# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 15, 2023 – 11:15 AM EDT

| | | |
|---|---|---|
| PDB ID | : | 2YYA |
| Title | : | Crystal structure of GAR synthetase from Aquifex aeolicus |
| Authors | : | Baba, S.; Kanagawa, M.; Kuramitsu, S.; Yokoyama, S.; Kawai, G.; Sampei, G.; RIKEN Structural Genomics/Proteomics Initiative (RSGI) |
| Deposited on | : | 2007-04-27 |
| Resolution | : | 2.40 Å(reported) |

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

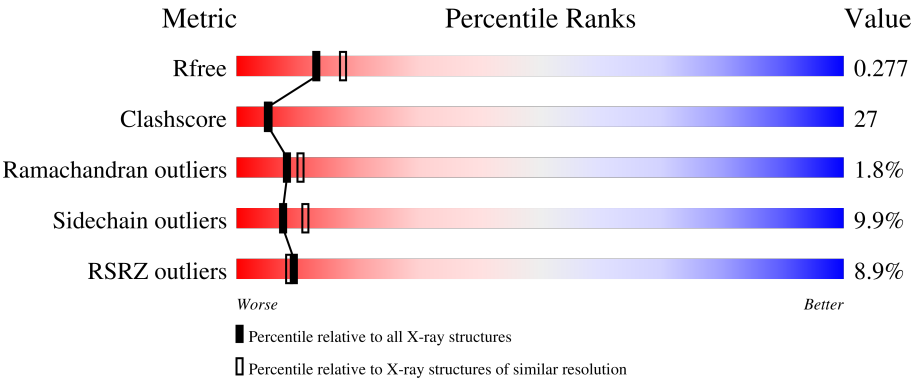
| | | |
|---|---|---|
| MolProbity | : | 4.02b-467 |
| Xtriage (Phenix) | : | 1.13 |
| EDS | : | 2.36 |
| Percentile statistics | : | 20191225.v01 (using entries in the PDB archive December 25th 2019) |
| Refmac | : | 5.8.0158 |
| CCP4 | : | 7.0.044 (Gargrove) |
| Ideal geometry (proteins) | : | Engh & Huber (2001) |
| Ideal geometry (DNA, RNA) | : | Parkinson et al. (1996) |
| Validation Pipeline (wwPDB-VP) | : | 2.36 |

# 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 2.40 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 | 3907 (2.40-2.40) |
| Clashscore | 141614 | 4398 (2.40-2.40) |
| Ramachandran outliers | 138981 | 4318 (2.40-2.40) |
| Sidechain outliers | 138945 | 4319 (2.40-2.40) |
| RSRZ outliers | 127900 | 3811 (2.40-2.40) |

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

| Mol | Chain | Length | Quality of chain |
|---|---|---|---|
| 1 | A | 424 | 8% 47% 38% 12% · |
| 1 | B | 424 | 10% 47% 38% 10% · |

# 2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 6553 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 Phosphoribosylamine--glycine ligase.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| 1 | A | 423 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 3236 | 2069 | 548 | 608 | 11 | | | |
| 1 | B | 423 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 3228 | 2065 | 548 | 604 | 11 | | | |

- Molecule 2 is water.

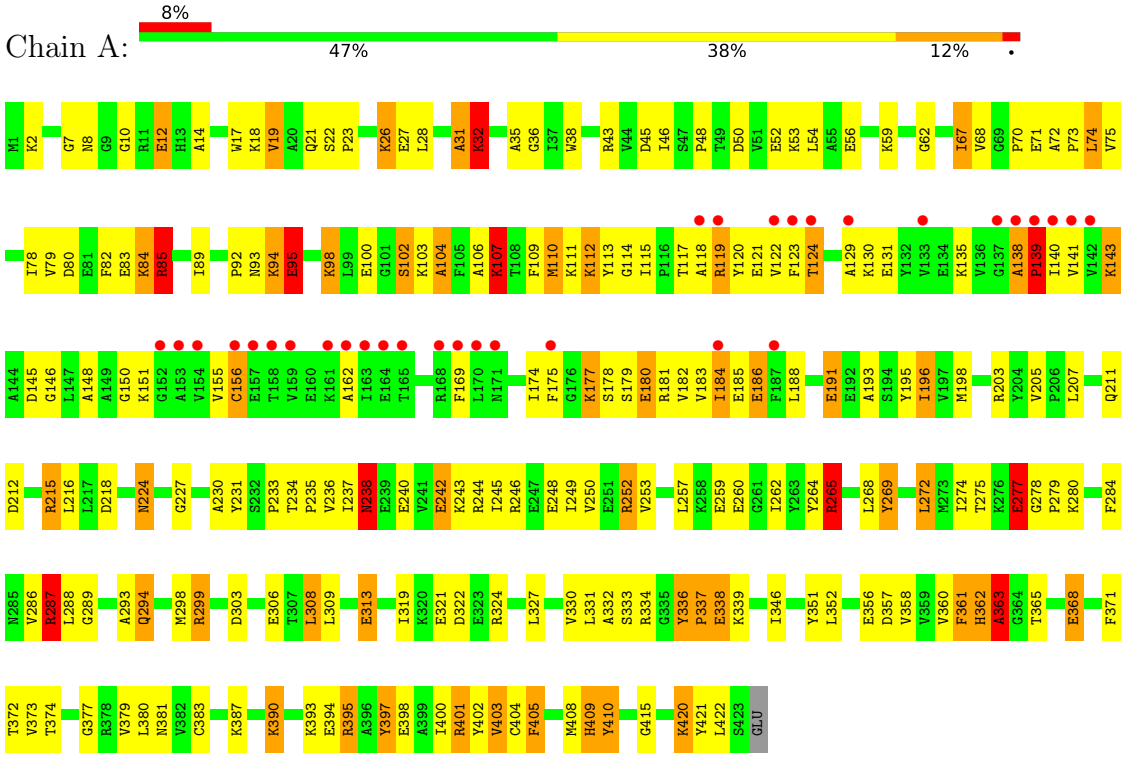
| Mol | Chain | Residues | Atoms | | ZeroOcc | AltConf |
|---|---|---|---|---|---|---|
| 2 | A | 38 | Total | O | 0 | 0 |
| | | | 38 | 38 | | |
| 2 | B | 51 | Total | O | 0 | 0 |
| | | | 51 | 51 | | |

# 3 Residue-property plots (i)

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

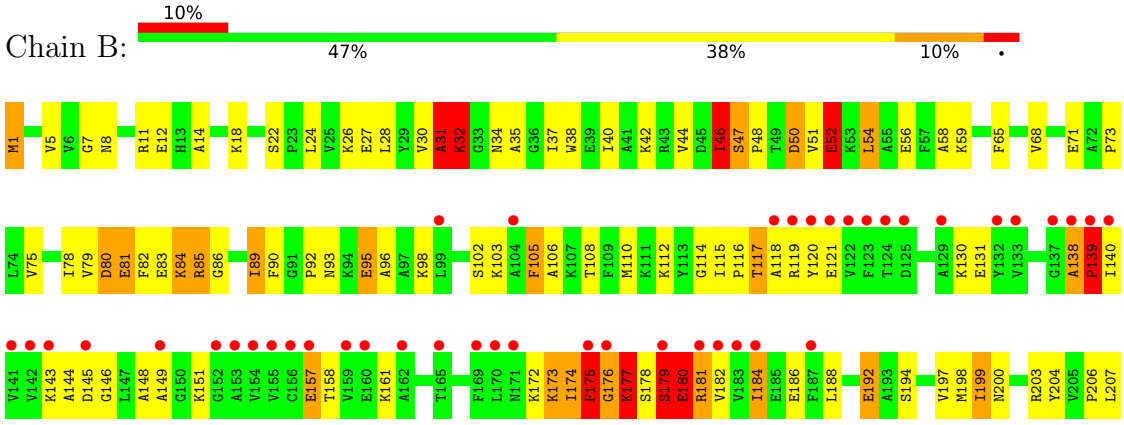
• Molecule 1: Phosphoribosylamine--glycine ligase

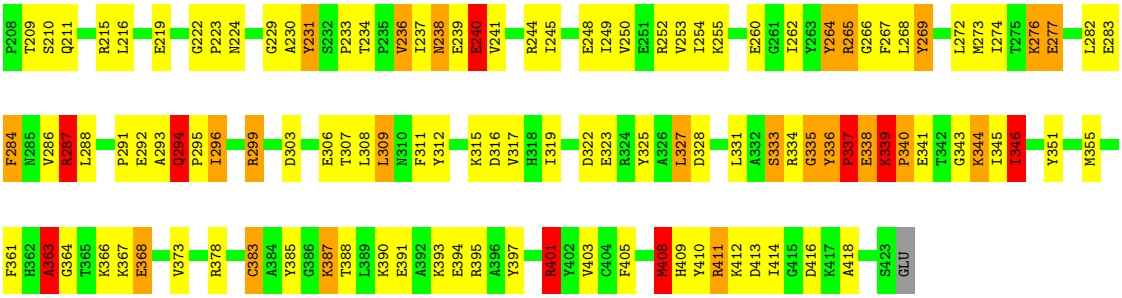
Chain A:




• Molecule 1: Phosphoribosylamine--glycine ligase

Chain B:




P208 T209 S210 Q211 R215 L216 E219 G222 P223 N224 G229 A230 Y231 S232 P233 T234 P235 V236 I237 N238 E239 E240 V241 R244 I245 E248 I249 V250 E251 R252 V253 I254 K255 E260 G261 I262 Y263 Y264 R265 G266 F267 L268 Y269 L272 M273 I274 T275 K276 E277 L282 E283
F284 N285 V286 R287 L288 P291 E292 A293 Q294 P295 I296 R299 D303 E306 T307 L308 L309 N310 F311 Y312 K315 D316 V317 H318 I319 D322 E323 R324 Y325 A326 L327 D328 L331 A332 S333 R334 G335 Y336 P337 E338 K339 P340 E341 T342 G343 K344 I345 I346 Y351 M355
F361 H362 A363 G364 T365 K366 K367 E368 V373 R378 C383 A384 Y385 G386 K387 T388 L389 K390 E391 A392 K393 E394 R395 A396 Y397 R401 Y402 V403 C404 F405 M408 H409 Y410 R411 K412 D413 I414 G415 D416 K417 A418 S423 GLU

# 4 Data and refinement statistics (i)

| Property | Value | Source |
|---|---|---|
| Space group | P 1 21 1 | Depositor |
| Cell constants<br>a, b, c, $\alpha$, $\beta$, $\gamma$ | 97.26Å 45.15Å 103.48Å<br>90.00° 103.87° 90.00° | Depositor |
| Resolution (Å) | 49.55 – 2.40<br>49.55 – 2.39 | Depositor<br>EDS |
| % Data completeness<br>(in resolution range) | 92.9 (49.55-2.40)<br>96.2 (49.55-2.39) | Depositor<br>EDS |
| $R_{merge}$ | 0.07 | Depositor |
| $R_{sym}$ | (Not available) | Depositor |
| $< I/\sigma(I) >$ [1] | 3.10 (at 2.39Å) | Xtriage |
| Refinement program | CNS 1.1 | Depositor |
| R, $R_{free}$ | 0.225 , 0.249<br>0.228 , 0.277 | Depositor<br>DCC |
| $R_{free}$ test set | 1694 reflections (4.99%) | wwPDB-VP |
| Wilson B-factor (Å$^2$) | 34.6 | Xtriage |
| Anisotropy | 1.100 | Xtriage |
| Bulk solvent $k_{sol}$(e/Å$^3$), $B_{sol}$(Å$^2$) | 0.35 , 54.9 | EDS |
| L-test for twinning[2] | $< \|L\| > = 0.49$, $< L^2 > = 0.32$ | Xtriage |
| Estimated twinning fraction | No twinning to report. | Xtriage |
| $F_o$,$F_c$ correlation | 0.93 | EDS |
| Total number of atoms | 6553 | wwPDB-VP |
| Average B, all atoms (Å$^2$) | 51.0 | wwPDB-VP |

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.32% 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

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 | 1.78 | 35/3297 (1.1%) | 1.72 | 76/4447 (1.7%) |
| 1 | B | 1.74 | 36/3289 (1.1%) | 1.68 | 64/4436 (1.4%) |
| All | All | 1.76 | 71/6586 (1.1%) | 1.70 | 140/8883 (1.6%) |

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 | A | 0 | 5 |
| 1 | B | 0 | 11 |
| All | All | 0 | 16 |

All (71) bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|---|---|---|---|---|---|---|---|
| 1 | B | 175 | PHE | C-N | 6.58 | 1.44 | 1.33 |
| 1 | B | 283 | GLU | CD-OE1 | 5.95 | 1.32 | 1.25 |
| 1 | A | 321 | GLU | CD-OE2 | 5.95 | 1.32 | 1.25 |
| 1 | B | 401 | ARG | CG-CD | 5.92 | 1.66 | 1.51 |
| 1 | A | 401 | ARG | C-O | 5.88 | 1.34 | 1.23 |
| 1 | A | 336 | TYR | CD1-CE1 | 5.87 | 1.48 | 1.39 |
| 1 | B | 240 | GLU | CB-CG | 5.86 | 1.63 | 1.52 |
| 1 | A | 405 | PHE | CG-CD1 | 5.85 | 1.47 | 1.38 |
| 1 | A | 95 | GLU | CB-CG | 5.84 | 1.63 | 1.52 |
| 1 | A | 398 | GLU | CG-CD | 5.83 | 1.60 | 1.51 |
| 1 | B | 391 | GLU | CD-OE2 | 5.83 | 1.32 | 1.25 |
| 1 | B | 56 | GLU | CD-OE2 | 5.76 | 1.31 | 1.25 |
| 1 | A | 373 | VAL | CB-CG2 | -5.72 | 1.40 | 1.52 |
| 1 | A | 94 | LYS | CD-CE | 5.71 | 1.65 | 1.51 |
| 1 | A | 2 | LYS | C-O | -5.66 | 1.12 | 1.23 |
| 1 | B | 37 | ILE | C-O | 5.62 | 1.34 | 1.23 |

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| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|---|---|---|---|---|---|---|---|
| 1 | A | 52 | GLU | CD-OE2 | 5.62 | 1.31 | 1.25 |
| 1 | A | 264 | TYR | CG-CD2 | 5.59 | 1.46 | 1.39 |
| 1 | A | 403 | VAL | CB-CG1 | -5.58 | 1.41 | 1.52 |
| 1 | A | 250 | VAL | CB-CG1 | 5.55 | 1.64 | 1.52 |
| 1 | A | 313 | GLU | CB-CG | -5.55 | 1.41 | 1.52 |
| 1 | A | 277 | GLU | CD-OE1 | 5.54 | 1.31 | 1.25 |
| 1 | B | 42 | LYS | CD-CE | 5.53 | 1.65 | 1.51 |
| 1 | B | 192 | GLU | CG-CD | 5.50 | 1.60 | 1.51 |
| 1 | B | 231 | TYR | CD2-CE2 | -5.49 | 1.31 | 1.39 |
| 1 | A | 332 | ALA | C-O | 5.47 | 1.33 | 1.23 |
| 1 | B | 294 | GLN | CB-CG | 5.46 | 1.67 | 1.52 |
| 1 | B | 351 | TYR | CG-CD2 | 5.44 | 1.46 | 1.39 |
| 1 | B | 410 | TYR | CG-CD2 | 5.43 | 1.46 | 1.39 |
| 1 | B | 105 | PHE | CB-CG | -5.41 | 1.42 | 1.51 |
| 1 | A | 62 | GLY | C-O | 5.41 | 1.32 | 1.23 |
| 1 | A | 68 | VAL | CB-CG1 | 5.40 | 1.64 | 1.52 |
| 1 | A | 242 | GLU | CB-CG | -5.39 | 1.42 | 1.52 |
| 1 | B | 269 | TYR | CD1-CE1 | -5.38 | 1.31 | 1.39 |
| 1 | B | 403 | VAL | CA-CB | 5.35 | 1.66 | 1.54 |
| 1 | B | 65 | PHE | CE2-CZ | 5.33 | 1.47 | 1.37 |
| 1 | B | 240 | GLU | CD-OE1 | 5.33 | 1.31 | 1.25 |
| 1 | B | 385 | TYR | CD2-CE2 | 5.33 | 1.47 | 1.39 |
| 1 | A | 363 | ALA | C-O | 5.31 | 1.33 | 1.23 |
| 1 | A | 193 | ALA | CA-CB | -5.31 | 1.41 | 1.52 |
| 1 | A | 17 | TRP | CE3-CZ3 | 5.27 | 1.47 | 1.38 |
| 1 | A | 98 | LYS | CE-NZ | 5.26 | 1.62 | 1.49 |
| 1 | B | 363 | ALA | C-O | 5.24 | 1.33 | 1.23 |
| 1 | B | 323 | GLU | CD-OE2 | 5.24 | 1.31 | 1.25 |
| 1 | A | 119 | ARG | CG-CD | 5.21 | 1.65 | 1.51 |
| 1 | B | 299 | ARG | CA-CB | 5.21 | 1.65 | 1.53 |
| 1 | A | 409 | HIS | C-O | -5.20 | 1.13 | 1.23 |
| 1 | B | 239 | GLU | CD-OE2 | 5.19 | 1.31 | 1.25 |
| 1 | A | 338 | GLU | CD-OE1 | 5.17 | 1.31 | 1.25 |
| 1 | B | 327 | LEU | CG-CD2 | 5.17 | 1.71 | 1.51 |
| 1 | B | 131 | GLU | C-O | 5.16 | 1.33 | 1.23 |
| 1 | A | 43 | ARG | N-CA | -5.16 | 1.36 | 1.46 |
| 1 | A | 224 | ASN | N-CA | -5.16 | 1.36 | 1.46 |
| 1 | B | 383 | CYS | CB-SG | -5.15 | 1.73 | 1.81 |
| 1 | A | 358 | VAL | CB-CG2 | 5.14 | 1.63 | 1.52 |
| 1 | A | 227 | GLY | N-CA | 5.14 | 1.53 | 1.46 |
| 1 | A | 390 | LYS | CD-CE | 5.14 | 1.64 | 1.51 |
| 1 | B | 157 | GLU | C-O | 5.13 | 1.33 | 1.23 |

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| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|---|---|---|---|---|---|---|---|
| 1 | B | 328 | ASP | CG-OD1 | -5.13 | 1.13 | 1.25 |
| 1 | A | 19 | VAL | CA-CB | 5.12 | 1.65 | 1.54 |
| 1 | A | 191 | GLU | CD-OE1 | 5.12 | 1.31 | 1.25 |
| 1 | A | 337 | PRO | C-N | 5.11 | 1.45 | 1.34 |
| 1 | B | 343 | GLY | C-O | -5.10 | 1.15 | 1.23 |
| 1 | B | 284 | PHE | CA-C | -5.09 | 1.39 | 1.52 |
| 1 | A | 12 | GLU | CD-OE1 | -5.08 | 1.20 | 1.25 |
| 1 | B | 52 | GLU | CD-OE1 | 5.06 | 1.31 | 1.25 |
| 1 | B | 267 | PHE | CE1-CZ | 5.06 | 1.47 | 1.37 |
| 1 | B | 367 | LYS | CB-CG | 5.05 | 1.66 | 1.52 |
| 1 | B | 80 | ASP | CB-CG | 5.03 | 1.62 | 1.51 |
| 1 | B | 411 | ARG | C-O | 5.03 | 1.32 | 1.23 |
| 1 | B | 264 | TYR | CD1-CE1 | 5.01 | 1.46 | 1.39 |

All (140) bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 1 | B | 287 | ARG | NE-CZ-NH1 | 14.95 | 127.77 | 120.30 |
| 1 | A | 287 | ARG | NE-CZ-NH2 | -14.23 | 113.19 | 120.30 |
| 1 | B | 287 | ARG | NE-CZ-NH2 | -13.66 | 113.47 | 120.30 |
| 1 | A | 395 | ARG | NE-CZ-NH2 | -12.08 | 114.26 | 120.30 |
| 1 | B | 139 | PRO | O-C-N | -11.88 | 103.69 | 122.70 |
| 1 | A | 174 | ILE | O-C-N | 11.84 | 141.65 | 122.70 |
| 1 | A | 395 | ARG | NE-CZ-NH1 | 10.53 | 125.57 | 120.30 |
| 1 | B | 175 | PHE | O-C-N | 10.38 | 140.84 | 123.20 |
| 1 | B | 309 | LEU | CB-CG-CD1 | -9.88 | 94.20 | 111.00 |
| 1 | A | 265 | ARG | NE-CZ-NH1 | 9.80 | 125.20 | 120.30 |
| 1 | A | 356 | GLU | O-C-N | 9.72 | 138.26 | 122.70 |
| 1 | A | 107 | LYS | O-C-N | -9.63 | 107.28 | 122.70 |
| 1 | B | 157 | GLU | O-C-N | -9.50 | 107.49 | 122.70 |
| 1 | B | 341 | GLU | O-C-N | 9.49 | 137.88 | 122.70 |
| 1 | B | 177 | LYS | O-C-N | -9.41 | 107.65 | 122.70 |
| 1 | B | 378 | ARG | NE-CZ-NH2 | -9.24 | 115.68 | 120.30 |
| 1 | B | 139 | PRO | CA-C-N | 9.21 | 137.46 | 117.20 |
| 1 | B | 175 | PHE | CA-C-N | -9.00 | 98.19 | 116.20 |
| 1 | B | 157 | GLU | CA-C-N | 8.72 | 136.39 | 117.20 |
| 1 | A | 334 | ARG | NE-CZ-NH1 | 8.70 | 124.65 | 120.30 |
| 1 | A | 397 | TYR | CZ-CE2-CD2 | 8.50 | 127.45 | 119.80 |
| 1 | B | 408 | MET | CG-SD-CE | -8.48 | 86.63 | 100.20 |
| 1 | A | 196 | ILE | CG1-CB-CG2 | -8.48 | 92.75 | 111.40 |
| 1 | A | 85 | ARG | NE-CZ-NH1 | 8.45 | 124.53 | 120.30 |
| 1 | A | 246 | ARG | NE-CZ-NH1 | -8.40 | 116.10 | 120.30 |

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| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 1 | B | 395 | ARG | NE-CZ-NH2 | -8.35 | 116.13 | 120.30 |
| 1 | B | 85 | ARG | NE-CZ-NH1 | -8.28 | 116.16 | 120.30 |
| 1 | B | 31 | ALA | CA-C-N | -8.21 | 99.14 | 117.20 |
| 1 | A | 287 | ARG | NE-CZ-NH1 | 8.20 | 124.40 | 120.30 |
| 1 | A | 361 | PHE | O-C-N | 8.18 | 135.78 | 122.70 |
| 1 | A | 31 | ALA | C-N-CA | 8.12 | 141.99 | 121.70 |
| 1 | B | 339 | LYS | C-N-CD | -8.06 | 102.87 | 120.60 |
| 1 | A | 174 | ILE | CA-C-N | -7.95 | 99.71 | 117.20 |
| 1 | A | 84 | LYS | CD-CE-NZ | 7.94 | 129.97 | 111.70 |
| 1 | B | 172 | LYS | C-N-CA | 7.93 | 141.52 | 121.70 |
| 1 | B | 26 | LYS | CD-CE-NZ | 7.88 | 129.82 | 111.70 |
| 1 | A | 410 | TYR | CZ-CE2-CD2 | 7.84 | 126.86 | 119.80 |
| 1 | A | 357 | ASP | CB-CG-OD2 | -7.80 | 111.28 | 118.30 |
| 1 | A | 238 | ASN | CA-C-O | 7.75 | 136.38 | 120.10 |
| 1 | A | 356 | GLU | CA-C-N | -7.74 | 100.17 | 117.20 |
| 1 | A | 299 | ARG | NE-CZ-NH2 | -7.73 | 116.43 | 120.30 |
| 1 | B | 299 | ARG | NE-CZ-NH1 | -7.65 | 116.47 | 120.30 |
| 1 | A | 84 | LYS | O-C-N | 7.59 | 134.85 | 122.70 |
| 1 | B | 32 | LYS | CB-CA-C | 7.57 | 125.54 | 110.40 |
| 1 | A | 324 | ARG | NE-CZ-NH1 | -7.50 | 116.55 | 120.30 |
| 1 | A | 265 | ARG | NE-CZ-NH2 | -7.33 | 116.64 | 120.30 |
| 1 | B | 85 | ARG | NE-CZ-NH2 | 7.14 | 123.87 | 120.30 |
| 1 | A | 357 | ASP | CB-CG-OD1 | 7.12 | 124.71 | 118.30 |
| 1 | B | 50 | ASP | CB-CG-OD1 | -7.02 | 111.98 | 118.30 |
| 1 | A | 309 | LEU | CA-CB-CG | -6.99 | 99.22 | 115.30 |
| 1 | B | 346 | ILE | CG1-CB-CG2 | -6.88 | 96.26 | 111.40 |
| 1 | A | 237 | ILE | CA-C-N | -6.83 | 102.17 | 117.20 |
| 1 | A | 410 | TYR | CG-CD2-CE2 | -6.80 | 115.86 | 121.30 |
| 1 | B | 180 | GLU | O-C-N | 6.72 | 133.45 | 122.70 |
| 1 | A | 309 | LEU | CB-CG-CD1 | -6.66 | 99.68 | 111.00 |
| 1 | A | 139 | PRO | C-N-CA | 6.65 | 138.32 | 121.70 |
| 1 | B | 1 | MET | CG-SD-CE | -6.58 | 89.67 | 100.20 |
| 1 | A | 50 | ASP | CB-CG-OD1 | -6.55 | 112.41 | 118.30 |
| 1 | B | 219 | GLU | C-N-CA | 6.55 | 138.07 | 121.70 |
| 1 | A | 237 | ILE | O-C-N | 6.49 | 133.09 | 122.70 |
| 1 | A | 238 | ASN | CA-C-N | -6.42 | 103.08 | 117.20 |
| 1 | A | 174 | ILE | C-N-CA | -6.37 | 105.78 | 121.70 |
| 1 | B | 294 | GLN | O-C-N | 6.32 | 133.11 | 121.10 |
| 1 | A | 422 | LEU | CA-CB-CG | 6.31 | 129.81 | 115.30 |
| 1 | A | 107 | LYS | CA-C-N | 6.24 | 130.92 | 117.20 |
| 1 | B | 31 | ALA | O-C-N | 6.20 | 132.62 | 122.70 |
| 1 | A | 84 | LYS | CA-C-N | -6.16 | 103.64 | 117.20 |

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| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 1 | A | 104 | ALA | C-N-CA | 6.15 | 137.07 | 121.70 |
| 1 | A | 395 | ARG | CD-NE-CZ | 6.12 | 132.18 | 123.60 |
| 1 | B | 401 | ARG | NE-CZ-NH2 | -6.10 | 117.25 | 120.30 |
| 1 | B | 287 | ARG | CB-CG-CD | 6.08 | 127.41 | 111.60 |
| 1 | B | 199 | ILE | CG1-CB-CG2 | -6.06 | 98.07 | 111.40 |
| 1 | B | 395 | ARG | NE-CZ-NH1 | 6.06 | 123.33 | 120.30 |
| 1 | A | 156 | CYS | C-N-CA | 6.01 | 136.73 | 121.70 |
| 1 | A | 246 | ARG | NE-CZ-NH2 | 5.99 | 123.30 | 120.30 |
| 1 | A | 351 | TYR | CZ-CE2-CD2 | -5.99 | 114.41 | 119.80 |
| 1 | A | 107 | LYS | C-N-CA | 5.98 | 136.65 | 121.70 |
| 1 | B | 355 | MET | CA-C-N | -5.96 | 104.09 | 117.20 |
| 1 | B | 355 | MET | O-C-N | 5.94 | 132.21 | 122.70 |
| 1 | A | 401 | ARG | NE-CZ-NH2 | -5.92 | 117.34 | 120.30 |
| 1 | B | 308 | LEU | CB-CG-CD1 | -5.92 | 100.94 | 111.00 |
| 1 | B | 368 | GLU | CB-CA-C | 5.91 | 122.22 | 110.40 |
| 1 | A | 218 | ASP | C-N-CA | 5.90 | 136.45 | 121.70 |
| 1 | A | 244 | ARG | NE-CZ-NH1 | -5.87 | 117.36 | 120.30 |
| 1 | A | 31 | ALA | N-CA-CB | 5.83 | 118.26 | 110.10 |
| 1 | A | 2 | LYS | CD-CE-NZ | -5.79 | 98.38 | 111.70 |
| 1 | B | 229 | GLY | N-CA-C | -5.79 | 98.63 | 113.10 |
| 1 | B | 344 | LYS | CD-CE-NZ | -5.79 | 98.39 | 111.70 |
| 1 | B | 336 | TYR | O-C-N | 5.76 | 132.05 | 121.10 |
| 1 | B | 177 | LYS | CA-C-N | 5.76 | 129.87 | 117.20 |
| 1 | B | 336 | TYR | C-N-CD | -5.75 | 107.96 | 120.60 |
| 1 | B | 346 | ILE | N-CA-C | -5.75 | 95.49 | 111.00 |
| 1 | A | 361 | PHE | CA-C-N | -5.72 | 104.62 | 117.20 |
| 1 | A | 224 | ASN | N-CA-C | -5.70 | 95.61 | 111.00 |
| 1 | B | 31 | ALA | C-N-CA | 5.69 | 135.93 | 121.70 |
| 1 | A | 401 | ARG | CD-NE-CZ | 5.64 | 131.49 | 123.60 |
| 1 | B | 174 | ILE | O-C-N | -5.62 | 113.71 | 122.70 |
| 1 | A | 212 | ASP | CB-CG-OD2 | -5.62 | 113.25 | 118.30 |
| 1 | B | 31 | ALA | N-CA-CB | 5.61 | 117.96 | 110.10 |
| 1 | A | 357 | ASP | C-N-CA | 5.59 | 135.68 | 121.70 |
| 1 | B | 337 | PRO | C-N-CA | 5.54 | 135.55 | 121.70 |
| 1 | A | 143 | LYS | C-N-CA | -5.52 | 107.89 | 121.70 |
| 1 | A | 334 | ARG | NE-CZ-NH2 | -5.52 | 117.54 | 120.30 |
| 1 | B | 335 | GLY | O-C-N | -5.51 | 113.88 | 122.70 |
| 1 | A | 308 | LEU | CA-CB-CG | -5.50 | 102.64 | 115.30 |
| 1 | A | 306 | GLU | OE1-CD-OE2 | 5.49 | 129.88 | 123.30 |
| 1 | A | 243 | LYS | CB-CG-CD | 5.48 | 125.85 | 111.60 |
| 1 | A | 67 | ILE | CA-CB-CG1 | 5.47 | 121.40 | 111.00 |
| 1 | A | 32 | LYS | N-CA-C | -5.47 | 96.23 | 111.00 |

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| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 1 | B | 50 | ASP | CB-CG-OD2 | 5.47 | 123.22 | 118.30 |
| 1 | A | 110 | MET | O-C-N | -5.44 | 113.99 | 122.70 |
| 1 | A | 106 | ALA | O-C-N | 5.41 | 131.36 | 122.70 |
| 1 | B | 11 | ARG | NE-CZ-NH2 | 5.41 | 123.00 | 120.30 |
| 1 | A | 26 | LYS | CD-CE-NZ | 5.39 | 124.09 | 111.70 |
| 1 | A | 387 | LYS | CD-CE-NZ | 5.35 | 124.00 | 111.70 |
| 1 | B | 181 | ARG | NE-CZ-NH2 | -5.34 | 117.63 | 120.30 |
| 1 | B | 299 | ARG | CG-CD-NE | -5.32 | 100.64 | 111.80 |
| 1 | A | 32 | LYS | CB-CA-C | 5.30 | 120.99 | 110.40 |
| 1 | A | 397 | TYR | CE1-CZ-CE2 | -5.30 | 111.33 | 119.80 |
| 1 | A | 287 | ARG | CB-CG-CD | 5.29 | 125.35 | 111.60 |
| 1 | B | 315 | LYS | CA-C-N | -5.26 | 105.63 | 117.20 |
| 1 | A | 143 | LYS | O-C-N | 5.24 | 131.08 | 122.70 |
| 1 | B | 222 | GLY | N-CA-C | -5.22 | 100.05 | 113.10 |
| 1 | B | 363 | ALA | C-N-CA | 5.21 | 133.25 | 122.30 |
| 1 | B | 299 | ARG | NH1-CZ-NH2 | 5.20 | 125.11 | 119.40 |
| 1 | B | 32 | LYS | CD-CE-NZ | 5.17 | 123.59 | 111.70 |
| 1 | A | 357 | ASP | O-C-N | -5.17 | 114.44 | 122.70 |
| 1 | A | 272 | LEU | CB-CG-CD2 | -5.14 | 102.25 | 111.00 |
| 1 | B | 84 | LYS | CD-CE-NZ | 5.14 | 123.53 | 111.70 |
| 1 | A | 74 | LEU | CA-CB-CG | -5.14 | 103.48 | 115.30 |
| 1 | B | 413 | ASP | CB-CG-OD2 | 5.13 | 122.92 | 118.30 |
| 1 | B | 47 | SER | C-N-CD | 5.11 | 139.13 | 128.40 |
| 1 | B | 236 | VAL | CB-CA-C | -5.11 | 101.69 | 111.40 |
| 1 | B | 385 | TYR | CD1-CE1-CZ | 5.10 | 124.39 | 119.80 |
| 1 | B | 32 | LYS | N-CA-C | -5.09 | 97.24 | 111.00 |
| 1 | A | 362 | HIS | C-N-CA | 5.06 | 134.35 | 121.70 |
| 1 | A | 129 | ALA | C-N-CA | 5.05 | 134.34 | 121.70 |
| 1 | B | 46 | ILE | CB-CA-C | -5.04 | 101.51 | 111.60 |
| 1 | A | 72 | ALA | C-N-CD | 5.04 | 138.98 | 128.40 |
| 1 | A | 368 | GLU | N-CA-C | -5.00 | 97.49 | 111.00 |

There are no chirality outliers.

All (16) planarity outliers are listed below:

| Mol | Chain | Res | Type | Group |
|---|---|---|---|---|
| 1 | A | 138 | ALA | Peptide |
| 1 | A | 139 | PRO | Peptide |
| 1 | A | 238 | ASN | Peptide |
| 1 | A | 31 | ALA | Peptide |
| 1 | A | 371 | PHE | Peptide |
| 1 | B | 138 | ALA | Peptide |

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| Mol | Chain | Res | Type | Group |
|---|---|---|---|---|
| 1 | B | 139 | PRO | Peptide |
| 1 | B | 173 | LYS | Peptide |
| 1 | B | 174 | ILE | Peptide |
| 1 | B | 179 | SER | Peptide |
| 1 | B | 31 | ALA | Peptide |
| 1 | B | 337 | PRO | Peptide |
| 1 | B | 338 | GLU | Peptide |
| 1 | B | 339 | LYS | Peptide |
| 1 | B | 340 | PRO | Peptide |
| 1 | B | 50 | ASP | 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 | 3236 | 0 | 3194 | 173 | 0 |
| 1 | B | 3228 | 0 | 3180 | 171 | 0 |
| 2 | A | 38 | 0 | 0 | 4 | 0 |
| 2 | B | 51 | 0 | 0 | 1 | 0 |
| All | All | 6553 | 0 | 6374 | 342 | 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 27.

All (342) 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:337:PRO:HD2 | 1:B:338:GLU:CD | 1.49 | 1.32 |
| 1:B:337:PRO:HD2 | 1:B:338:GLU:OE2 | 1.38 | 1.18 |
| 1:A:103:LYS:HD2 | 1:A:143:LYS:HE2 | 1.27 | 1.11 |
| 1:B:265:ARG:HG2 | 1:B:265:ARG:HH11 | 0.94 | 1.09 |
| 1:A:103:LYS:CD | 1:A:143:LYS:HE2 | 1.85 | 1.05 |
| 1:A:46:ILE:HD13 | 1:A:53:LYS:HG2 | 1.51 | 0.93 |
| 1:B:194:SER:HB3 | 1:B:269:TYR:HE1 | 1.30 | 0.93 |
| 1:A:71:GLU:HB3 | 1:A:287:ARG:HD2 | 1.50 | 0.92 |
| 1:B:265:ARG:HG2 | 1:B:265:ARG:NH1 | 1.68 | 0.91 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:B:207:LEU:HD23 | 1:B:319:ILE:CD1 | 2.00 | 0.91 |
| 1:B:103:LYS:CD | 1:B:143:LYS:HE2 | 2.01 | 0.91 |
| 1:B:337:PRO:CD | 1:B:338:GLU:OE2 | 2.19 | 0.90 |
| 1:B:265:ARG:HH11 | 1:B:265:ARG:CG | 1.84 | 0.88 |
| 1:A:184:ILE:N | 1:A:184:ILE:HD12 | 1.90 | 0.86 |
| 1:A:215:ARG:NH1 | 1:A:224:ASN:HD22 | 1.73 | 0.86 |
| 1:A:124:THR:HG21 | 1:A:181:ARG:NH1 | 1.90 | 0.86 |
| 1:B:90:PHE:CE2 | 1:B:266:GLY:HA2 | 2.10 | 0.86 |
| 1:B:103:LYS:HD3 | 1:B:143:LYS:HE2 | 1.57 | 0.85 |
| 1:B:110:MET:HG2 | 1:B:115:ILE:HB | 1.60 | 0.83 |
| 1:B:116:PRO:HG2 | 1:B:249:ILE:HD11 | 1.58 | 0.83 |
| 1:A:59:LYS:HE2 | 1:A:85:ARG:HH21 | 1.44 | 0.82 |
| 1:B:177:LYS:HE2 | 1:B:180:GLU:OE2 | 1.78 | 0.82 |
| 1:A:207:LEU:HD23 | 1:A:319:ILE:HD12 | 1.60 | 0.82 |
| 1:A:140:ILE:HG23 | 1:A:141:VAL:H | 1.45 | 0.81 |
| 1:B:138:ALA:HB1 | 1:B:157:GLU:O | 1.80 | 0.81 |
| 1:B:120:TYR:O | 1:B:121:GLU:HG2 | 1.80 | 0.81 |
| 1:A:103:LYS:HE3 | 1:A:143:LYS:HE3 | 1.63 | 0.80 |
| 1:B:294:GLN:HE21 | 1:B:294:GLN:N | 1.79 | 0.80 |
| 1:B:79:VAL:HG22 | 1:B:89:ILE:HD12 | 1.63 | 0.80 |
| 1:B:210:SER:HB3 | 1:B:296:ILE:HD11 | 1.63 | 0.78 |
| 1:B:51:VAL:HG23 | 1:B:81:GLU:OE2 | 1.84 | 0.78 |
| 1:A:115:ILE:O | 1:A:117:THR:HG22 | 1.86 | 0.76 |
| 1:A:140:ILE:HG23 | 1:A:141:VAL:N | 2.02 | 0.75 |
| 1:B:336:TYR:CD1 | 1:B:337:PRO:HA | 2.20 | 0.75 |
| 1:A:260:GLU:HB2 | 1:A:262:ILE:HG13 | 1.67 | 0.75 |
| 1:B:194:SER:HB3 | 1:B:269:TYR:CE1 | 2.18 | 0.75 |
| 1:B:337:PRO:CD | 1:B:338:GLU:CD | 2.44 | 0.75 |
| 1:B:176:GLY:O | 1:B:180:GLU:HG2 | 1.87 | 0.74 |
| 1:A:207:LEU:HD23 | 1:A:319:ILE:CD1 | 2.18 | 0.74 |
| 1:B:390:LYS:HE2 | 1:B:394:GLU:OE2 | 1.88 | 0.73 |
| 1:A:216:LEU:O | 1:A:409:HIS:HE1 | 1.71 | 0.73 |
| 1:B:236:VAL:HG12 | 1:B:274:ILE:HG13 | 1.70 | 0.72 |
| 1:B:71:GLU:HB3 | 1:B:287:ARG:HD2 | 1.71 | 0.72 |
| 1:A:403:VAL:O | 1:A:404:CYS:HB2 | 1.89 | 0.72 |
| 1:B:405:PHE:O | 1:B:408:MET:HG2 | 1.90 | 0.72 |
| 1:A:215:ARG:HH12 | 1:A:224:ASN:HD22 | 1.38 | 0.71 |
| 1:A:95:GLU:OE1 | 1:A:95:GLU:HA | 1.90 | 0.71 |
| 1:A:207:LEU:CD2 | 1:A:319:ILE:CD1 | 2.69 | 0.71 |
| 1:B:238:ASN:C | 1:B:238:ASN:HD22 | 1.94 | 0.70 |
| 1:A:124:THR:HG22 | 1:A:181:ARG:HG3 | 1.72 | 0.69 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:B:393:LYS:O | 1:B:397:TYR:HD2 | 1.75 | 0.69 |
| 1:A:215:ARG:HH12 | 1:A:224:ASN:HB2 | 1.56 | 0.69 |
| 1:A:265:ARG:HH11 | 1:A:265:ARG:HG2 | 1.57 | 0.69 |
| 1:A:177:LYS:HE2 | 1:A:180:GLU:OE2 | 1.92 | 0.68 |
| 1:A:95:GLU:OE1 | 1:A:98:LYS:HE2 | 1.92 | 0.68 |
| 1:A:112:LYS:O | 1:A:112:LYS:HG2 | 1.95 | 0.67 |
| 1:A:124:THR:CG2 | 1:A:181:ARG:NH1 | 2.58 | 0.67 |
| 1:B:114:GLY:O | 1:B:252:ARG:NH1 | 2.27 | 0.67 |
| 1:A:245:ILE:HA | 1:A:249:ILE:HD13 | 1.75 | 0.67 |
| 1:B:116:PRO:HG2 | 1:B:249:ILE:CD1 | 2.25 | 0.67 |
| 1:A:103:LYS:CD | 1:A:143:LYS:CE | 2.70 | 0.66 |
| 1:B:276:LYS:HG3 | 1:B:277:GLU:OE2 | 1.95 | 0.66 |
| 1:A:14:ALA:HA | 1:A:361:PHE:CE1 | 2.31 | 0.66 |
| 1:A:103:LYS:HD2 | 1:A:143:LYS:CE | 2.15 | 0.66 |
| 1:B:294:GLN:H | 1:B:294:GLN:NE2 | 1.95 | 0.65 |
| 1:A:277:GLU:H | 1:A:277:GLU:CD | 2.00 | 0.65 |
| 1:B:68:VAL:HG23 | 1:B:89:ILE:HD11 | 1.79 | 0.65 |
| 1:B:175:PHE:CD1 | 1:B:175:PHE:N | 2.59 | 0.65 |
| 1:A:114:GLY:O | 1:A:252:ARG:NH1 | 2.29 | 0.65 |
| 1:B:175:PHE:H | 1:B:175:PHE:HD1 | 1.42 | 0.65 |
| 1:A:119:ARG:O | 1:A:185:GLU:HA | 1.96 | 0.64 |
| 1:A:146:GLY:HA3 | 1:A:178:SER:HB2 | 1.79 | 0.64 |
| 1:B:59:LYS:HD3 | 1:B:85:ARG:HB3 | 1.78 | 0.64 |
| 1:B:199:ILE:CD1 | 1:B:254:ILE:HD11 | 2.26 | 0.64 |
| 1:A:111:LYS:O | 1:A:113:TYR:N | 2.30 | 0.64 |
| 1:A:8:ASN:OD1 | 1:A:32:LYS:HB2 | 1.97 | 0.64 |
| 1:B:210:SER:HB3 | 1:B:296:ILE:CD1 | 2.27 | 0.64 |
| 1:B:8:ASN:OD1 | 1:B:32:LYS:HB2 | 1.98 | 0.64 |
| 1:A:103:LYS:HE3 | 1:A:143:LYS:CE | 2.27 | 0.63 |
| 1:A:195:TYR:C | 1:A:196:ILE:HD12 | 2.19 | 0.63 |
| 1:A:207:LEU:CD2 | 1:A:319:ILE:HD12 | 2.27 | 0.63 |
| 1:B:393:LYS:NZ | 1:B:416:ASP:OD1 | 2.31 | 0.63 |
| 1:A:109:PHE:O | 1:A:113:TYR:HB2 | 1.98 | 0.63 |
| 1:A:115:ILE:HD13 | 1:A:253:VAL:HG23 | 1.80 | 0.63 |
| 1:B:294:GLN:N | 1:B:294:GLN:NE2 | 2.46 | 0.63 |
| 1:A:191:GLU:HG3 | 1:A:421:TYR:OH | 1.99 | 0.63 |
| 1:A:140:ILE:CG2 | 1:A:141:VAL:N | 2.61 | 0.63 |
| 1:A:184:ILE:N | 1:A:184:ILE:CD1 | 2.59 | 0.62 |
| 1:A:333:SER:HB2 | 2:A:428:HOH:O | 2.00 | 0.62 |
| 1:A:215:ARG:NH1 | 1:A:224:ASN:HB2 | 2.15 | 0.61 |
| 1:B:116:PRO:HD2 | 1:B:249:ILE:HD13 | 1.81 | 0.61 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:B:176:GLY:O | 1:B:180:GLU:CG | 2.49 | 0.61 |
| 1:B:199:ILE:HD12 | 1:B:254:ILE:HD11 | 1.82 | 0.61 |
| 1:A:84:LYS:O | 1:B:86:GLY:HA2 | 2.00 | 0.61 |
| 1:A:7:GLY:HA3 | 1:A:12:GLU:HG2 | 1.84 | 0.60 |
| 1:A:139:PRO:HB2 | 1:A:140:ILE:HG13 | 1.84 | 0.60 |
| 1:B:51:VAL:CG2 | 1:B:81:GLU:OE2 | 2.49 | 0.60 |
| 1:A:183:VAL:C | 1:A:184:ILE:HD12 | 2.23 | 0.59 |
| 1:B:95:GLU:OE2 | 1:B:262:ILE:HD12 | 2.02 | 0.59 |
| 1:A:288:LEU:HB3 | 1:A:293:ALA:HB2 | 1.82 | 0.59 |
| 1:B:95:GLU:OE1 | 1:B:98:LYS:HE2 | 2.02 | 0.59 |
| 1:B:117:THR:HG23 | 1:B:118:ALA:O | 2.03 | 0.59 |
| 1:B:92:PRO:HG3 | 1:B:286:VAL:HB | 1.83 | 0.59 |
| 1:A:115:ILE:CD1 | 1:A:253:VAL:HG23 | 2.32 | 0.59 |
| 1:A:111:LYS:C | 1:A:113:TYR:H | 2.06 | 0.59 |
| 1:A:156:CYS:SG | 1:A:162:ALA:HA | 2.43 | 0.59 |
| 1:B:216:LEU:O | 1:B:409:HIS:HE1 | 1.85 | 0.59 |
| 1:A:330:VAL:HG22 | 1:A:381:ASN:OD1 | 2.02 | 0.59 |
| 1:A:120:TYR:CE1 | 1:A:122:VAL:HG23 | 2.37 | 0.58 |
| 1:A:253:VAL:HG21 | 1:A:284:PHE:CZ | 2.38 | 0.58 |
| 1:A:113:TYR:OH | 1:A:259:GLU:HB2 | 2.03 | 0.58 |
| 1:A:131:GLU:O | 1:A:135:LYS:N | 2.36 | 0.58 |
| 1:A:46:ILE:CD1 | 1:A:53:LYS:HG2 | 2.32 | 0.57 |
| 1:A:59:LYS:HD3 | 1:A:85:ARG:HE | 1.67 | 0.57 |
| 1:A:238:ASN:O | 1:A:242:GLU:HB3 | 2.03 | 0.57 |
| 1:B:277:GLU:CD | 1:B:277:GLU:N | 2.56 | 0.57 |
| 1:A:36:GLY:HA3 | 1:A:362:HIS:CG | 2.40 | 0.57 |
| 1:A:119:ARG:HB2 | 1:A:186:GLU:HG2 | 1.87 | 0.57 |
| 1:B:288:LEU:HB3 | 1:B:293:ALA:HB2 | 1.86 | 0.57 |
| 1:A:224:ASN:ND2 | 2:A:449:HOH:O | 2.38 | 0.56 |
| 1:A:141:VAL:HG22 | 1:A:155:VAL:HA | 1.87 | 0.56 |
| 1:A:393:LYS:O | 1:A:397:TYR:HD2 | 1.89 | 0.56 |
| 1:B:22:SER:HB2 | 1:B:303:ASP:OD1 | 2.05 | 0.56 |
| 1:B:337:PRO:HD2 | 1:B:338:GLU:OE1 | 2.03 | 0.56 |
| 1:B:210:SER:HA | 1:B:231:TYR:O | 2.06 | 0.56 |
| 1:A:294:GLN:HE21 | 1:A:294:GLN:N | 2.03 | 0.56 |
| 1:A:83:GLU:HB3 | 1:B:84:LYS:HA | 1.88 | 0.56 |
| 1:B:79:VAL:HB | 1:B:93:ASN:HA | 1.88 | 0.56 |
| 1:B:309:LEU:O | 1:B:312:TYR:HB3 | 2.05 | 0.56 |
| 1:A:123:PHE:CD2 | 1:A:184:ILE:HD11 | 2.41 | 0.56 |
| 1:B:31:ALA:O | 1:B:48:PRO:HG3 | 2.06 | 0.55 |
| 1:A:107:LYS:HE2 | 1:A:117:THR:OG1 | 2.07 | 0.55 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:B:103:LYS:CE | 1:B:143:LYS:HE2 | 2.35 | 0.55 |
| 1:A:35:ALA:HA | 1:A:38:TRP:CE3 | 2.42 | 0.55 |
| 1:A:207:LEU:CD2 | 1:A:319:ILE:HD11 | 2.37 | 0.55 |
| 1:B:89:ILE:HD13 | 1:B:90:PHE:C | 2.27 | 0.55 |
| 1:A:403:VAL:O | 1:A:404:CYS:CB | 2.49 | 0.55 |
| 1:A:73:PRO:O | 1:A:78:ILE:HG22 | 2.07 | 0.54 |
| 1:A:110:MET:HB3 | 1:A:117:THR:HG21 | 1.89 | 0.54 |
| 1:A:123:PHE:CD2 | 1:A:184:ILE:CD1 | 2.90 | 0.54 |
| 1:A:233:PRO:HB3 | 1:A:299:ARG:NH2 | 2.23 | 0.54 |
| 1:A:175:PHE:HB2 | 1:A:179:SER:HB3 | 1.88 | 0.54 |
| 1:B:7:GLY:HA3 | 1:B:12:GLU:HG2 | 1.90 | 0.54 |
| 1:B:215:ARG:HH11 | 1:B:224:ASN:HD22 | 1.54 | 0.54 |
| 1:B:179:SER:C | 1:B:181:ARG:H | 2.10 | 0.54 |
| 1:B:199:ILE:HD13 | 1:B:204:TYR:HB2 | 1.89 | 0.54 |
| 1:B:34:ASN:ND2 | 1:B:363:ALA:O | 2.41 | 0.54 |
| 1:B:238:ASN:HD21 | 1:B:240:GLU:HG3 | 1.73 | 0.54 |
| 1:B:138:ALA:CB | 1:B:157:GLU:O | 2.53 | 0.53 |
| 1:A:95:GLU:OE1 | 1:A:95:GLU:CA | 2.56 | 0.53 |
| 1:B:245:ILE:HD13 | 1:B:272:LEU:HD11 | 1.91 | 0.53 |
| 1:A:420:LYS:HG2 | 2:A:439:HOH:O | 2.08 | 0.53 |
| 1:B:215:ARG:NH1 | 1:B:224:ASN:HD22 | 2.07 | 0.53 |
| 1:A:26:LYS:O | 1:A:27:GLU:HG3 | 2.08 | 0.53 |
| 1:A:346:ILE:HD12 | 1:A:372:THR:HG22 | 1.91 | 0.52 |
| 1:B:335:GLY:O | 1:B:338:GLU:OE1 | 2.26 | 0.52 |
| 1:B:387:LYS:HG2 | 1:B:388:THR:HG23 | 1.91 | 0.52 |
| 1:A:140:ILE:HG21 | 1:A:184:ILE:HG22 | 1.91 | 0.52 |
| 1:A:215:ARG:HG2 | 1:A:215:ARG:HH11 | 1.74 | 0.52 |
| 1:B:345:ILE:HG22 | 1:B:346:ILE:N | 2.23 | 0.52 |
| 1:A:148:ALA:O | 1:A:151:LYS:HB2 | 2.10 | 0.52 |
| 1:B:238:ASN:ND2 | 1:B:241:VAL:H | 2.08 | 0.52 |
| 1:A:115:ILE:HG12 | 1:A:252:ARG:HB2 | 1.91 | 0.51 |
| 1:A:299:ARG:NH1 | 1:A:322:ASP:O | 2.40 | 0.51 |
| 1:B:144:ALA:CB | 1:B:179:SER:OG | 2.58 | 0.51 |
| 1:A:103:LYS:CE | 1:A:143:LYS:CE | 2.89 | 0.51 |
| 1:A:110:MET:HG2 | 1:A:115:ILE:HB | 1.91 | 0.51 |
| 1:A:249:ILE:HD12 | 1:A:249:ILE:N | 2.26 | 0.51 |
| 1:B:197:VAL:HG12 | 1:B:206:PRO:HB3 | 1.91 | 0.51 |
| 1:A:120:TYR:HE1 | 1:A:122:VAL:HG23 | 1.75 | 0.51 |
| 1:B:83:GLU:O | 1:B:86:GLY:N | 2.42 | 0.51 |
| 1:A:277:GLU:CD | 1:A:277:GLU:N | 2.63 | 0.51 |
| 1:B:75:VAL:HG12 | 1:B:75:VAL:O | 2.10 | 0.51 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:B:291:PRO:O | 1:B:295:PRO:HD2 | 2.10 | 0.51 |
| 1:B:277:GLU:CD | 1:B:277:GLU:H | 2.14 | 0.51 |
| 1:A:215:ARG:NH1 | 1:A:224:ASN:ND2 | 2.52 | 0.50 |
| 1:B:207:LEU:HD23 | 1:B:319:ILE:HD13 | 1.90 | 0.50 |
| 1:A:177:LYS:CE | 1:A:180:GLU:OE2 | 2.58 | 0.50 |
| 1:A:182:VAL:HG23 | 1:A:184:ILE:HD11 | 1.93 | 0.50 |
| 1:A:405:PHE:CE1 | 1:A:408:MET:HA | 2.47 | 0.50 |
| 1:B:260:GLU:OE1 | 1:B:260:GLU:HA | 2.12 | 0.50 |
| 1:A:287:ARG:NH2 | 1:A:289:GLY:HA2 | 2.26 | 0.50 |
| 1:A:104:ALA:HB1 | 1:A:122:VAL:HG21 | 1.93 | 0.50 |
| 1:A:245:ILE:HD13 | 1:A:279:PRO:HB2 | 1.92 | 0.50 |
| 1:A:118:ALA:HB2 | 1:A:188:LEU:HD11 | 1.94 | 0.50 |
| 1:B:276:LYS:HG3 | 1:B:277:GLU:CD | 2.32 | 0.50 |
| 1:A:56:GLU:HG2 | 1:A:85:ARG:CZ | 2.41 | 0.49 |
| 1:A:102:SER:HA | 1:A:145:ASP:O | 2.11 | 0.49 |
| 1:B:207:LEU:HD23 | 1:B:319:ILE:HD12 | 1.92 | 0.49 |
| 1:B:345:ILE:CG2 | 1:B:346:ILE:N | 2.74 | 0.49 |
| 1:B:46:ILE:O | 1:B:47:SER:C | 2.47 | 0.49 |
| 1:A:124:THR:HG21 | 1:A:181:ARG:HH12 | 1.74 | 0.49 |
| 1:A:327:LEU:O | 1:A:383:CYS:HA | 2.11 | 0.49 |
| 1:B:103:LYS:HE3 | 1:B:143:LYS:HE2 | 1.94 | 0.49 |
| 1:B:148:ALA:CB | 1:B:175:PHE:CD2 | 2.95 | 0.49 |
| 1:B:192:GLU:HA | 1:B:272:LEU:O | 2.12 | 0.49 |
| 1:B:244:ARG:O | 1:B:248:GLU:HG3 | 2.13 | 0.49 |
| 1:A:110:MET:SD | 1:A:117:THR:HB | 2.53 | 0.49 |
| 1:B:105:PHE:HD2 | 1:B:106:ALA:N | 2.09 | 0.49 |
| 1:B:89:ILE:HD13 | 1:B:90:PHE:O | 2.13 | 0.49 |
| 1:A:111:LYS:C | 1:A:113:TYR:N | 2.66 | 0.49 |
| 1:B:73:PRO:O | 1:B:78:ILE:HG22 | 2.12 | 0.49 |
| 1:B:366:LYS:NZ | 2:B:452:HOH:O | 2.42 | 0.49 |
| 1:A:245:ILE:HD12 | 1:A:272:LEU:HD13 | 1.95 | 0.48 |
| 1:B:105:PHE:O | 1:B:108:THR:HB | 2.13 | 0.48 |
| 1:B:146:GLY:HA3 | 1:B:178:SER:HB3 | 1.95 | 0.48 |
| 1:B:238:ASN:C | 1:B:238:ASN:ND2 | 2.66 | 0.48 |
| 1:B:115:ILE:HD13 | 1:B:253:VAL:HG23 | 1.96 | 0.48 |
| 1:A:18:LYS:O | 1:A:21:GLN:HB2 | 2.14 | 0.48 |
| 1:B:90:PHE:CE2 | 1:B:266:GLY:CA | 2.90 | 0.48 |
| 1:A:82:PHE:HB2 | 1:A:89:ILE:HG21 | 1.95 | 0.48 |
| 1:B:265:ARG:NH1 | 1:B:265:ARG:CG | 2.49 | 0.48 |
| 1:A:248:GLU:HB2 | 1:A:249:ILE:HD12 | 1.96 | 0.48 |
| 1:A:333:SER:N | 1:A:377:GLY:O | 2.38 | 0.47 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:B:231:TYR:OH | 1:B:418:ALA:HB2 | 2.14 | 0.47 |
| 1:B:144:ALA:HB1 | 1:B:179:SER:OG | 2.14 | 0.47 |
| 1:B:408:MET:HE3 | 1:B:408:MET:HB3 | 1.21 | 0.47 |
| 1:B:268:LEU:HD11 | 1:B:284:PHE:CD1 | 2.49 | 0.47 |
| 1:A:48:PRO:HA | 1:A:54:LEU:HD11 | 1.96 | 0.47 |
| 1:A:80:ASP:OD2 | 1:A:94:LYS:HB2 | 2.15 | 0.47 |
| 1:A:275:THR:HG21 | 1:A:280:LYS:HD2 | 1.97 | 0.47 |
| 1:A:95:GLU:OE1 | 1:A:98:LYS:CE | 2.61 | 0.47 |
| 1:A:124:THR:CG2 | 1:A:181:ARG:HH11 | 2.27 | 0.47 |
| 1:B:299:ARG:NH1 | 1:B:322:ASP:O | 2.45 | 0.47 |
| 1:A:257:LEU:HD23 | 1:A:262:ILE:HD12 | 1.96 | 0.47 |
| 1:A:362:HIS:ND1 | 1:A:365:THR:HG21 | 2.30 | 0.47 |
| 1:B:14:ALA:HA | 1:B:361:PHE:CE1 | 2.50 | 0.47 |
| 1:A:92:PRO:HG3 | 1:A:286:VAL:HB | 1.96 | 0.47 |
| 1:B:105:PHE:CD2 | 1:B:106:ALA:N | 2.83 | 0.47 |
| 1:B:241:VAL:O | 1:B:245:ILE:HG13 | 2.14 | 0.47 |
| 1:B:35:ALA:HA | 1:B:38:TRP:CE3 | 2.50 | 0.46 |
| 1:B:68:VAL:CG2 | 1:B:89:ILE:HD11 | 2.42 | 0.46 |
| 1:A:336:TYR:CD1 | 1:A:337:PRO:HA | 2.51 | 0.46 |
| 1:B:207:LEU:HD23 | 1:B:319:ILE:HD11 | 1.92 | 0.46 |
| 1:B:393:LYS:HD2 | 1:B:414:ILE:O | 2.15 | 0.46 |
| 1:B:34:ASN:OD1 | 1:B:34:ASN:C | 2.53 | 0.46 |
| 1:B:96:ALA:HB1 | 1:B:264:TYR:CD1 | 2.51 | 0.46 |
| 1:B:112:LYS:HG2 | 1:B:112:LYS:O | 2.16 | 0.46 |
| 1:B:209:THR:HG21 | 1:B:237:ILE:HG21 | 1.97 | 0.46 |
| 1:A:32:LYS:HE2 | 1:A:45:ASP:HA | 1.96 | 0.46 |
| 1:B:344:LYS:O | 1:B:373:VAL:HA | 2.16 | 0.46 |
| 1:A:374:THR:HG22 | 1:A:379:VAL:HG11 | 1.97 | 0.46 |
| 1:B:307:THR:HG23 | 1:B:317:VAL:HB | 1.97 | 0.46 |
| 1:B:327:LEU:O | 1:B:383:CYS:HA | 2.15 | 0.46 |
| 1:A:245:ILE:HD13 | 1:A:279:PRO:CB | 2.45 | 0.46 |
| 1:A:32:LYS:HE2 | 1:A:45:ASP:OD1 | 2.15 | 0.45 |
| 1:B:408:MET:HE2 | 1:B:408:MET:HB2 | 1.76 | 0.45 |
| 1:B:105:PHE:CD2 | 1:B:105:PHE:C | 2.90 | 0.45 |
| 1:B:188:LEU:HD12 | 1:B:282:LEU:CD2 | 2.46 | 0.45 |
| 1:A:253:VAL:HG21 | 1:A:284:PHE:HZ | 1.79 | 0.45 |
| 1:B:188:LEU:HB2 | 1:B:273:MET:HG2 | 1.99 | 0.45 |
| 1:B:234:THR:OG1 | 1:B:236:VAL:HG23 | 2.17 | 0.45 |
| 1:A:107:LYS:HA | 1:A:107:LYS:HD3 | 1.70 | 0.45 |
| 1:B:44:VAL:HG12 | 1:B:46:ILE:HG12 | 1.99 | 0.45 |
| 1:A:245:ILE:CD1 | 1:A:272:LEU:HD13 | 2.47 | 0.44 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:A:363:ALA:HB3 | 1:A:379:VAL:C | 2.37 | 0.44 |
| 1:B:250:VAL:O | 1:B:253:VAL:HB | 2.17 | 0.44 |
| 1:B:58:ALA:CB | 1:B:82:PHE:CE2 | 3.00 | 0.44 |
| 1:B:92:PRO:HB2 | 1:B:96:ALA:HB3 | 1.98 | 0.44 |
| 1:B:198:MET:O | 1:B:204:TYR:HA | 2.18 | 0.44 |
| 1:B:333:SER:O | 1:B:334:ARG:C | 2.54 | 0.44 |
| 1:A:245:ILE:HD12 | 1:A:272:LEU:CD1 | 2.47 | 0.44 |
| 1:A:253:VAL:HG11 | 1:A:268:LEU:HD21 | 1.99 | 0.44 |
| 1:B:237:ILE:HG22 | 1:B:237:ILE:O | 2.16 | 0.44 |
| 1:A:70:PRO:HB2 | 2:A:454:HOH:O | 2.17 | 0.44 |
| 1:B:139:PRO:HB2 | 1:B:140:ILE:HD12 | 2.00 | 0.44 |
| 1:B:146:GLY:CA | 1:B:178:SER:HB3 | 2.46 | 0.44 |
| 1:A:238:ASN:O | 1:A:242:GLU:CB | 2.65 | 0.44 |
| 1:B:89:ILE:HD13 | 1:B:89:ILE:C | 2.38 | 0.44 |
| 1:B:119:ARG:NE | 1:B:186:GLU:OE2 | 2.48 | 0.44 |
| 1:B:236:VAL:CG1 | 1:B:274:ILE:HG13 | 2.43 | 0.44 |
| 1:B:401:ARG:HE | 1:B:401:ARG:HB3 | 1.47 | 0.44 |
| 1:A:275:THR:OG1 | 1:A:278:GLY:O | 2.33 | 0.44 |
| 1:B:148:ALA:HB2 | 1:B:175:PHE:CD2 | 2.52 | 0.43 |
| 1:B:54:LEU:HD23 | 1:B:54:LEU:HA | 1.81 | 0.43 |
| 1:A:393:LYS:O | 1:A:397:TYR:CD2 | 2.69 | 0.43 |
| 1:B:387:LYS:HB3 | 1:B:387:LYS:HE3 | 1.87 | 0.43 |
| 1:A:28:LEU:HA | 1:A:28:LEU:HD12 | 1.76 | 0.43 |
| 1:A:360:VAL:CG1 | 1:A:380:LEU:HD22 | 2.48 | 0.43 |
| 1:A:75:VAL:O | 1:A:94:LYS:HG3 | 2.17 | 0.43 |
| 1:B:18:LYS:HA | 1:B:18:LYS:HD2 | 1.81 | 0.43 |
| 1:B:90:PHE:CD2 | 1:B:266:GLY:HA2 | 2.52 | 0.43 |
| 1:B:148:ALA:HB1 | 1:B:175:PHE:CD2 | 2.52 | 0.43 |
| 1:A:80:ASP:O | 1:A:84:LYS:HG3 | 2.19 | 0.43 |
| 1:A:215:ARG:HH12 | 1:A:224:ASN:ND2 | 2.10 | 0.43 |
| 1:A:352:LEU:HD11 | 1:A:402:TYR:HB2 | 2.00 | 0.43 |
| 1:A:121:GLU:O | 1:A:184:ILE:HD13 | 2.19 | 0.43 |
| 1:A:196:ILE:HG13 | 1:A:269:TYR:HA | 2.01 | 0.43 |
| 1:A:401:ARG:HE | 1:A:401:ARG:HB3 | 1.54 | 0.43 |
| 1:B:52:GLU:HB2 | 1:B:85:ARG:HH22 | 1.82 | 0.43 |
| 1:B:139:PRO:HB2 | 1:B:140:ILE:CD1 | 2.49 | 0.43 |
| 1:A:294:GLN:O | 1:A:298:MET:HG3 | 2.19 | 0.42 |
| 1:B:158:THR:O | 1:B:161:LYS:N | 2.51 | 0.42 |
| 1:B:252:ARG:HH11 | 1:B:252:ARG:HD2 | 1.65 | 0.42 |
| 1:B:102:SER:OG | 1:B:145:ASP:OD1 | 2.27 | 0.42 |
| 1:A:74:LEU:HA | 1:A:74:LEU:HD23 | 1.53 | 0.42 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:B:28:LEU:HD12 | 1:B:28:LEU:HA | 1.81 | 0.42 |
| 1:A:100:GLU:OE1 | 1:A:287:ARG:HD3 | 2.19 | 0.42 |
| 1:B:216:LEU:HB3 | 1:B:223:PRO:HD2 | 2.00 | 0.42 |
| 1:B:24:LEU:HD11 | 1:B:306:GLU:HB2 | 2.00 | 0.42 |
| 1:B:233:PRO:HD2 | 1:B:325:TYR:CD1 | 2.54 | 0.42 |
| 1:A:211:GLN:O | 1:A:230:ALA:HA | 2.19 | 0.42 |
| 1:A:59:LYS:HE2 | 1:A:85:ARG:NH2 | 2.24 | 0.42 |
| 1:A:260:GLU:HB2 | 1:A:262:ILE:CG1 | 2.43 | 0.42 |
| 1:B:95:GLU:OE2 | 1:B:262:ILE:CD1 | 2.67 | 0.42 |
| 1:A:7:GLY:CA | 1:A:12:GLU:HG2 | 2.49 | 0.41 |
| 1:A:79:VAL:HB | 1:A:93:ASN:HA | 2.02 | 0.41 |
| 1:A:138:ALA:HA | 1:A:139:PRO:C | 2.41 | 0.41 |
| 1:A:216:LEU:O | 1:A:409:HIS:CE1 | 2.61 | 0.41 |
| 1:A:269:TYR:CD1 | 1:A:269:TYR:C | 2.94 | 0.41 |
| 1:A:400:ILE:HG21 | 1:A:410:TYR:CZ | 2.55 | 0.41 |
| 1:A:22:SER:HA | 1:A:23:PRO:HD3 | 1.72 | 0.41 |
| 1:B:200:ASN:HB2 | 1:B:311:PHE:CE2 | 2.55 | 0.41 |
| 1:B:276:LYS:CG | 1:B:277:GLU:OE2 | 2.65 | 0.41 |
| 1:A:390:LYS:HE2 | 1:A:394:GLU:OE2 | 2.20 | 0.41 |
| 1:A:196:ILE:HG13 | 1:A:269:TYR:HB2 | 2.03 | 0.41 |
| 1:A:236:VAL:CG1 | 1:A:274:ILE:HD13 | 2.51 | 0.41 |
| 1:A:119:ARG:H | 1:A:186:GLU:CG | 2.33 | 0.41 |
| 1:B:197:VAL:HA | 1:B:206:PRO:HA | 2.02 | 0.41 |
| 1:B:199:ILE:CD1 | 1:B:204:TYR:HB2 | 2.50 | 0.41 |
| 1:B:211:GLN:O | 1:B:230:ALA:HA | 2.21 | 0.41 |
| 1:A:234:THR:HA | 1:A:235:PRO:HD2 | 1.91 | 0.41 |
| 1:A:308:LEU:HA | 1:A:308:LEU:HD23 | 1.74 | 0.41 |
| 1:B:84:LYS:HE2 | 1:B:84:LYS:HB3 | 1.65 | 0.41 |
| 1:B:149:ALA:C | 1:B:151:LYS:H | 2.23 | 0.41 |
| 1:A:120:TYR:CD1 | 1:A:122:VAL:HG23 | 2.55 | 0.41 |
| 1:A:231:TYR:CE2 | 1:A:415:GLY:HA2 | 2.56 | 0.41 |
| 1:B:339:LYS:HA | 1:B:340:PRO:HD2 | 1.71 | 0.41 |
| 1:A:19:VAL:C | 1:A:21:GLN:H | 2.24 | 0.41 |
| 1:B:144:ALA:HB2 | 1:B:179:SER:OG | 2.21 | 0.41 |
| 1:A:393:LYS:HG3 | 1:A:397:TYR:HE2 | 1.86 | 0.40 |
| 1:B:5:VAL:O | 1:B:30:VAL:HA | 2.21 | 0.40 |
| 1:B:188:LEU:HD12 | 1:B:282:LEU:HD23 | 2.03 | 0.40 |
| 1:A:198:MET:N | 1:A:205:VAL:O | 2.52 | 0.40 |
| 1:A:395:ARG:HE | 1:A:395:ARG:HB2 | 1.65 | 0.40 |
| 1:A:253:VAL:CG2 | 1:A:284:PHE:CZ | 3.03 | 0.40 |
| 1:B:22:SER:HG | 1:B:24:LEU:HG | 1.86 | 0.40 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:B:140:ILE:HG21 | 1:B:184:ILE:CG2 | 2.52 | 0.40 |
| 1:B:269:TYR:OH | 1:B:292:GLU:OE2 | 2.26 | 0.40 |
| 1:A:10:GLY:HA2 | 1:A:362:HIS:O | 2.21 | 0.40 |
| 1:B:294:GLN:N | 1:B:295:PRO:HD2 | 2.36 | 0.40 |
| 1:A:169:PHE:O | 1:A:179:SER:HB2 | 2.22 | 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 | 421/424 (99%) | 383 (91%) | 30 (7%) | 8 (2%) | 8 | 10 |
| 1 | B | 421/424 (99%) | 366 (87%) | 48 (11%) | 7 (2%) | 9 | 11 |
| All | All | 842/848 (99%) | 749 (89%) | 78 (9%) | 15 (2%) | 8 | 10 |

All (15) Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | A | 32 | LYS |
| 1 | A | 112 | LYS |
| 1 | A | 139 | PRO |
| 1 | B | 32 | LYS |
| 1 | B | 130 | LYS |
| 1 | B | 364 | GLY |
| 1 | A | 130 | LYS |
| 1 | A | 277 | GLU |
| 1 | B | 173 | LYS |
| 1 | B | 176 | GLY |
| 1 | B | 363 | ALA |
| 1 | A | 303 | ASP |
| 1 | A | 363 | ALA |

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| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | B | 139 | PRO |
| 1 | A | 150 | GLY |

### 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 | 324/351 (92%) | 299 (92%) | 25 (8%) | 13 20 |
| 1 | B | 321/351 (92%) | 282 (88%) | 39 (12%) | 5 6 |
| All | All | 645/702 (92%) | 581 (90%) | 64 (10%) | 8 11 |

All (64) residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | A | 67 | ILE |
| 1 | A | 85 | ARG |
| 1 | A | 95 | GLU |
| 1 | A | 102 | SER |
| 1 | A | 107 | LYS |
| 1 | A | 124 | THR |
| 1 | A | 139 | PRO |
| 1 | A | 177 | LYS |
| 1 | A | 180 | GLU |
| 1 | A | 184 | ILE |
| 1 | A | 186 | GLU |
| 1 | A | 203 | ARG |
| 1 | A | 215 | ARG |
| 1 | A | 240 | GLU |
| 1 | A | 252 | ARG |
| 1 | A | 265 | ARG |
| 1 | A | 269 | TYR |
| 1 | A | 287 | ARG |
| 1 | A | 294 | GLN |
| 1 | A | 313 | GLU |
| 1 | A | 331 | LEU |

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| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | A | 338 | GLU |
| 1 | A | 339 | LYS |
| 1 | A | 368 | GLU |
| 1 | A | 420 | LYS |
| 1 | B | 1 | MET |
| 1 | B | 27 | GLU |
| 1 | B | 40 | ILE |
| 1 | B | 46 | ILE |
| 1 | B | 52 | GLU |
| 1 | B | 54 | LEU |
| 1 | B | 80 | ASP |
| 1 | B | 81 | GLU |
| 1 | B | 89 | ILE |
| 1 | B | 95 | GLU |
| 1 | B | 117 | THR |
| 1 | B | 139 | PRO |
| 1 | B | 175 | PHE |
| 1 | B | 177 | LYS |
| 1 | B | 179 | SER |
| 1 | B | 180 | GLU |
| 1 | B | 182 | VAL |
| 1 | B | 184 | ILE |
| 1 | B | 203 | ARG |
| 1 | B | 238 | ASN |
| 1 | B | 240 | GLU |
| 1 | B | 255 | LYS |
| 1 | B | 265 | ARG |
| 1 | B | 276 | LYS |
| 1 | B | 277 | GLU |
| 1 | B | 287 | ARG |
| 1 | B | 294 | GLN |
| 1 | B | 296 | ILE |
| 1 | B | 316 | ASP |
| 1 | B | 331 | LEU |
| 1 | B | 333 | SER |
| 1 | B | 339 | LYS |
| 1 | B | 346 | ILE |
| 1 | B | 368 | GLU |
| 1 | B | 387 | LYS |
| 1 | B | 401 | ARG |
| 1 | B | 408 | MET |
| 1 | B | 411 | ARG |

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| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | B | 412 | LYS |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | A | 224 | ASN |
| 1 | A | 285 | ASN |
| 1 | A | 294 | GLN |
| 1 | A | 310 | ASN |
| 1 | A | 370 | ASN |
| 1 | A | 409 | HIS |
| 1 | B | 224 | ASN |
| 1 | B | 238 | ASN |
| 1 | B | 294 | GLN |
| 1 | B | 310 | ASN |
| 1 | B | 318 | HIS |
| 1 | B | 370 | ASN |
| 1 | B | 409 | HIS |

#### 5.3.3 RNA

There are no RNA molecules in this entry.

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

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

### 5.5 Carbohydrates

There are no monosaccharides in this entry.

### 5.6 Ligand geometry

There are no ligands in this entry.

### 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues (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 | 423/424 (99%) | 0.17 | 32 (7%) 13 12 | 21, 43, 103, 125 | 0 |
| 1 | B | 423/424 (99%) | 0.42 | 43 (10%) 6 6 | 21, 46, 114, 137 | 0 |
| All | All | 846/848 (99%) | 0.30 | 75 (8%) 9 9 | 21, 44, 109, 137 | 0 |

All (75) RSRZ outliers are listed below:

| Mol | Chain | Res | Type | RSRZ |
|---|---|---|---|---|
| 1 | B | 162 | ALA | 7.8 |
| 1 | B | 179 | SER | 7.6 |
| 1 | B | 184 | ILE | 7.2 |
| 1 | B | 142 | VAL | 6.7 |
| 1 | B | 182 | VAL | 6.5 |
| 1 | B | 123 | PHE | 6.4 |
| 1 | B | 153 | ALA | 6.4 |
| 1 | B | 140 | ILE | 6.2 |
| 1 | B | 154 | VAL | 5.8 |
| 1 | B | 118 | ALA | 5.7 |
| 1 | A | 165 | THR | 5.3 |
| 1 | B | 141 | VAL | 5.3 |
| 1 | B | 143 | LYS | 4.9 |
| 1 | B | 149 | ALA | 4.9 |
| 1 | A | 140 | ILE | 4.8 |
| 1 | B | 129 | ALA | 4.7 |
| 1 | B | 124 | THR | 4.3 |
| 1 | B | 183 | VAL | 4.3 |
| 1 | A | 162 | ALA | 4.3 |
| 1 | B | 139 | PRO | 4.2 |
| 1 | A | 170 | LEU | 4.2 |
| 1 | B | 119 | ARG | 4.1 |
| 1 | A | 154 | VAL | 4.1 |
| 1 | B | 122 | VAL | 4.1 |

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| Mol | Chain | Res | Type | RSRZ |
|---|---|---|---|---|
| 1 | B | 170 | LEU | 4.0 |
| 1 | A | 169 | PHE | 4.0 |
| 1 | B | 156 | CYS | 4.0 |
| 1 | B | 175 | PHE | 4.0 |
| 1 | B | 137 | GLY | 3.9 |
| 1 | A | 141 | VAL | 3.8 |
| 1 | B | 152 | GLY | 3.8 |
| 1 | B | 133 | VAL | 3.7 |
| 1 | B | 120 | TYR | 3.6 |
| 1 | A | 159 | VAL | 3.6 |
| 1 | A | 124 | THR | 3.5 |
| 1 | B | 155 | VAL | 3.5 |
| 1 | A | 164 | GLU | 3.4 |
| 1 | A | 184 | ILE | 3.3 |
| 1 | B | 138 | ALA | 3.3 |
| 1 | B | 125 | ASP | 3.3 |
| 1 | A | 161 | LYS | 3.2 |
| 1 | A | 156 | CYS | 3.1 |
| 1 | A | 158 | THR | 3.1 |
| 1 | A | 123 | PHE | 3.0 |
| 1 | A | 175 | PHE | 3.0 |
| 1 | B | 169 | PHE | 2.9 |
| 1 | B | 160 | GLU | 2.9 |
| 1 | B | 187 | PHE | 2.9 |
| 1 | B | 165 | THR | 2.9 |
| 1 | A | 122 | VAL | 2.9 |
| 1 | B | 176 | GLY | 2.8 |
| 1 | B | 159 | VAL | 2.8 |
| 1 | A | 171 | ASN | 2.8 |
| 1 | B | 132 | TYR | 2.8 |
| 1 | B | 181 | ARG | 2.7 |
| 1 | B | 121 | GLU | 2.7 |
| 1 | A | 133 | VAL | 2.7 |
| 1 | A | 153 | ALA | 2.6 |
| 1 | A | 168 | ARG | 2.6 |
| 1 | A | 129 | ALA | 2.5 |
| 1 | A | 163 | ILE | 2.5 |
| 1 | A | 119 | ARG | 2.4 |
| 1 | B | 99 | LEU | 2.4 |
| 1 | A | 137 | GLY | 2.4 |
| 1 | A | 118 | ALA | 2.3 |
| 1 | A | 138 | ALA | 2.3 |

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| Mol | Chain | Res | Type | RSRZ |
|---|---|---|---|---|
| 1 | A | 157 | GLU | 2.2 |
| 1 | A | 139 | PRO | 2.2 |
| 1 | A | 152 | GLY | 2.2 |
| 1 | B | 104 | ALA | 2.2 |
| 1 | B | 145 | ASP | 2.1 |
| 1 | B | 171 | ASN | 2.1 |
| 1 | A | 142 | VAL | 2.1 |
| 1 | A | 187 | PHE | 2.0 |
| 1 | B | 157 | GLU | 2.0 |

## 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 monosaccharides in this entry.

## 6.4 Ligands (i)

There are no ligands in this entry.

## 6.5 Other polymers (i)

There are no such residues in this entry.