# Full wwPDB X-ray Structure Validation Report (i)

Mar 9, 2024 – 07:37 PM EST

| | | |
|---|---|---|
| PDB ID | : | 3LPX |
| Title | : | Crystal structure of GyrA |
| Authors | : | Jung, H.Y.; Heo, Y.S. |
| Deposited on | : | 2010-02-07 |
| Resolution | : | 2.60 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 (i) 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 (1)) were used in the production of this report:

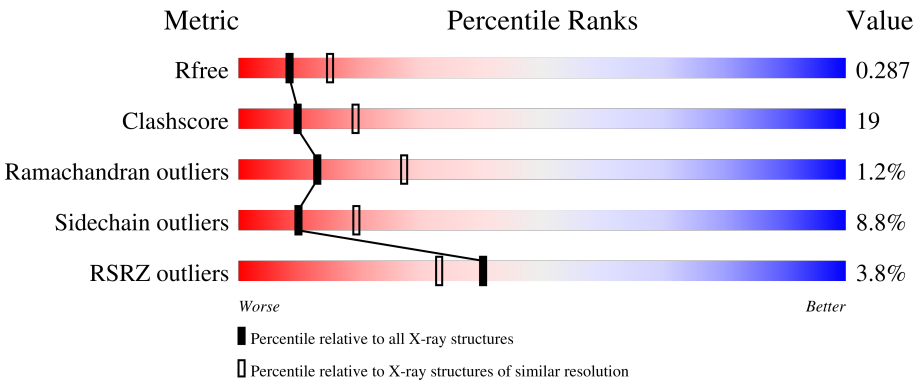
| | | |
|---|---|---|
| MolProbity | : | 4.02b-467 |
| Xtriage (Phenix) | : | 1.13 |
| EDS | : | 2.36 |
| Percentile statistics | : | 20191225.v01 (using entries in the PDB archive December 25th 2019) |
| Refmac | : | 5.8.0158 |
| CCP4 | : | 7.0.044 (Gargrove) |
| Ideal geometry (proteins) | : | Engh & 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 2.60 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 | 3163 (2.60-2.60) |
| Clashscore | 141614 | 3518 (2.60-2.60) |
| Ramachandran outliers | 138981 | 3455 (2.60-2.60) |
| Sidechain outliers | 138945 | 3455 (2.60-2.60) |
| RSRZ outliers | 127900 | 3104 (2.60-2.60) |

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 | 500 | 2%, 58%, 30%, •, 8% |
| 1 | B | 500 | 5%, 57%, 29%, 5%, •, 8% |

# 2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 7331 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called DNA gyrase, A subunit.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | | |
| 1 | A | 462 | 3644 | 2296 | 643 | 687 | 18 | 0 | 0 | 0 |
| 1 | B | 458 | 3608 | 2275 | 637 | 678 | 18 | 0 | 0 | 0 |

There are 18 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|---|---|---|---|---|---|
| A | 31 | MET | - | expression tag | UNP Q482G7 |
| A | 523 | LEU | - | expression tag | UNP Q482G7 |
| A | 524 | GLU | - | expression tag | UNP Q482G7 |
| A | 525 | HIS | - | expression tag | UNP Q482G7 |
| A | 526 | HIS | - | expression tag | UNP Q482G7 |
| A | 527 | HIS | - | expression tag | UNP Q482G7 |
| A | 528 | HIS | - | expression tag | UNP Q482G7 |
| A | 529 | HIS | - | expression tag | UNP Q482G7 |
| A | 530 | HIS | - | expression tag | UNP Q482G7 |
| B | 31 | MET | - | expression tag | UNP Q482G7 |
| B | 523 | LEU | - | expression tag | UNP Q482G7 |
| B | 524 | GLU | - | expression tag | UNP Q482G7 |
| B | 525 | HIS | - | expression tag | UNP Q482G7 |
| B | 526 | HIS | - | expression tag | UNP Q482G7 |
| B | 527 | HIS | - | expression tag | UNP Q482G7 |
| B | 528 | HIS | - | expression tag | UNP Q482G7 |
| B | 529 | HIS | - | expression tag | UNP Q482G7 |
| B | 530 | HIS | - | expression tag | UNP Q482G7 |

- Molecule 2 is water.

| Mol | Chain | Residues | Atoms | | ZeroOcc | AltConf |
|---|---|---|---|---|---|---|
| | | | Total | O | | |
| 2 | A | 44 | 44 | 44 | 0 | 0 |

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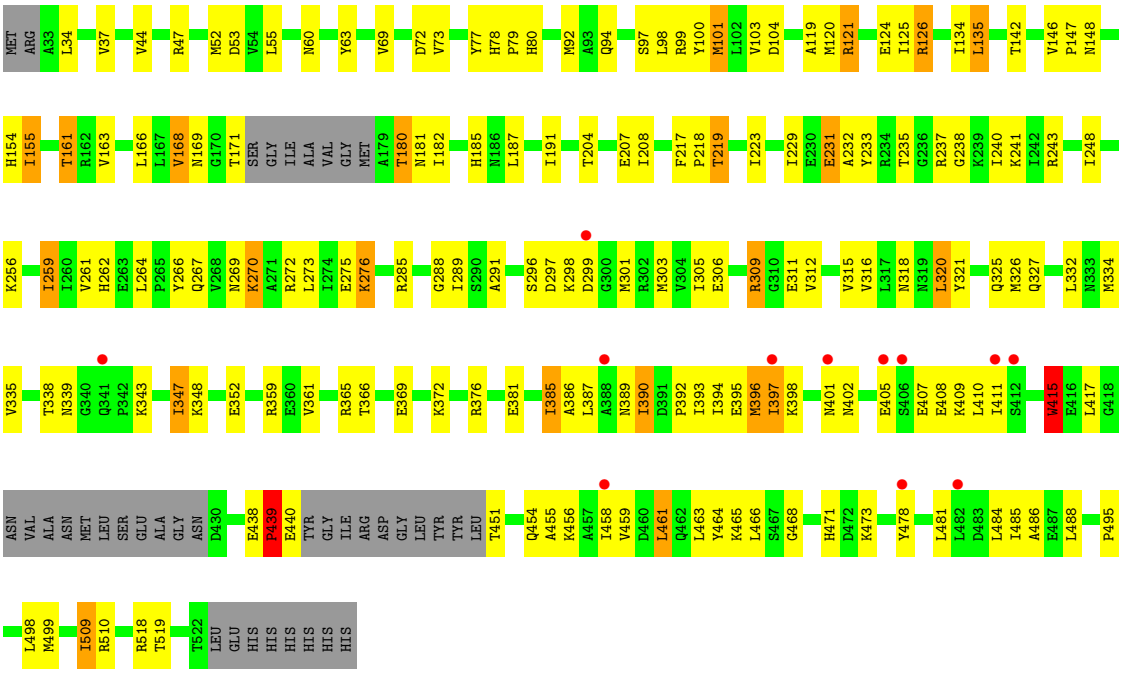
| Mol | Chain | Residues | Atoms | | ZeroOcc | AltConf |
|---|---|---|---|---|---|---|
| | | | Total | O | | |
| 2 | B | 35 | 35 | 35 | 0 | 0 |

# 3 Residue-property plots (i)

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

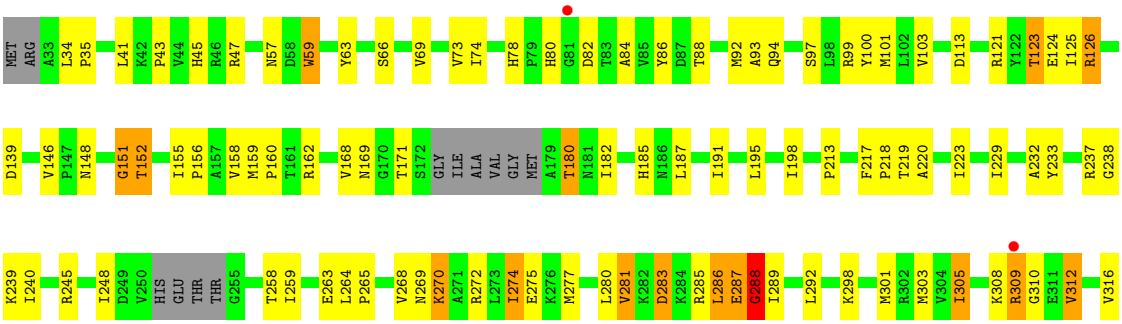
• Molecule 1: DNA gyrase, A subunit

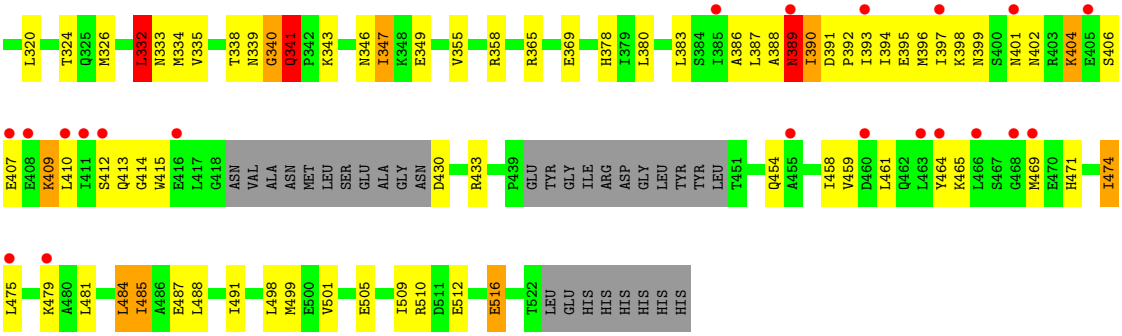
Chain A:




• Molecule 1: DNA gyrase, A subunit

Chain B:




L320
T324
Q325
M326
L332
N333
M334
V335
T338
N339
G340
Q341
P342
K343
N346
I347
K348
E349
V355
R358
R365
E369
H378
I379
L380
L383
S384
I385
A386
L387
A388
N389
I390
D391
P392
I393
I394
E395
M396
I397
K398
N399
S400
N401
N402
R403
K404
E405
S406
E407
E408
K409
L410
I411
S412
Q413
G414
W415
E416
L417
G418
ASN
VAL
ALA
ASN
MET
LEU
SER
GLU
ALA
GLY
ASN
D430
R433
P439
GLU
TYR
GLY
ILE
ARG
ASP
GLY
LEU
TYR
TYR
LEU
T451
Q454
A455
I458
V459
D460
L461
Q462
L463
Y464
K465
L466
S467
G468
M469
E470
H471
I474
L475
K479
A480
L481
L484
I485
A486
E487
L488
I491
L498
M499
E500
V501
E505
I509
R510
D511
E512
E516
T522
LEU
GLU
HIS
HIS
HIS
HIS
HIS
HIS

# 4 Data and refinement statistics (i)

| Property | Value | Source |
|---|---|---|
| Space group | P 21 21 21 | Depositor |
| Cell constants<br>a, b, c, $\alpha$, $\beta$, $\gamma$ | 98.98Å 101.56Å 141.83Å<br>90.00° 90.00° 90.00° | Depositor |
| Resolution (Å) | 41.29 – 2.60<br>41.28 – 2.60 | Depositor<br>EDS |
| % Data completeness<br>(in resolution range) | 97.1 (41.29-2.60)<br>96.9 (41.28-2.60) | Depositor<br>EDS |
| $R_{merge}$ | (Not available) | Depositor |
| $R_{sym}$ | (Not available) | Depositor |
| $< I/\sigma(I) >$ [1] | 3.02 (at 2.61Å) | Xtriage |
| Refinement program | CNS | Depositor |
| R, $R_{free}$ | 0.262 , 0.287<br>0.262 , 0.287 | Depositor<br>DCC |
| $R_{free}$ test set | 2169 reflections (5.00%) | wwPDB-VP |
| Wilson B-factor (Å$^2$) | 50.6 | Xtriage |
| Anisotropy | 0.467 | Xtriage |
| Bulk solvent $k_{sol}$(e/Å$^3$), $B_{sol}$(Å$^2$) | 0.39 , 54.6 | EDS |
| L-test for twinning[2] | $< \|L\| > = 0.49$, $< L^2 > = 0.31$ | Xtriage |
| Estimated twinning fraction | 0.017 for k,h,-l | Xtriage |
| $F_o$,$F_c$ correlation | 0.91 | EDS |
| Total number of atoms | 7331 | wwPDB-VP |
| Average B, all atoms (Å$^2$) | 49.0 | wwPDB-VP |

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.18% 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 (i)

## 5.1 Standard geometry (i)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

| Mol | Chain | Bond lengths | | Bond angles | |
|---|---|---|---|---|---|
| | | RMSZ | $\#\|Z\|>5$ | RMSZ | $\#\|Z\|>5$ |
| 1 | A | 0.52 | 0/3700 | 0.84 | 5/4995 (0.1%) |
| 1 | B | 0.55 | 0/3662 | 0.87 | 8/4941 (0.2%) |
| All | All | 0.53 | 0/7362 | 0.85 | 13/9936 (0.1%) |

There are no bond length outliers.

All (13) bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 1 | A | 80 | HIS | N-CA-C | 6.19 | 127.72 | 111.00 |
| 1 | A | 397 | ILE | N-CA-C | -6.12 | 94.49 | 111.00 |
| 1 | B | 340 | GLY | N-CA-C | -5.73 | 98.76 | 113.10 |
| 1 | A | 417 | LEU | CA-CB-CG | 5.68 | 128.36 | 115.30 |
| 1 | B | 341 | GLN | CB-CA-C | -5.61 | 99.17 | 110.40 |
| 1 | B | 151 | GLY | N-CA-C | -5.41 | 99.59 | 113.10 |
| 1 | A | 415 | TRP | N-CA-C | 5.29 | 125.29 | 111.00 |
| 1 | B | 288 | GLY | N-CA-C | 5.29 | 126.31 | 113.10 |
| 1 | B | 414 | GLY | N-CA-C | -5.24 | 100.01 | 113.10 |
| 1 | A | 396 | MET | CB-CA-C | -5.22 | 99.95 | 110.40 |
| 1 | B | 332 | LEU | CA-CB-CG | 5.16 | 127.17 | 115.30 |
| 1 | B | 310 | GLY | N-CA-C | -5.14 | 100.24 | 113.10 |
| 1 | B | 152 | THR | N-CA-C | 5.08 | 124.70 | 111.00 |

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|---|---|---|---|---|---|---|
| 1 | A | 3644 | 0 | 3700 | 142 | 0 |
| 1 | B | 3608 | 0 | 3671 | 147 | 0 |
| 2 | A | 44 | 0 | 0 | 3 | 0 |
| 2 | B | 35 | 0 | 0 | 0 | 0 |
| All | All | 7331 | 0 | 7371 | 282 | 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 19.

All (282) 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:308:LYS:O | 1:B:309:ARG:HG3 | 1.22 | 1.36 |
| 1:A:321:TYR:O | 1:A:327:GLN:HG2 | 1.61 | 1.00 |
| 1:B:308:LYS:O | 1:B:309:ARG:CG | 2.12 | 0.96 |
| 1:A:395:GLU:HG3 | 1:A:398:LYS:HB2 | 1.51 | 0.93 |
| 1:A:459:VAL:HG13 | 1:B:464:TYR:HB3 | 1.48 | 0.92 |
| 1:A:291:ALA:HB3 | 1:A:306:GLU:HG3 | 1.51 | 0.92 |
| 1:B:289:ILE:HD11 | 1:B:316:VAL:HG11 | 1.54 | 0.90 |
| 1:B:155:ILE:HG13 | 1:B:156:PRO:HD2 | 1.52 | 0.89 |
| 1:A:243:ARG:NH1 | 1:A:327:GLN:HB2 | 1.92 | 0.85 |
| 1:B:182:ILE:HD11 | 1:B:334:MET:HA | 1.59 | 0.84 |
| 1:A:461:LEU:HD22 | 1:A:465:LYS:HG3 | 1.58 | 0.83 |
| 1:B:100:TYR:H | 1:B:169:ASN:HD21 | 1.26 | 0.83 |
| 1:A:297:ASP:HB3 | 1:A:299:ASP:H | 1.44 | 0.82 |
| 1:A:134:ILE:HG23 | 1:A:161:THR:HG23 | 1.61 | 0.82 |
| 1:B:410:LEU:HA | 1:B:415:TRP:HH2 | 1.46 | 0.80 |
| 1:A:395:GLU:HG2 | 1:A:396:MET:H | 1.44 | 0.80 |
| 1:A:248:ILE:O | 1:A:248:ILE:HG13 | 1.80 | 0.79 |
| 1:B:287:GLU:HG2 | 1:B:288:GLY:H | 1.48 | 0.78 |
| 1:A:191:ILE:HD11 | 1:A:509:ILE:HD11 | 1.65 | 0.78 |
| 1:A:180:THR:HG23 | 1:A:335:VAL:H | 1.48 | 0.77 |
| 1:B:388:ALA:H | 1:B:390:ILE:HD11 | 1.49 | 0.77 |
| 1:A:408:GLU:HA | 1:A:411:ILE:HG12 | 1.64 | 0.77 |
| 1:A:464:TYR:HB3 | 1:B:459:VAL:HG13 | 1.68 | 0.76 |
| 1:A:395:GLU:C | 1:A:397:ILE:H | 1.86 | 0.76 |
| 1:A:269:ASN:HB3 | 1:A:272:ARG:HE | 1.51 | 0.76 |
| 1:B:191:ILE:HD11 | 1:B:509:ILE:HD11 | 1.68 | 0.76 |
| 1:B:269:ASN:ND2 | 1:B:272:ARG:HE | 1.84 | 0.75 |
| 1:A:223:ILE:HD12 | 1:A:240:ILE:HD12 | 1.69 | 0.75 |
| 1:A:217:PHE:HE2 | 1:A:223:ILE:HD11 | 1.52 | 0.74 |
| 1:A:276:LYS:HE3 | 1:A:325:GLN:HG3 | 1.70 | 0.73 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:B:113:ASP:OD1 | 1:B:270:LYS:HB3 | 1.90 | 0.72 |
| 1:B:410:LEU:HA | 1:B:415:TRP:CH2 | 2.27 | 0.70 |
| 1:A:219:THR:HG21 | 1:A:266:TYR:HA | 1.75 | 0.69 |
| 1:A:261:VAL:HB | 1:A:303:MET:HB2 | 1.74 | 0.69 |
| 1:B:383:LEU:HD23 | 1:B:458:ILE:HD13 | 1.76 | 0.68 |
| 1:B:516:GLU:CD | 1:B:516:GLU:H | 1.94 | 0.68 |
| 1:B:103:VAL:HG11 | 1:B:125:ILE:HD12 | 1.74 | 0.68 |
| 1:B:407:GLU:HA | 1:B:410:LEU:HD12 | 1.74 | 0.68 |
| 1:B:491:ILE:HG22 | 1:B:498:LEU:HD12 | 1.76 | 0.67 |
| 1:A:204:THR:HG23 | 1:A:207:GLU:H | 1.59 | 0.67 |
| 1:A:410:LEU:HA | 1:A:415:TRP:HZ3 | 1.60 | 0.67 |
| 1:B:180:THR:HG23 | 1:B:335:VAL:HB | 1.76 | 0.67 |
| 1:A:464:TYR:HB3 | 1:B:459:VAL:CG1 | 2.26 | 0.66 |
| 1:B:217:PHE:HE2 | 1:B:223:ILE:HD11 | 1.61 | 0.66 |
| 1:A:273:LEU:HA | 1:A:276:LYS:HE2 | 1.78 | 0.66 |
| 1:A:389:ASN:O | 1:A:393:ILE:HG12 | 1.96 | 0.65 |
| 1:B:481:LEU:O | 1:B:485:ILE:HG23 | 1.97 | 0.65 |
| 1:B:43:PRO:O | 1:B:47:ARG:HG3 | 1.97 | 0.65 |
| 1:B:289:ILE:HD11 | 1:B:316:VAL:CG1 | 2.26 | 0.64 |
| 1:A:218:PRO:HA | 1:A:518:ARG:HH11 | 1.63 | 0.64 |
| 1:A:261:VAL:HG11 | 1:A:326:MET:HE1 | 1.79 | 0.63 |
| 1:B:387:LEU:HA | 1:B:390:ILE:HG13 | 1.80 | 0.63 |
| 1:B:269:ASN:HD22 | 1:B:272:ARG:HE | 1.46 | 0.62 |
| 1:B:396:MET:SD | 1:B:409:LYS:HB3 | 2.39 | 0.62 |
| 1:B:402:ASN:ND2 | 1:B:404:LYS:HB2 | 2.14 | 0.62 |
| 1:A:44:VAL:HG23 | 2:A:14:HOH:O | 2.00 | 0.61 |
| 1:B:233:TYR:HB3 | 1:B:347:ILE:CG1 | 2.30 | 0.61 |
| 1:A:259:ILE:HG12 | 1:A:305:ILE:HD13 | 1.82 | 0.61 |
| 1:A:94:GLN:HB2 | 1:A:97:SER:HB2 | 1.83 | 0.61 |
| 1:A:410:LEU:HA | 1:A:415:TRP:CZ3 | 2.36 | 0.61 |
| 1:B:182:ILE:HG13 | 1:B:334:MET:HG2 | 1.81 | 0.61 |
| 1:B:338:THR:O | 1:B:339:ASN:HB2 | 2.00 | 0.61 |
| 1:A:120:MET:HG2 | 1:A:121:ARG:HH12 | 1.65 | 0.60 |
| 1:B:454:GLN:O | 1:B:458:ILE:HG12 | 2.00 | 0.60 |
| 1:A:161:THR:HG22 | 1:A:163:VAL:H | 1.66 | 0.60 |
| 1:A:100:TYR:H | 1:A:169:ASN:HD21 | 1.50 | 0.60 |
| 1:B:265:PRO:O | 1:B:268:VAL:HG22 | 2.02 | 0.60 |
| 1:B:390:ILE:HD12 | 1:B:390:ILE:H | 1.66 | 0.60 |
| 1:A:389:ASN:O | 1:A:392:PRO:HD2 | 2.02 | 0.59 |
| 1:A:204:THR:HG22 | 1:A:207:GLU:OE1 | 2.03 | 0.59 |
| 1:A:219:THR:HG21 | 1:A:266:TYR:CA | 2.33 | 0.59 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:B:395:GLU:O | 1:B:398:LYS:HB2 | 2.01 | 0.59 |
| 1:B:475:LEU:O | 1:B:479:LYS:HG3 | 2.04 | 0.58 |
| 1:A:288:GLY:HA2 | 1:A:311:GLU:HG3 | 1.84 | 0.58 |
| 1:A:390:ILE:HD12 | 1:A:466:LEU:HD23 | 1.84 | 0.58 |
| 1:B:182:ILE:CD1 | 1:B:334:MET:HA | 2.32 | 0.58 |
| 1:B:277:MET:O | 1:B:281:VAL:HG12 | 2.04 | 0.58 |
| 1:A:465:LYS:HE3 | 2:A:547:HOH:O | 2.03 | 0.58 |
| 1:B:155:ILE:HG13 | 1:B:156:PRO:CD | 2.28 | 0.58 |
| 1:A:359:ARG:HD3 | 1:A:499:MET:SD | 2.44 | 0.58 |
| 1:B:316:VAL:O | 1:B:320:LEU:HB2 | 2.04 | 0.57 |
| 1:A:401:ASN:O | 1:B:469:MET:HG2 | 2.05 | 0.57 |
| 1:B:365:ARG:O | 1:B:369:GLU:HG2 | 2.05 | 0.57 |
| 1:A:365:ARG:O | 1:A:369:GLU:HG2 | 2.05 | 0.56 |
| 1:A:182:ILE:HG12 | 1:A:334:MET:HG2 | 1.88 | 0.56 |
| 1:B:100:TYR:CD2 | 1:B:168:VAL:HG13 | 2.40 | 0.56 |
| 1:A:101:MET:H | 1:A:101:MET:CE | 2.19 | 0.56 |
| 1:B:410:LEU:O | 1:B:415:TRP:HZ3 | 1.87 | 0.56 |
| 1:A:262:HIS:C | 1:A:301:MET:HE2 | 2.26 | 0.56 |
| 1:A:309:ARG:HH11 | 1:A:309:ARG:HG2 | 1.70 | 0.56 |
| 1:B:474:ILE:HD13 | 1:B:475:LEU:N | 2.20 | 0.56 |
| 1:A:146:VAL:HB | 1:A:147:PRO:HD2 | 1.87 | 0.56 |
| 1:B:198:ILE:HD12 | 1:B:499:MET:CE | 2.36 | 0.56 |
| 1:B:387:LEU:HD13 | 1:B:471:HIS:ND1 | 2.20 | 0.56 |
| 1:A:261:VAL:HG12 | 1:A:301:MET:HE3 | 1.88 | 0.55 |
| 1:B:82:ASP:HB3 | 1:B:84:ALA:H | 1.71 | 0.55 |
| 1:B:280:LEU:HB3 | 1:B:286:LEU:HB2 | 1.88 | 0.55 |
| 1:A:63:TYR:HB3 | 1:A:124:GLU:HB3 | 1.88 | 0.55 |
| 1:A:466:LEU:H | 1:A:466:LEU:HD12 | 1.72 | 0.55 |
| 1:B:180:THR:HG22 | 1:B:182:ILE:CD1 | 2.36 | 0.55 |
| 1:B:474:ILE:HD13 | 1:B:475:LEU:H | 1.72 | 0.55 |
| 1:A:390:ILE:HD12 | 1:B:398:LYS:HE2 | 1.89 | 0.55 |
| 1:B:180:THR:HG21 | 1:B:335:VAL:O | 2.07 | 0.55 |
| 1:A:264:LEU:HD11 | 1:A:270:LYS:HG3 | 1.89 | 0.55 |
| 1:A:37:VAL:HA | 1:A:166:LEU:HD22 | 1.90 | 0.55 |
| 1:B:389:ASN:O | 1:B:393:ILE:HG12 | 2.07 | 0.54 |
| 1:A:338:THR:HG23 | 1:A:339:ASN:H | 1.71 | 0.54 |
| 1:B:233:TYR:CG | 1:B:347:ILE:HG12 | 2.42 | 0.54 |
| 1:B:430:ASP:O | 1:B:433:ARG:HG2 | 2.07 | 0.54 |
| 1:A:134:ILE:HA | 1:A:161:THR:HG23 | 1.90 | 0.54 |
| 1:B:338:THR:O | 1:B:338:THR:HG23 | 2.08 | 0.53 |
| 1:A:218:PRO:HA | 1:A:518:ARG:NH1 | 2.23 | 0.53 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:A:395:GLU:C | 1:A:397:ILE:N | 2.56 | 0.53 |
| 1:A:466:LEU:HD12 | 1:A:466:LEU:N | 2.24 | 0.53 |
| 1:A:187:LEU:O | 1:A:191:ILE:HG12 | 2.09 | 0.53 |
| 1:A:387:LEU:HB3 | 1:A:471:HIS:CE1 | 2.43 | 0.53 |
| 1:A:55:LEU:HD11 | 1:A:72:ASP:OD2 | 2.08 | 0.52 |
| 1:A:229:ILE:HD13 | 1:A:240:ILE:HG21 | 1.92 | 0.52 |
| 1:B:245:ARG:HB3 | 1:B:263:GLU:CG | 2.39 | 0.52 |
| 1:A:458:ILE:O | 1:A:461:LEU:HB2 | 2.09 | 0.52 |
| 1:A:407:GLU:OE2 | 1:A:456:LYS:HG2 | 2.10 | 0.52 |
| 1:A:185:HIS:HE1 | 1:A:233:TYR:OH | 1.93 | 0.52 |
| 1:B:340:GLY:O | 1:B:341:GLN:HB2 | 2.11 | 0.51 |
| 1:B:66:SER:OG | 1:B:123:THR:HG23 | 2.10 | 0.51 |
| 1:B:103:VAL:CG1 | 1:B:125:ILE:HD12 | 2.38 | 0.51 |
| 1:A:312:VAL:HG11 | 1:A:315:VAL:HG23 | 1.92 | 0.51 |
| 1:A:99:ARG:HA | 1:A:218:PRO:HB3 | 1.93 | 0.51 |
| 1:A:142:THR:HB | 1:A:361:VAL:HG13 | 1.91 | 0.51 |
| 1:B:484:LEU:HD22 | 1:B:488:LEU:HG | 1.92 | 0.51 |
| 1:B:94:GLN:HB2 | 1:B:97:SER:HB2 | 1.93 | 0.50 |
| 1:B:69:VAL:O | 1:B:73:VAL:HG23 | 2.10 | 0.50 |
| 1:B:63:TYR:CE1 | 1:B:126:ARG:HD2 | 2.46 | 0.50 |
| 1:B:346:ASN:ND2 | 1:B:349:GLU:HG3 | 2.27 | 0.50 |
| 1:B:378:HIS:CE1 | 1:B:454:GLN:HG3 | 2.47 | 0.50 |
| 1:B:248:ILE:HG12 | 1:B:259:ILE:HD13 | 1.92 | 0.50 |
| 1:B:404:LYS:HE3 | 1:B:404:LYS:N | 2.26 | 0.50 |
| 1:B:182:ILE:HD12 | 1:B:182:ILE:N | 2.27 | 0.50 |
| 1:A:100:TYR:CD2 | 1:A:168:VAL:HG13 | 2.47 | 0.49 |
| 1:B:237:ARG:HA | 1:B:332:LEU:O | 2.12 | 0.49 |
| 1:A:119:ALA:HB1 | 1:A:121:ARG:CZ | 2.42 | 0.49 |
| 1:B:233:TYR:HB3 | 1:B:347:ILE:HD11 | 1.94 | 0.49 |
| 1:A:393:ILE:O | 1:A:397:ILE:HD13 | 2.13 | 0.49 |
| 1:A:231:GLU:O | 1:A:235:THR:HB | 2.13 | 0.49 |
| 1:B:74:ILE:HA | 1:B:78:HIS:O | 2.13 | 0.49 |
| 1:B:245:ARG:HB3 | 1:B:263:GLU:HG2 | 1.94 | 0.49 |
| 1:A:261:VAL:HG12 | 1:A:301:MET:CE | 2.43 | 0.48 |
| 1:B:285:ARG:HG3 | 1:B:285:ARG:HH11 | 1.78 | 0.48 |
| 1:B:63:TYR:HB3 | 1:B:124:GLU:HB3 | 1.95 | 0.48 |
| 1:B:223:ILE:HD12 | 1:B:240:ILE:HD12 | 1.95 | 0.48 |
| 1:A:134:ILE:CG2 | 1:A:161:THR:HG23 | 2.39 | 0.48 |
| 1:A:264:LEU:HG | 1:A:301:MET:CE | 2.44 | 0.48 |
| 1:A:366:THR:HG23 | 1:A:488:LEU:HD22 | 1.96 | 0.48 |
| 1:A:223:ILE:HG12 | 1:A:519:THR:HG21 | 1.95 | 0.48 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:A:264:LEU:HG | 1:A:301:MET:SD | 2.54 | 0.48 |
| 1:A:395:GLU:O | 1:A:396:MET:HB2 | 2.13 | 0.48 |
| 1:A:101:MET:H | 1:A:101:MET:HE3 | 1.78 | 0.48 |
| 1:B:380:LEU:HD23 | 1:B:383:LEU:HD12 | 1.96 | 0.48 |
| 1:B:274:ILE:HG22 | 1:B:292:LEU:HD13 | 1.96 | 0.48 |
| 1:A:219:THR:HG21 | 1:A:266:TYR:N | 2.30 | 0.47 |
| 1:B:171:THR:HG22 | 1:B:182:ILE:HB | 1.95 | 0.47 |
| 1:A:389:ASN:O | 1:A:389:ASN:OD1 | 2.32 | 0.47 |
| 1:A:455:ALA:O | 1:A:459:VAL:HB | 2.15 | 0.47 |
| 1:A:464:TYR:CB | 1:B:459:VAL:HG13 | 2.42 | 0.47 |
| 1:A:509:ILE:HG13 | 1:A:510:ARG:N | 2.29 | 0.47 |
| 1:B:396:MET:SD | 1:B:409:LYS:O | 2.72 | 0.47 |
| 1:B:413:GLN:HB2 | 1:B:415:TRP:CZ3 | 2.50 | 0.47 |
| 1:B:461:LEU:HD11 | 1:B:465:LYS:HB2 | 1.97 | 0.47 |
| 1:B:35:PRO:HG3 | 1:B:171:THR:HG21 | 1.97 | 0.47 |
| 1:A:297:ASP:HB3 | 1:A:299:ASP:N | 2.22 | 0.47 |
| 1:A:134:ILE:HG12 | 1:A:161:THR:CG2 | 2.45 | 0.47 |
| 1:B:125:ILE:CG2 | 1:B:126:ARG:N | 2.78 | 0.47 |
| 1:A:270:LYS:HE2 | 1:A:296:SER:OG | 2.15 | 0.46 |
| 1:A:338:THR:HG23 | 1:A:339:ASN:N | 2.30 | 0.46 |
| 1:A:390:ILE:O | 1:A:394:ILE:HG12 | 2.15 | 0.46 |
| 1:A:395:GLU:HG2 | 1:A:396:MET:N | 2.23 | 0.46 |
| 1:A:103:VAL:HG13 | 1:A:125:ILE:HG13 | 1.97 | 0.46 |
| 1:A:454:GLN:O | 1:A:458:ILE:HD13 | 2.16 | 0.46 |
| 1:B:180:THR:CG2 | 1:B:335:VAL:O | 2.64 | 0.46 |
| 1:A:163:VAL:HG22 | 1:A:509:ILE:HD13 | 1.97 | 0.46 |
| 1:A:335:VAL:HA | 1:A:343:LYS:O | 2.15 | 0.46 |
| 1:B:99:ARG:HA | 1:B:218:PRO:HB3 | 1.98 | 0.46 |
| 1:B:113:ASP:OD1 | 1:B:270:LYS:NZ | 2.48 | 0.46 |
| 1:B:237:ARG:HE | 1:B:333:ASN:ND2 | 2.14 | 0.46 |
| 1:B:413:GLN:HB2 | 1:B:415:TRP:CH2 | 2.51 | 0.46 |
| 1:B:501:VAL:O | 1:B:505:GLU:HG3 | 2.16 | 0.46 |
| 1:B:100:TYR:H | 1:B:169:ASN:ND2 | 2.05 | 0.46 |
| 1:B:185:HIS:HE1 | 1:B:233:TYR:OH | 1.98 | 0.46 |
| 1:A:63:TYR:CE1 | 1:A:126:ARG:HD2 | 2.50 | 0.46 |
| 1:B:80:HIS:C | 1:B:82:ASP:H | 2.18 | 0.46 |
| 1:B:88:THR:O | 1:B:92:MET:HG3 | 2.15 | 0.46 |
| 1:B:264:LEU:HD12 | 1:B:301:MET:HE1 | 1.97 | 0.46 |
| 1:B:387:LEU:HA | 1:B:390:ILE:CG1 | 2.44 | 0.46 |
| 1:A:235:THR:HG22 | 1:A:237:ARG:H | 1.81 | 0.46 |
| 1:B:217:PHE:CE2 | 1:B:223:ILE:HD11 | 2.47 | 0.46 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:A:312:VAL:CG1 | 1:A:315:VAL:HG23 | 2.46 | 0.45 |
| 1:B:59:TRP:HA | 1:B:126:ARG:HG3 | 1.97 | 0.45 |
| 1:B:407:GLU:O | 1:B:410:LEU:HB2 | 2.16 | 0.45 |
| 1:B:265:PRO:HD2 | 1:B:268:VAL:HG21 | 1.97 | 0.45 |
| 1:A:171:THR:HG22 | 1:A:182:ILE:HB | 1.97 | 0.45 |
| 1:B:461:LEU:CD1 | 1:B:465:LYS:HB2 | 2.46 | 0.45 |
| 1:A:52:MET:HE3 | 1:A:125:ILE:HG23 | 1.99 | 0.45 |
| 1:A:451:THR:HB | 2:A:556:HOH:O | 2.17 | 0.45 |
| 1:B:233:TYR:HB3 | 1:B:347:ILE:HG12 | 1.97 | 0.45 |
| 1:A:104:ASP:OD2 | 1:A:126:ARG:HD3 | 2.16 | 0.45 |
| 1:A:208:ILE:HD13 | 1:A:347:ILE:HG23 | 1.98 | 0.45 |
| 1:B:386:ALA:CB | 1:B:458:ILE:HD12 | 2.47 | 0.45 |
| 1:A:439:PRO:HB2 | 1:A:440:GLU:OE2 | 2.16 | 0.44 |
| 1:B:198:ILE:HD11 | 1:B:355:VAL:CG1 | 2.46 | 0.44 |
| 1:B:402:ASN:ND2 | 1:B:404:LYS:H | 2.14 | 0.44 |
| 1:A:395:GLU:O | 1:A:397:ILE:N | 2.50 | 0.44 |
| 1:B:324:THR:OG1 | 1:B:326:MET:HG2 | 2.17 | 0.44 |
| 1:A:407:GLU:HA | 1:A:410:LEU:HD13 | 1.98 | 0.44 |
| 1:B:335:VAL:HA | 1:B:343:LYS:O | 2.18 | 0.44 |
| 1:A:376:ARG:HG2 | 1:A:481:LEU:HD21 | 2.00 | 0.44 |
| 1:A:395:GLU:CG | 1:A:396:MET:H | 2.22 | 0.44 |
| 1:B:233:TYR:CB | 1:B:347:ILE:CG1 | 2.96 | 0.44 |
| 1:A:395:GLU:O | 1:A:396:MET:CB | 2.65 | 0.44 |
| 1:B:195:LEU:HD23 | 1:B:195:LEU:HA | 1.86 | 0.44 |
| 1:A:121:ARG:H | 1:A:121:ARG:HG2 | 1.64 | 0.44 |
| 1:A:348:LYS:HG2 | 1:A:352:GLU:OE2 | 2.17 | 0.44 |
| 1:A:396:MET:HE2 | 1:A:409:LYS:O | 2.18 | 0.43 |
| 1:B:402:ASN:HD22 | 1:B:404:LYS:HB2 | 1.82 | 0.43 |
| 1:A:47:ARG:NH1 | 1:A:78:HIS:HD2 | 2.16 | 0.43 |
| 1:B:162:ARG:HG3 | 1:B:358:ARG:NH2 | 2.33 | 0.43 |
| 1:B:233:TYR:CB | 1:B:347:ILE:HG12 | 2.48 | 0.43 |
| 1:B:264:LEU:HD21 | 1:B:303:MET:HE2 | 2.00 | 0.43 |
| 1:A:385:ILE:HD13 | 1:A:386:ALA:N | 2.34 | 0.43 |
| 1:B:34:LEU:HD12 | 1:B:34:LEU:N | 2.34 | 0.43 |
| 1:B:93:ALA:O | 1:B:101:MET:HE3 | 2.19 | 0.43 |
| 1:B:213:PRO:O | 1:B:229:ILE:HG21 | 2.18 | 0.43 |
| 1:A:289:ILE:HD11 | 1:A:316:VAL:HG13 | 2.01 | 0.43 |
| 1:B:219:THR:O | 1:B:220:ALA:HB3 | 2.18 | 0.43 |
| 1:B:233:TYR:HB3 | 1:B:347:ILE:CD1 | 2.49 | 0.43 |
| 1:A:402:ASN:OD1 | 1:A:405:GLU:HB3 | 2.19 | 0.43 |
| 1:B:168:VAL:HG21 | 1:B:187:LEU:HD13 | 2.01 | 0.43 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:A:69:VAL:O | 1:A:73:VAL:HG23 | 2.19 | 0.43 |
| 1:B:287:GLU:CG | 1:B:288:GLY:H | 2.17 | 0.43 |
| 1:B:347:ILE:H | 1:B:347:ILE:HG13 | 1.66 | 0.43 |
| 1:A:381:GLU:HG3 | 1:A:478:TYR:CZ | 2.54 | 0.42 |
| 1:B:391:ASP:HB2 | 1:B:392:PRO:HD3 | 2.01 | 0.42 |
| 1:A:464:TYR:HA | 1:B:397:ILE:HG21 | 2.00 | 0.42 |
| 1:B:159:MET:HA | 1:B:160:PRO:HD3 | 1.77 | 0.42 |
| 1:B:288:GLY:O | 1:B:289:ILE:HD13 | 2.19 | 0.42 |
| 1:A:273:LEU:HD21 | 1:A:326:MET:HE2 | 2.01 | 0.42 |
| 1:B:270:LYS:O | 1:B:274:ILE:HG12 | 2.20 | 0.42 |
| 1:B:283:ASP:HB2 | 1:B:285:ARG:HG3 | 2.01 | 0.42 |
| 1:A:485:ILE:HG13 | 1:A:486:ALA:N | 2.34 | 0.42 |
| 1:B:66:SER:OG | 1:B:123:THR:CG2 | 2.67 | 0.42 |
| 1:B:41:LEU:HD22 | 1:B:45:HIS:HB3 | 2.01 | 0.42 |
| 1:B:148:ASN:OD1 | 1:B:151:GLY:O | 2.38 | 0.42 |
| 1:B:312:VAL:HG23 | 1:B:312:VAL:O | 2.18 | 0.42 |
| 1:A:229:ILE:CD1 | 1:A:240:ILE:HG21 | 2.50 | 0.41 |
| 1:B:198:ILE:HD11 | 1:B:355:VAL:HG11 | 2.01 | 0.41 |
| 1:A:99:ARG:HG3 | 1:A:100:TYR:CE2 | 2.55 | 0.41 |
| 1:A:267:GLN:HE21 | 1:A:267:GLN:HB2 | 1.61 | 0.41 |
| 1:A:77:TYR:CD1 | 1:A:155:ILE:HD12 | 2.56 | 0.41 |
| 1:B:390:ILE:HG22 | 1:B:394:ILE:CD1 | 2.50 | 0.41 |
| 1:A:325:GLN:C | 1:A:327:GLN:N | 2.73 | 0.41 |
| 1:A:148:ASN:HB3 | 1:A:155:ILE:HD11 | 2.03 | 0.41 |
| 1:A:347:ILE:O | 1:A:347:ILE:HG13 | 2.21 | 0.41 |
| 1:A:320:LEU:HD12 | 1:A:320:LEU:HA | 1.85 | 0.41 |
| 1:B:125:ILE:HG22 | 1:B:126:ARG:N | 2.35 | 0.41 |
| 1:A:134:ILE:HG12 | 1:A:161:THR:HG23 | 2.03 | 0.41 |
| 1:A:395:GLU:HA | 1:A:398:LYS:HG3 | 2.02 | 0.41 |
| 1:A:92:MET:HA | 1:A:98:LEU:HD22 | 2.01 | 0.41 |
| 1:A:180:THR:HG22 | 1:A:181:ASN:H | 1.85 | 0.41 |
| 1:B:232:ALA:HB2 | 1:B:238:GLY:HA3 | 2.01 | 0.41 |
| 1:B:292:LEU:HD12 | 1:B:292:LEU:O | 2.20 | 0.41 |
| 1:B:409:LYS:HD3 | 1:B:412:SER:OG | 2.21 | 0.41 |
| 1:B:410:LEU:HD23 | 1:B:415:TRP:CH2 | 2.56 | 0.41 |
| 1:A:53:ASP:HB2 | 1:A:135:LEU:HD12 | 2.02 | 0.41 |
| 1:A:389:ASN:HD21 | 1:A:415:TRP:HD1 | 1.69 | 0.40 |
| 1:A:438:GLU:O | 1:A:440:GLU:N | 2.54 | 0.40 |
| 1:B:86:TYR:OH | 1:B:123:THR:HG21 | 2.22 | 0.40 |
| 1:B:406:SER:O | 1:B:410:LEU:HG | 2.21 | 0.40 |
| 1:B:484:LEU:HD22 | 1:B:484:LEU:O | 2.22 | 0.40 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:A:237:ARG:HA | 1:A:332:LEU:O | 2.22 | 0.40 |
| 1:B:191:ILE:HG21 | 1:B:510:ARG:HB2 | 2.03 | 0.40 |
| 1:A:180:THR:CG2 | 1:A:335:VAL:H | 2.24 | 0.40 |
| 1:A:232:ALA:HB2 | 1:A:238:GLY:HA3 | 2.03 | 0.40 |
| 1:B:259:ILE:HB | 1:B:305:ILE:HG23 | 2.03 | 0.40 |
| 1:A:180:THR:HG23 | 1:A:335:VAL:N | 2.27 | 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 | 454/500 (91%) | 430 (95%) | 21 (5%) | 3 (1%) | 22 43 |
| 1 | B | 448/500 (90%) | 410 (92%) | 30 (7%) | 8 (2%) | 8 16 |
| All | All | 902/1000 (90%) | 840 (93%) | 51 (6%) | 11 (1%) | 13 27 |

All (11) Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | A | 439 | PRO |
| 1 | B | 152 | THR |
| 1 | B | 287 | GLU |
| 1 | B | 309 | ARG |
| 1 | B | 312 | VAL |
| 1 | B | 389 | ASN |
| 1 | B | 288 | GLY |
| 1 | B | 399 | ASN |
| 1 | B | 341 | GLN |
| 1 | A | 79 | PRO |
| 1 | A | 468 | 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 | 394/424 (93%) | 357 (91%) | 37 (9%) | 8 17 |
| 1 | B | 390/424 (92%) | 358 (92%) | 32 (8%) | 11 22 |
| All | All | 784/848 (92%) | 715 (91%) | 69 (9%) | 10 19 |

All (69) residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | A | 34 | LEU |
| 1 | A | 60 | ASN |
| 1 | A | 101 | MET |
| 1 | A | 121 | ARG |
| 1 | A | 126 | ARG |
| 1 | A | 135 | LEU |
| 1 | A | 154 | HIS |
| 1 | A | 155 | ILE |
| 1 | A | 161 | THR |
| 1 | A | 168 | VAL |
| 1 | A | 180 | THR |
| 1 | A | 219 | THR |
| 1 | A | 231 | GLU |
| 1 | A | 241 | LYS |
| 1 | A | 256 | LYS |
| 1 | A | 259 | ILE |
| 1 | A | 270 | LYS |
| 1 | A | 275 | GLU |
| 1 | A | 276 | LYS |
| 1 | A | 285 | ARG |
| 1 | A | 298 | LYS |
| 1 | A | 309 | ARG |
| 1 | A | 318 | ASN |
| 1 | A | 320 | LEU |
| 1 | A | 347 | ILE |
| 1 | A | 372 | LYS |
| 1 | A | 385 | ILE |

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| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | A | 390 | ILE |
| 1 | A | 415 | TRP |
| 1 | A | 439 | PRO |
| 1 | A | 461 | LEU |
| 1 | A | 463 | LEU |
| 1 | A | 473 | LYS |
| 1 | A | 484 | LEU |
| 1 | A | 495 | PRO |
| 1 | A | 498 | LEU |
| 1 | A | 509 | ILE |
| 1 | B | 57 | ASN |
| 1 | B | 59 | TRP |
| 1 | B | 121 | ARG |
| 1 | B | 123 | THR |
| 1 | B | 126 | ARG |
| 1 | B | 139 | ASP |
| 1 | B | 146 | VAL |
| 1 | B | 158 | VAL |
| 1 | B | 180 | THR |
| 1 | B | 239 | LYS |
| 1 | B | 258 | THR |
| 1 | B | 270 | LYS |
| 1 | B | 274 | ILE |
| 1 | B | 275 | GLU |
| 1 | B | 281 | VAL |
| 1 | B | 283 | ASP |
| 1 | B | 286 | LEU |
| 1 | B | 298 | LYS |
| 1 | B | 305 | ILE |
| 1 | B | 332 | LEU |
| 1 | B | 347 | ILE |
| 1 | B | 389 | ASN |
| 1 | B | 390 | ILE |
| 1 | B | 401 | ASN |
| 1 | B | 404 | LYS |
| 1 | B | 409 | LYS |
| 1 | B | 474 | ILE |
| 1 | B | 484 | LEU |
| 1 | B | 485 | ILE |
| 1 | B | 487 | GLU |
| 1 | B | 512 | GLU |
| 1 | B | 516 | GLU |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (23) such sidechains are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | A | 78 | HIS |
| 1 | A | 106 | GLN |
| 1 | A | 169 | ASN |
| 1 | A | 185 | HIS |
| 1 | A | 192 | ASN |
| 1 | A | 267 | GLN |
| 1 | A | 318 | ASN |
| 1 | A | 339 | ASN |
| 1 | A | 413 | GLN |
| 1 | A | 471 | HIS |
| 1 | B | 57 | ASN |
| 1 | B | 106 | GLN |
| 1 | B | 169 | ASN |
| 1 | B | 181 | ASN |
| 1 | B | 185 | HIS |
| 1 | B | 262 | HIS |
| 1 | B | 319 | ASN |
| 1 | B | 333 | ASN |
| 1 | B | 357 | HIS |
| 1 | B | 389 | ASN |
| 1 | B | 401 | ASN |
| 1 | B | 402 | ASN |
| 1 | B | 413 | GLN |

### 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 monosaccharides in this entry.

## 5.6 Ligand geometry (i)

There are no ligands in this entry.

## 5.7 Other polymers (i)

There are no such residues in this entry.

## 5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

# 6 Fit of model and data (i)

## 6.1 Protein, DNA and RNA chains (i)

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 | 462/500 (92%) | 0.19 | 12 (2%) | 56 | 50 | 32, 47, 70, 87 | 0 |
| 1 | B | 458/500 (91%) | 0.28 | 23 (5%) | 28 | 23 | 31, 47, 74, 87 | 0 |
| All | All | 920/1000 (92%) | 0.24 | 35 (3%) | 40 | 33 | 31, 47, 72, 87 | 0 |

All (35) RSRZ outliers are listed below:

| Mol | Chain | Res | Type | RSRZ |
|---|---|---|---|---|
| 1 | B | 411 | ILE | 8.1 |
| 1 | B | 397 | ILE | 5.7 |
| 1 | B | 401 | ASN | 4.7 |
| 1 | B | 393 | ILE | 4.4 |
| 1 | A | 412 | SER | 4.0 |
| 1 | A | 411 | ILE | 4.0 |
| 1 | A | 397 | ILE | 3.4 |
| 1 | B | 463 | LEU | 3.4 |
| 1 | B | 412 | SER | 3.2 |
| 1 | B | 385 | ILE | 3.1 |
| 1 | B | 81 | GLY | 3.0 |
| 1 | B | 466 | LEU | 2.9 |
| 1 | B | 407 | GLU | 2.8 |
| 1 | A | 388 | ALA | 2.7 |
| 1 | B | 309 | ARG | 2.7 |
| 1 | B | 408 | GLU | 2.7 |
| 1 | B | 475 | LEU | 2.6 |
| 1 | B | 416 | GLU | 2.6 |
| 1 | A | 299 | ASP | 2.6 |
| 1 | A | 406 | SER | 2.6 |
| 1 | A | 401 | ASN | 2.5 |
| 1 | B | 405 | GLU | 2.4 |
| 1 | B | 479 | LYS | 2.4 |
| 1 | B | 455 | ALA | 2.4 |

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| Mol | Chain | Res | Type | RSRZ |
|---|---|---|---|---|
| 1 | A | 458 | ILE | 2.4 |
| 1 | B | 468 | GLY | 2.4 |
| 1 | A | 405 | GLU | 2.4 |
| 1 | B | 460 | ASP | 2.3 |
| 1 | B | 464 | TYR | 2.2 |
| 1 | B | 469 | MET | 2.2 |
| 1 | B | 410 | LEU | 2.2 |
| 1 | A | 478 | TYR | 2.2 |
| 1 | B | 389 | ASN | 2.1 |
| 1 | A | 341 | GLN | 2.1 |
| 1 | A | 482 | LEU | 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 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.