD1 | 1:C:179:PHE:C | 1.84 | 0.81 |
| 1:C:286:LEU:HA | 1:C:287:THR:OG1 | 1.79 | 0.81 |
| 1:A:87:VAL:HG13 | 1:A:92:VAL:C | 2.01 | 0.81 |
| 1:B:268:LYS:HE2 | 4:B:2083:HOH:O | 1.81 | 0.81 |
| 1:C:286:LEU:CA | 1:C:287:THR:CB | 2.50 | 0.81 |
| 1:C:285:TYR:CD2 | 1:C:287:THR:CG2 | 2.65 | 0.80 |
| 1:C:140:PHE:CG | 1:C:184:MET:HE3 | 2.17 | 0.80 |
| 1:C:286:LEU:CA | 1:C:287:THR:OG1 | 2.30 | 0.80 |
| 1:C:60:PHE:C | 1:C:62:ASN:H | 1.81 | 0.80 |
| 1:C:259:LEU:CD2 | 1:C:259:LEU:N | 2.41 | 0.79 |
| 1:C:238:SER:CB | 1:C:284:TYR:CE2 | 2.65 | 0.79 |
| 1:A:87:VAL:HG13 | 1:A:92:VAL:O | 1.83 | 0.79 |
| 1:A:87:VAL:HG22 | 1:A:93:VAL:HA | 1.63 | 0.78 |
| 1:C:286:LEU:CD2 | 1:C:287:THR:OG1 | 2.30 | 0.78 |
| 1:C:61:ILE:O | 1:C:61:ILE:CG2 | 2.31 | 0.78 |
| 1:C:61:ILE:O | 1:C:61:ILE:HG22 | 1.83 | 0.78 |
| 1:C:140:PHE:CB | 1:C:184:MET:HE3 | 2.13 | 0.78 |
| 1:C:238:SER:HB3 | 1:C:284:TYR:HH | 0.98 | 0.78 |
| 1:C:251:ASN:HA | 4:C:2025:HOH:O | 1.84 | 0.78 |
| 1:B:117:VAL:O | 1:B:118:LEU:HD23 | 1.83 | 0.78 |
| 1:C:285:TYR:HE2 | 1:C:287:THR:HG22 | 1.46 | 0.77 |
| 1:C:144:LEU:HD23 | 4:C:2009:HOH:O | 1.83 | 0.77 |
| 1:C:273:LEU:O | 1:C:311:LEU:HA | 1.84 | 0.77 |
| 1:C:285:TYR:CD2 | 1:C:287:THR:HG22 | 2.19 | 0.77 |
| 1:C:287:THR:CB | 1:C:290:GLU:HB2 | 2.12 | 0.75 |
| 1:C:34:TYR:O | 1:C:313:GLU:HB2 | 1.86 | 0.75 |
| 1:C:140:PHE:O | 1:C:141:ALA:C | 2.22 | 0.75 |
| 1:C:165:VAL:O | 1:C:198:ARG:NH2 | 2.20 | 0.75 |
| 1:C:285:TYR:CZ | 1:C:288:PRO:HD3 | 2.21 | 0.74 |
| 1:C:238:SER:OG | 1:C:284:TYR:CE2 | 2.40 | 0.74 |
| 1:A:181:TYR:O | 1:A:185:VAL:HG23 | 1.87 | 0.74 |
| 1:C:284:TYR:O | 1:C:284:TYR:CD1 | 2.40 | 0.73 |
| 1:A:80:GLN:HE22 | 1:A:102:GLN:HE21 | 1.33 | 0.73 |
| 1:C:286:LEU:CG | 1:C:287:THR:OG1 | 2.36 | 0.73 |
| 1:C:327:TYR:O | 1:C:331:MET:HG2 | 1.89 | 0.73 |
| 1:C:141:ALA:HA | 1:C:188:PHE:CZ | 2.23 | 0.73 |
| 1:C:161:PHE:O | 1:C:164:VAL:HG23 | 1.90 | 0.72 |
| 2:B:1340:KLS:NAA | 2:B:1340:KLS:HAI | 2.04 | 0.71 |
| 1:C:286:LEU:H | 1:C:287:THR:HG23 | 1.56 | 0.71 |
| 1:C:132:LEU:HA | 1:C:179:PHE:CE2 | 2.23 | 0.71 |
| 1:A:85:VAL:HA | 1:A:96:LEU:O | 1.91 | 0.70 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:B:229:ILE:CD1 | 1:B:269:LEU:HD21 | 2.21 | 0.70 |
| 1:C:140:PHE:O | 1:C:143:PHE:N | 2.24 | 0.70 |
| 1:C:255:TRP:O | 1:C:259:LEU:HG | 1.91 | 0.70 |
| 1:C:131:ILE:N | 1:C:131:ILE:HD12 | 1.99 | 0.70 |
| 1:C:240:LYS:HD3 | 1:C:284:TYR:CB | 2.22 | 0.70 |
| 1:C:242:PHE:HE1 | 1:C:294:LEU:HA | 1.58 | 0.69 |
| 1:B:80:GLN:HE22 | 1:B:102:GLN:HB2 | 1.58 | 0.69 |
| 1:C:286:LEU:CD1 | 1:C:287:THR:OG1 | 2.30 | 0.69 |
| 1:C:62:ASN:C | 1:C:62:ASN:OD1 | 2.30 | 0.69 |
| 1:C:161:PHE:CB | 1:C:164:VAL:HB | 2.23 | 0.69 |
| 1:C:232:TYR:HA | 1:C:284:TYR:OH | 1.94 | 0.68 |
| 1:C:103:ILE:C | 1:C:105:GLU:H | 1.96 | 0.68 |
| 1:C:285:TYR:CD2 | 1:C:287:THR:HG23 | 2.29 | 0.67 |
| 1:A:149:GLY:O | 1:A:165:VAL:HG22 | 1.94 | 0.66 |
| 1:C:219:ILE:HB | 4:C:2019:HOH:O | 1.95 | 0.66 |
| 1:C:60:PHE:CD1 | 1:C:122:GLY:C | 2.68 | 0.66 |
| 1:C:140:PHE:CG | 1:C:184:MET:CE | 2.79 | 0.65 |
| 1:C:216:SER:O | 4:C:2019:HOH:O | 2.15 | 0.65 |
| 1:C:255:TRP:O | 1:C:259:LEU:CG | 2.44 | 0.65 |
| 1:B:194:GLN:O | 1:B:196:PRO:HD3 | 1.98 | 0.64 |
| 1:C:60:PHE:C | 1:C:62:ASN:N | 2.49 | 0.64 |
| 1:C:104:MET:HA | 1:C:164:VAL:HG21 | 1.78 | 0.64 |
| 1:C:179:PHE:HD1 | 1:C:179:PHE:O | 1.80 | 0.64 |
| 1:C:258:VAL:CG1 | 1:C:259:LEU:HD23 | 2.22 | 0.63 |
| 1:B:186:ASN:O | 1:B:190:GLN:HG3 | 1.97 | 0.63 |
| 1:B:254:ALA:O | 1:B:258:VAL:HG23 | 1.99 | 0.63 |
| 1:C:259:LEU:O | 1:C:265:LYS:HA | 1.98 | 0.63 |
| 1:C:138:VAL:O | 1:C:140:PHE:N | 2.28 | 0.62 |
| 1:C:251:ASN:CA | 4:C:2025:HOH:O | 2.38 | 0.62 |
| 1:A:196:PRO:HD2 | 1:A:197:GLU:OE1 | 1.99 | 0.62 |
| 1:A:150:PRO:HA | 1:A:165:VAL:HG21 | 1.80 | 0.62 |
| 1:C:255:TRP:O | 1:C:259:LEU:HD23 | 1.98 | 0.61 |
| 1:C:232:TYR:HE1 | 1:C:272:GLY:O | 1.84 | 0.61 |
| 1:C:275:ALA:HB3 | 1:C:312:TRP:C | 2.20 | 0.61 |
| 1:B:177:GLY:H | 1:B:214:GLN:HE21 | 1.49 | 0.61 |
| 1:C:229:ILE:HD11 | 1:C:269:LEU:HD11 | 1.82 | 0.61 |
| 1:C:298:TYR:C | 4:C:2032:HOH:O | 2.39 | 0.60 |
| 1:C:33:ILE:HD12 | 1:C:311:LEU:HD12 | 1.82 | 0.60 |
| 1:B:117:VAL:O | 1:B:167:ASP:HB2 | 2.02 | 0.60 |
| 1:C:61:ILE:CG1 | 1:C:119:LEU:HD11 | 2.32 | 0.60 |
| 1:C:149:GLY:C | 1:C:165:VAL:HG23 | 2.23 | 0.59 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:C:255:TRP:O | 1:C:259:LEU:HD21 | 2.01 | 0.59 |
| 1:A:155:TRP:CZ2 | 1:A:157:GLY:HA3 | 2.38 | 0.59 |
| 1:C:131:ILE:HG12 | 1:C:184:MET:SD | 2.43 | 0.59 |
| 1:C:285:TYR:CE2 | 1:C:287:THR:HA | 2.38 | 0.59 |
| 1:C:60:PHE:CD1 | 1:C:122:GLY:O | 2.56 | 0.59 |
| 1:C:326:PRO:O | 1:C:329:ASP:HB2 | 2.03 | 0.58 |
| 1:C:61:ILE:HD11 | 1:C:119:LEU:CD1 | 2.23 | 0.58 |
| 1:A:333:ASP:O | 1:A:337:HIS:HB2 | 2.04 | 0.58 |
| 1:C:238:SER:CB | 1:C:284:TYR:HH | 1.91 | 0.58 |
| 1:A:125:TYR:HB2 | 4:A:2028:HOH:O | 2.03 | 0.57 |
| 1:A:131:ILE:HG21 | 1:A:137:ALA:HB2 | 1.86 | 0.57 |
| 1:C:145:TRP:O | 1:C:149:GLY:HA3 | 2.03 | 0.57 |
| 1:B:295:VAL:HG21 | 1:B:309:ILE:HD11 | 1.86 | 0.57 |
| 1:C:240:LYS:HB2 | 1:C:284:TYR:CD1 | 2.40 | 0.57 |
| 1:A:65:PRO:HB3 | 1:A:71:HIS:O | 2.05 | 0.57 |
| 1:B:80:GLN:O | 1:B:81:CYS:HB2 | 2.05 | 0.57 |
| 1:C:140:PHE:CD2 | 1:C:184:MET:HE1 | 2.38 | 0.57 |
| 1:A:287:THR:O | 1:A:291:VAL:HG23 | 2.05 | 0.56 |
| 1:B:292:GLU:CD | 1:B:292:GLU:C | 2.63 | 0.56 |
| 1:C:103:ILE:C | 1:C:105:GLU:N | 2.59 | 0.56 |
| 1:C:143:PHE:CD2 | 4:C:2009:HOH:O | 2.44 | 0.56 |
| 1:B:170:ASP:OD1 | 1:B:203:SER:OG | 2.18 | 0.55 |
| 1:C:220:PHE:HA | 1:C:262:SER:HB2 | 1.88 | 0.55 |
| 1:C:286:LEU:CB | 1:C:287:THR:OG1 | 2.55 | 0.55 |
| 1:A:38:GLY:HA3 | 4:A:2079:HOH:O | 2.07 | 0.55 |
| 1:C:103:ILE:O | 1:C:105:GLU:N | 2.40 | 0.55 |
| 1:C:242:PHE:CE1 | 1:C:294:LEU:HA | 2.41 | 0.55 |
| 1:C:144:LEU:HA | 4:C:2009:HOH:O | 2.07 | 0.54 |
| 1:C:310:MET:SD | 1:C:311:LEU:N | 2.80 | 0.54 |
| 1:B:294:LEU:HD23 | 1:B:294:LEU:C | 2.27 | 0.54 |
| 1:C:232:TYR:CE1 | 1:C:272:GLY:O | 2.61 | 0.54 |
| 1:C:328:ALA:HA | 1:C:331:MET:HG3 | 1.88 | 0.54 |
| 1:B:87:VAL:HA | 1:B:92:VAL:O | 2.07 | 0.54 |
| 1:C:187:THR:O | 1:C:188:PHE:C | 2.45 | 0.54 |
| 1:C:287:THR:OG1 | 1:C:290:GLU:CA | 2.51 | 0.54 |
| 1:C:240:LYS:CB | 1:C:284:TYR:CG | 2.91 | 0.54 |
| 1:C:60:PHE:HE1 | 1:C:120:SER:HG | 1.55 | 0.54 |
| 1:C:203:SER:HA | 1:C:226:PHE:O | 2.08 | 0.54 |
| 1:A:220:PHE:HA | 1:A:262:SER:HB2 | 1.90 | 0.53 |
| 1:A:333:ASP:CB | 4:A:2089:HOH:O | 2.43 | 0.53 |
| 1:C:104:MET:O | 1:C:104:MET:HG2 | 2.08 | 0.53 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:C:168:GLY:HA3 | 1:C:201:TYR:O | 2.08 | 0.53 |
| 1:C:173:ILE:CG2 | 1:C:214:GLN:HG3 | 2.27 | 0.53 |
| 1:C:42:LEU:HD13 | 1:C:46:HIS:CD2 | 2.44 | 0.53 |
| 1:B:242:PHE:HD2 | 1:B:243:ILE:HD13 | 1.72 | 0.53 |
| 1:A:204:ALA:HB1 | 1:A:215:LEU:HD13 | 1.90 | 0.53 |
| 1:A:330:HIS:O | 1:A:334:ILE:HG13 | 2.08 | 0.53 |
| 1:B:72:TRP:CH2 | 1:B:158:PRO:HD3 | 2.44 | 0.52 |
| 1:B:66:ASP:OD2 | 1:B:136:SER:OG | 2.27 | 0.52 |
| 1:C:240:LYS:CG | 1:C:284:TYR:CB | 2.67 | 0.52 |
| 1:C:210:ILE:HD11 | 1:C:255:TRP:CD1 | 2.45 | 0.52 |
| 1:C:133:SER:O | 1:C:138:VAL:HG23 | 1.92 | 0.52 |
| 1:C:120:SER:O | 1:C:122:GLY:HA2 | 2.10 | 0.52 |
| 1:C:141:ALA:HB2 | 1:C:184:MET:O | 2.09 | 0.52 |
| 1:C:161:PHE:O | 1:C:164:VAL:CG2 | 2.57 | 0.52 |
| 1:C:235:ALA:O | 1:C:236:ALA:C | 2.47 | 0.51 |
| 1:B:80:GLN:O | 1:B:81:CYS:CB | 2.58 | 0.51 |
| 1:B:127:PRO:HA | 1:B:175:HIS:CD2 | 2.46 | 0.51 |
| 1:B:196:PRO:CD | 1:B:197:GLU:OE1 | 2.46 | 0.51 |
| 1:C:140:PHE:CB | 1:C:184:MET:CE | 2.86 | 0.51 |
| 1:C:240:LYS:HD3 | 1:C:284:TYR:C | 2.31 | 0.51 |
| 1:C:237:CYS:O | 1:C:238:SER:C | 2.47 | 0.51 |
| 1:C:140:PHE:O | 1:C:141:ALA:O | 2.28 | 0.51 |
| 1:C:240:LYS:HB2 | 1:C:284:TYR:CG | 2.45 | 0.51 |
| 1:A:145:TRP:CE2 | 1:A:191:TYR:HB3 | 2.46 | 0.50 |
| 1:C:229:ILE:CD1 | 1:C:269:LEU:HD11 | 2.41 | 0.50 |
| 1:C:286:LEU:HD23 | 1:C:287:THR:CG2 | 2.22 | 0.50 |
| 1:C:169:PHE:CE2 | 1:C:188:PHE:CE1 | 2.99 | 0.50 |
| 1:C:143:PHE:HB3 | 4:C:2009:HOH:O | 2.12 | 0.50 |
| 1:C:284:TYR:O | 1:C:285:TYR:O | 2.30 | 0.50 |
| 1:C:60:PHE:HD1 | 1:C:122:GLY:HA2 | 1.77 | 0.49 |
| 1:B:268:LYS:HE3 | 1:B:304:ASP:O | 2.12 | 0.49 |
| 1:A:65:PRO:O | 1:A:71:HIS:HA | 2.11 | 0.49 |
| 1:A:80:GLN:NE2 | 1:A:102:GLN:NE2 | 2.48 | 0.49 |
| 1:C:287:THR:O | 1:C:291:VAL:N | 2.45 | 0.49 |
| 1:A:240:LYS:HG3 | 1:A:240:LYS:O | 2.12 | 0.49 |
| 1:B:191:TYR:O | 1:B:192:PHE:C | 2.51 | 0.48 |
| 1:C:295:VAL:O | 1:C:299:MET:HB3 | 2.13 | 0.48 |
| 1:C:123:GLY:HA2 | 4:C:2007:HOH:O | 2.13 | 0.48 |
| 1:C:165:VAL:O | 1:C:165:VAL:HG13 | 2.13 | 0.48 |
| 1:C:232:TYR:HA | 1:C:284:TYR:CE1 | 2.48 | 0.48 |
| 1:A:282:GLN:HG3 | 1:A:282:GLN:O | 2.13 | 0.48 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:C:165:VAL:O | 1:C:165:VAL:HG22 | 2.13 | 0.48 |
| 1:B:124:ALA:HB1 | 2:B:1340:KLS:HAE | 1.96 | 0.48 |
| 1:B:311:LEU:HD11 | 1:B:331:MET:HG3 | 1.96 | 0.48 |
| 1:C:144:LEU:CA | 4:C:2009:HOH:O | 2.62 | 0.48 |
| 1:A:330:HIS:HE1 | 4:A:2082:HOH:O | 1.96 | 0.48 |
| 1:B:73:PRO:HG2 | 1:B:143:PHE:CD1 | 2.49 | 0.47 |
| 1:B:58:ILE:HD11 | 1:B:117:VAL:HG11 | 1.94 | 0.47 |
| 1:C:179:PHE:CD1 | 1:C:180:GLY:N | 2.81 | 0.47 |
| 1:C:62:ASN:O | 1:C:62:ASN:OD1 | 2.31 | 0.47 |
| 1:C:60:PHE:CG | 1:C:122:GLY:C | 2.83 | 0.47 |
| 1:B:124:ALA:HB1 | 2:B:1340:KLS:CAE | 2.45 | 0.47 |
| 1:B:80:GLN:OE1 | 1:B:102:GLN:OE1 | 2.33 | 0.47 |
| 1:C:189:ARG:NH2 | 1:C:223:ALA:O | 2.40 | 0.47 |
| 1:C:107:ILE:HG23 | 1:C:117:VAL:HG21 | 1.96 | 0.46 |
| 1:C:131:ILE:HG22 | 1:C:138:VAL:HG23 | 1.97 | 0.46 |
| 1:C:140:PHE:HD2 | 1:C:184:MET:HE3 | 1.66 | 0.46 |
| 1:C:233:ASN:HB2 | 4:C:2022:HOH:O | 2.14 | 0.46 |
| 1:C:43:ARG:NH2 | 1:C:106:ASP:OD1 | 2.49 | 0.46 |
| 1:A:155:TRP:CE2 | 1:A:157:GLY:HA3 | 2.51 | 0.46 |
| 1:A:108:PRO:HG3 | 1:A:164:VAL:HG22 | 1.98 | 0.46 |
| 1:C:295:VAL:O | 1:C:299:MET:CB | 2.64 | 0.46 |
| 1:A:75:SER:HB2 | 1:A:77:PHE:CE2 | 2.51 | 0.46 |
| 1:C:181:TYR:O | 1:C:185:VAL:HG23 | 2.16 | 0.46 |
| 1:C:212:ASP:OD2 | 1:C:215:LEU:N | 2.47 | 0.46 |
| 1:A:332:LYS:HD2 | 1:A:332:LYS:HA | 1.84 | 0.46 |
| 1:B:220:PHE:HA | 1:B:262:SER:HB2 | 1.97 | 0.45 |
| 1:A:33:ILE:HD12 | 1:A:311:LEU:HD12 | 1.96 | 0.45 |
| 1:A:87:VAL:CG1 | 1:A:91:GLY:C | 2.84 | 0.45 |
| 1:B:64:PHE:HB3 | 4:B:2037:HOH:O | 2.17 | 0.45 |
| 1:C:132:LEU:C | 1:C:179:PHE:CE2 | 2.90 | 0.45 |
| 1:C:285:TYR:O | 1:C:286:LEU:HB2 | 2.17 | 0.45 |
| 1:B:204:ALA:HB3 | 1:B:227:ILE:HG12 | 1.99 | 0.45 |
| 1:A:87:VAL:HA | 1:A:92:VAL:O | 2.16 | 0.45 |
| 1:C:173:ILE:HG21 | 1:C:181:TYR:CE2 | 2.51 | 0.45 |
| 1:C:104:MET:O | 1:C:104:MET:CG | 2.64 | 0.45 |
| 2:B:1340:KLS:OAJ | 2:B:1340:KLS:NAA | 2.50 | 0.45 |
| 1:C:141:ALA:HA | 1:C:188:PHE:CE1 | 2.51 | 0.44 |
| 1:C:204:ALA:HB1 | 1:C:215:LEU:HD13 | 1.98 | 0.44 |
| 1:B:191:TYR:O | 1:B:193:ASN:N | 2.51 | 0.44 |
| 1:B:292:GLU:O | 1:B:296:SER:HB3 | 2.17 | 0.44 |
| 1:A:322:ILE:O | 1:A:330:HIS:NE2 | 2.48 | 0.44 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:C:258:VAL:C | 1:C:259:LEU:CD2 | 2.77 | 0.44 |
| 1:C:145:TRP:CH2 | 1:C:200:PHE:CD2 | 3.05 | 0.44 |
| 1:B:140:PHE:CE1 | 1:B:144:LEU:HD11 | 2.52 | 0.44 |
| 1:C:322:ILE:O | 1:C:330:HIS:NE2 | 2.51 | 0.44 |
| 1:B:209:ILE:HG13 | 1:B:237:CYS:SG | 2.57 | 0.43 |
| 1:C:31:LEU:HD22 | 1:C:332:LYS:HB2 | 2.00 | 0.43 |
| 1:B:209:ILE:CD1 | 1:B:234:THR:HG21 | 2.47 | 0.43 |
| 1:B:228:TRP:HA | 1:B:270:TYR:HB2 | 1.99 | 0.43 |
| 1:B:29:SER:OG | 1:B:335:LEU:HD22 | 2.18 | 0.43 |
| 1:A:205:ALA:HB2 | 1:A:228:TRP:HD1 | 1.83 | 0.43 |
| 1:C:45:SER:HB3 | 1:C:106:ASP:CG | 2.38 | 0.43 |
| 1:C:311:LEU:HD11 | 1:C:331:MET:HG3 | 2.00 | 0.43 |
| 1:B:173:ILE:HG21 | 1:B:181:TYR:CE2 | 2.54 | 0.43 |
| 1:B:291:VAL:HG11 | 1:B:331:MET:SD | 2.59 | 0.43 |
| 1:C:161:PHE:HB3 | 1:C:164:VAL:HG21 | 2.01 | 0.43 |
| 1:C:313:GLU:C | 4:C:2001:HOH:O | 2.57 | 0.43 |
| 1:C:61:ILE:HG12 | 1:C:119:LEU:HD11 | 2.01 | 0.43 |
| 1:A:59:GLY:HA2 | 1:A:60:PHE:HA | 1.83 | 0.43 |
| 1:B:206:PRO:O | 1:B:230:GLN:HG3 | 2.19 | 0.43 |
| 1:A:206:PRO:O | 1:A:230:GLN:HG3 | 2.19 | 0.42 |
| 1:A:198:ARG:HG2 | 1:A:200:PHE:CE2 | 2.54 | 0.42 |
| 1:C:30:ASN:HB2 | 1:C:270:TYR:OH | 2.19 | 0.42 |
| 1:A:277:GLU:HG2 | 1:A:285:TYR:CD2 | 2.54 | 0.42 |
| 1:B:203:SER:HA | 1:B:226:PHE:O | 2.20 | 0.42 |
| 1:B:32:ALA:HA | 1:B:55:ILE:HB | 2.02 | 0.42 |
| 1:C:140:PHE:HB3 | 1:C:184:MET:CE | 2.49 | 0.42 |
| 1:C:107:ILE:HG23 | 1:C:117:VAL:HG11 | 2.02 | 0.42 |
| 1:C:254:ALA:O | 1:C:258:VAL:HB | 2.20 | 0.42 |
| 1:B:107:ILE:HG23 | 1:B:117:VAL:HG21 | 2.01 | 0.42 |
| 1:A:173:ILE:HG21 | 1:A:181:TYR:CE2 | 2.55 | 0.42 |
| 1:B:229:ILE:CD1 | 1:B:269:LEU:CD2 | 2.95 | 0.42 |
| 1:A:259:LEU:O | 1:A:265:LYS:HA | 2.20 | 0.41 |
| 1:B:58:ILE:HG21 | 1:B:58:ILE:HD13 | 1.91 | 0.41 |
| 1:A:254:ALA:O | 1:A:258:VAL:HG23 | 2.19 | 0.41 |
| 1:C:147:ALA:C | 1:C:149:GLY:H | 2.24 | 0.41 |
| 1:C:240:LYS:HD3 | 1:C:284:TYR:CA | 2.51 | 0.41 |
| 1:B:231:TYR:HD2 | 1:B:271:VAL:HG13 | 1.84 | 0.41 |
| 1:A:258:VAL:O | 1:A:259:LEU:HB2 | 2.21 | 0.41 |
| 1:A:269:LEU:HD12 | 1:A:269:LEU:HA | 1.95 | 0.41 |
| 1:A:330:HIS:ND1 | 4:A:2086:HOH:O | 2.36 | 0.41 |
| 1:B:57:ASN:HA | 1:B:118:LEU:O | 2.20 | 0.41 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:C:132:LEU:CA | 1:C:179:PHE:CE2 | 2.94 | 0.41 |
| 1:C:140:PHE:HB2 | 1:C:184:MET:HE3 | 1.94 | 0.41 |
| 2:B:1340:KLS:NAA | 2:B:1340:KLS:CAI | 2.71 | 0.41 |
| 1:B:252:PHE:CZ | 1:B:269:LEU:HD13 | 2.55 | 0.41 |
| 1:C:232:TYR:HA | 1:C:284:TYR:CZ | 2.55 | 0.41 |
| 1:B:242:PHE:CD2 | 1:B:243:ILE:HD13 | 2.55 | 0.41 |
| 1:C:138:VAL:HB | 1:C:139:ALA:H | 1.47 | 0.41 |
| 1:A:259:LEU:HD22 | 1:A:259:LEU:HA | 1.97 | 0.40 |
| 1:C:138:VAL:HG12 | 1:C:139:ALA:N | 2.36 | 0.40 |
| 1:C:141:ALA:HA | 1:C:188:PHE:CE2 | 2.56 | 0.40 |
| 1:C:60:PHE:HE2 | 1:C:312:TRP:CH2 | 2.39 | 0.40 |
| 1:B:209:ILE:HD12 | 1:B:234:THR:HG21 | 2.02 | 0.40 |
| 1:C:296:SER:CA | 4:C:2031:HOH:O | 2.35 | 0.40 |

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:A:323:ASP:OD2 | 1:B:90:ASP:O[2_554] | 1.74 | 0.46 |
| 1:A:153:GLU:OE1 | 1:C:278:THR:CG2[3_555] | 2.10 | 0.10 |
| 1:A:156:GLU:OE2 | 1:C:320:ASN:OD1[3_555] | 2.16 | 0.04 |

## 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 | 307/309 (99%) | 281 (92%) | 24 (8%) | 2 (1%) | 22 | 23 |
| 1 | B | 307/309 (99%) | 291 (95%) | 14 (5%) | 2 (1%) | 22 | 23 |
| 1 | C | 169/309 (55%) | 134 (79%) | 23 (14%) | 12 (7%) | 1 | 0 |
| All | All | 783/927 (84%) | 706 (90%) | 61 (8%) | 16 (2%) | 7 | 5 |

All (16) Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | A | 259 | LEU |
| 1 | C | 61 | ILE |
| 1 | C | 139 | ALA |
| 1 | C | 147 | ALA |
| 1 | C | 166 | VAL |
| 1 | C | 236 | ALA |
| 1 | C | 285 | TYR |
| 1 | C | 303 | PRO |
| 1 | A | 81 | CYS |
| 1 | C | 145 | TRP |
| 1 | C | 188 | PHE |
| 1 | C | 287 | THR |
| 1 | B | 192 | PHE |
| 1 | C | 122 | GLY |
| 1 | C | 304 | ASP |
| 1 | B | 81 | CYS |

### 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 | 252/252 (100%) | 243 (96%) | 9 (4%) | 35 43 |
| 1 | B | 252/252 (100%) | 238 (94%) | 14 (6%) | 21 23 |
| 1 | C | 168/252 (67%) | 139 (83%) | 29 (17%) | 2 1 |
| All | All | 672/756 (89%) | 620 (92%) | 52 (8%) | 13 12 |

All (52) residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | A | 67 | MET |
| 1 | A | 140 | PHE |
| 1 | A | 194 | GLN |
| 1 | A | 228 | TRP |
| 1 | A | 232 | TYR |

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| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | A | 237 | CYS |
| 1 | A | 240 | LYS |
| 1 | A | 323 | ASP |
| 1 | A | 337 | HIS |
| 1 | B | 67 | MET |
| 1 | B | 87 | VAL |
| 1 | B | 89 | ASN |
| 1 | B | 136 | SER |
| 1 | B | 153 | GLU |
| 1 | B | 165 | VAL |
| 1 | B | 228 | TRP |
| 1 | B | 259 | LEU |
| 1 | B | 269 | LEU |
| 1 | B | 293 | SER |
| 1 | B | 296 | SER |
| 1 | B | 313 | GLU |
| 1 | B | 323 | ASP |
| 1 | B | 332 | LYS |
| 1 | C | 50 | GLU |
| 1 | C | 61 | ILE |
| 1 | C | 62 | ASN |
| 1 | C | 102 | GLN |
| 1 | C | 119 | LEU |
| 1 | C | 128 | ASP |
| 1 | C | 131 | ILE |
| 1 | C | 132 | LEU |
| 1 | C | 140 | PHE |
| 1 | C | 179 | PHE |
| 1 | C | 188 | PHE |
| 1 | C | 214 | GLN |
| 1 | C | 228 | TRP |
| 1 | C | 238 | SER |
| 1 | C | 242 | PHE |
| 1 | C | 258 | VAL |
| 1 | C | 259 | LEU |
| 1 | C | 260 | LYS |
| 1 | C | 265 | LYS |
| 1 | C | 273 | LEU |
| 1 | C | 278 | THR |
| 1 | C | 284 | TYR |
| 1 | C | 286 | LEU |
| 1 | C | 287 | THR |

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| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | C | 302 | TYR |
| 1 | C | 313 | GLU |
| 1 | C | 319 | ASN |
| 1 | C | 327 | TYR |
| 1 | C | 331 | MET |

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | A | 102 | GLN |
| 1 | B | 71 | HIS |
| 1 | B | 80 | GLN |
| 1 | B | 214 | GLN |
| 1 | C | 46 | 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)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 for Mogul analysis.

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 | KLS | B | 1340 | - | 13,14,14 | 1.14 | 1 (7%) | 15,17,17 | 0.83 | 0 |
| 2 | KLS | A | 1338 | - | 13,14,14 | 1.24 | 2 (15%) | 15,17,17 | 1.30 | 1 (6%) |

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 | KLS | B | 1340 | - | - | 1/10/10/10 | 0/1/1/1 |
| 2 | KLS | A | 1338 | - | - | 1/10/10/10 | 0/1/1/1 |

All (3) bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|---|---|---|---|---|---|---|---|
| 2 | B | 1340 | KLS | CAD-NAC | -2.79 | 1.36 | 1.41 |
| 2 | A | 1338 | KLS | CAD-NAC | -2.69 | 1.36 | 1.41 |
| 2 | A | 1338 | KLS | CAB-NAC | -2.38 | 1.34 | 1.37 |

All (1) bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 2 | A | 1338 | KLS | CAB-NAN-CAK | 4.22 | 132.64 | 125.42 |

There are no chirality outliers.

All (2) torsion outliers are listed below:

| Mol | Chain | Res | Type | Atoms |
|---|---|---|---|---|
| 2 | B | 1340 | KLS | NAA-CAB-NAN-CAK |
| 2 | A | 1338 | KLS | NAA-CAB-NAN-CAK |

There are no ring outliers.

1 monomer is involved in 5 short contacts:

| Mol | Chain | Res | Type | Clashes | Symm-Clashes |
|---|---|---|---|---|---|
| 2 | B | 1340 | KLS | 5 | 0 |

## 5.7 Other polymers (i)

There are no such residues in this entry.

## 5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

| Mol | Chain | Number of breaks |
|---|---|---|
| 1 | B | 2 |
| 1 | A | 1 |

All chain breaks are listed below:

| Model | Chain | Residue-1 | Atom-1 | Residue-2 | Atom-2 | Distance (Å) |
|---|---|---|---|---|---|---|
| 1 | B | 277:GLU | C | 278:THR | N | 1.17 |
| 1 | B | 291:VAL | C | 292:GLU | N | 1.09 |
| 1 | A | 198:ARG | C | 199:LYS | N | 0.92 |

# 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 | 309/309 (100%) | 0.24 | 8 (2%) 56 65 | 2, 13, 27, 39 | 0 |
| 1 | B | 309/309 (100%) | 0.08 | 6 (1%) 66 76 | 2, 10, 23, 31 | 0 |
| 1 | C | 210/309 (67%) | 2.49 | 84 (40%) 0 0 | 7, 21, 63, 67 | 4 (1%) |
| All | All | 828/927 (89%) | 0.75 | 98 (11%) 4 7 | 2, 13, 38, 67 | 4 (0%) |

All (98) RSRZ outliers are listed below:

| Mol | Chain | Res | Type | RSRZ |
|---|---|---|---|---|
| 1 | C | 291 | VAL | 15.0 |
| 1 | C | 300 | ASP | 11.9 |
| 1 | C | 288 | PRO | 9.8 |
| 1 | C | 141 | ALA | 9.6 |
| 1 | C | 275 | ALA | 9.5 |
| 1 | C | 299 | MET | 9.4 |
| 1 | C | 293 | SER | 8.9 |
| 1 | C | 287 | THR | 8.7 |
| 1 | C | 296 | SER | 8.2 |
| 1 | C | 289 | ASP | 8.0 |
| 1 | C | 303 | PRO | 7.8 |
| 1 | C | 327 | TYR | 7.7 |
| 1 | C | 240 | LYS | 7.6 |
| 1 | C | 297 | THR | 7.6 |
| 1 | C | 131 | ILE | 7.5 |
| 1 | C | 98 | SER | 7.5 |
| 1 | C | 285 | TYR | 7.3 |
| 1 | C | 284 | TYR | 7.2 |
| 1 | C | 295 | VAL | 7.1 |
| 1 | C | 143 | PHE | 7.0 |
| 1 | C | 147 | ALA | 7.0 |
| 1 | C | 276 | SER | 7.0 |
| 1 | C | 286 | LEU | 6.8 |

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| Mol | Chain | Res | Type | RSRZ |
|---|---|---|---|---|
| 1 | C | 290 | GLU | 6.8 |
| 1 | C | 242 | PHE | 6.8 |
| 1 | C | 305 | THR | 6.7 |
| 1 | C | 294 | LEU | 6.4 |
| 1 | C | 241 | SER | 6.4 |
| 1 | C | 132 | LEU | 6.2 |
| 1 | C | 179 | PHE | 6.1 |
| 1 | C | 238 | SER | 6.0 |
| 1 | C | 278 | THR | 5.8 |
| 1 | C | 37 | GLN | 5.6 |
| 1 | C | 146 | GLY | 5.4 |
| 1 | C | 318 | GLU | 5.4 |
| 1 | C | 36 | GLY | 5.4 |
| 1 | C | 322 | ILE | 5.2 |
| 1 | C | 178 | GLY | 5.1 |
| 1 | B | 153 | GLU | 5.0 |
| 1 | C | 129 | GLN | 4.9 |
| 1 | C | 237 | CYS | 4.8 |
| 1 | C | 103 | ILE | 4.8 |
| 1 | A | 125 | TYR | 4.6 |
| 1 | C | 249 | THR | 4.6 |
| 1 | C | 302 | TYR | 4.6 |
| 1 | C | 292 | GLU | 4.5 |
| 1 | C | 319 | ASN | 4.4 |
| 1 | C | 320 | ASN | 4.4 |
| 1 | C | 333 | ASP | 4.3 |
| 1 | C | 104 | MET | 4.2 |
| 1 | C | 122 | GLY | 4.1 |
| 1 | C | 235 | ALA | 4.1 |
| 1 | C | 128 | ASP | 4.1 |
| 1 | C | 321 | GLN | 3.9 |
| 1 | C | 145 | TRP | 3.9 |
| 1 | A | 337 | HIS | 3.9 |
| 1 | C | 330 | HIS | 3.9 |
| 1 | C | 331 | MET | 3.8 |
| 1 | C | 326 | PRO | 3.7 |
| 1 | C | 165 | VAL | 3.6 |
| 1 | C | 298 | TYR | 3.6 |
| 1 | C | 236 | ALA | 3.6 |
| 1 | C | 62 | ASN | 3.6 |
| 1 | C | 304 | ASP | 3.4 |
| 1 | C | 187 | THR | 3.3 |

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| Mol | Chain | Res | Type | RSRZ |
|---|---|---|---|---|
| 1 | C | 259 | LEU | 3.3 |
| 1 | C | 162 | GLY | 3.1 |
| 1 | C | 161 | PHE | 3.0 |
| 1 | B | 199 | LYS | 3.0 |
| 1 | C | 199 | LYS | 3.0 |
| 1 | C | 61 | ILE | 3.0 |
| 1 | B | 196 | PRO | 2.9 |
| 1 | C | 233 | ASN | 2.9 |
| 1 | B | 337 | HIS | 2.9 |
| 1 | B | 125 | TYR | 2.9 |
| 1 | C | 130 | SER | 2.9 |
| 1 | C | 148 | PHE | 2.8 |
| 1 | A | 278 | THR | 2.7 |
| 1 | C | 313 | GLU | 2.6 |
| 1 | C | 134 | GLU | 2.6 |
| 1 | C | 144 | LEU | 2.6 |
| 1 | A | 258 | VAL | 2.5 |
| 1 | C | 138 | VAL | 2.5 |
| 1 | A | 89 | ASN | 2.5 |
| 1 | A | 156 | GLU | 2.4 |
| 1 | C | 163 | ASP | 2.4 |
| 1 | C | 248 | GLY | 2.4 |
| 1 | B | 323 | ASP | 2.4 |
| 1 | A | 154 | GLY | 2.3 |
| 1 | C | 306 | PHE | 2.3 |
| 1 | A | 196 | PRO | 2.3 |
| 1 | C | 188 | PHE | 2.3 |
| 1 | C | 312 | TRP | 2.2 |
| 1 | C | 277 | GLU | 2.2 |
| 1 | C | 332 | LYS | 2.2 |
| 1 | C | 252 | PHE | 2.2 |
| 1 | C | 307 | GLY | 2.1 |
| 1 | C | 169 | PHE | 2.1 |

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

There are no non-standard protein/DNA/RNA residues in this entry.

## 6.3 Carbohydrates (i)

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. The B-factors column lists the minimum, median, $95^{th}$ percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

| Mol | Type | Chain | Res | Atoms | RSCC | RSR | B-factors(Å$^2$) | Q<0.9 |
|---|---|---|---|---|---|---|---|---|
| 2 | KLS | B | 1340 | 14/14 | 0.89 | 0.26 | 24,32,39,39 | 0 |
| 2 | KLS | A | 1338 | 14/14 | 0.93 | 0.18 | 7,11,22,22 | 0 |
| 3 | CL | B | 1339 | 1/1 | 0.93 | 0.10 | 30,30,30,30 | 0 |
| 3 | CL | B | 1338 | 1/1 | 0.98 | 0.08 | 30,30,30,30 | 0 |

## 6.5 Other polymers

There are no such residues in this entry.