# Full wwPDB NMR Structure Validation Report (i)

Feb 17, 2022 – 07:27 AM EST

| | | |
|---|---|---|
| PDB ID | : | 1NY8 |
| Title | : | Solution structure of Protein yrbA from Escherichia Coli: Northeast Structural Genomics Consortium target ER115 |
| Authors | : | Swapna, G.V.T.; Huang, J.Y.; Acton, T.B.; Shastry, R.; Chiang, Y.-W.; Montelione, G.T.; Northeast Structural Genomics Consortium (NESG) |
| Deposited on | : | 2003-02-11 |

This is a Full wwPDB NMR 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/NMRValidationReportHelp
with specific help available everywhere you see the (i) symbol.

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

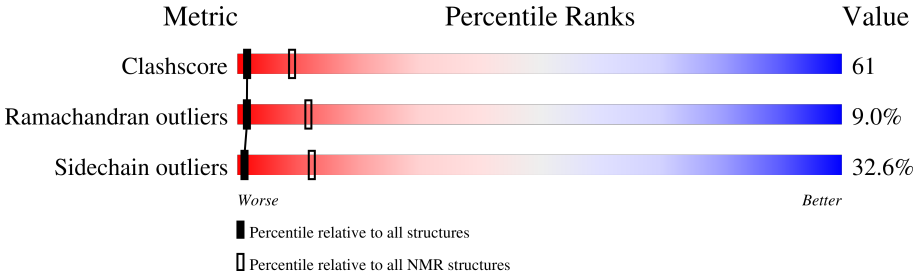
| | | |
|---|---|---|
| MolProbity | : | 4.02b-467 |
| Percentile statistics | : | 20191225.v01 (using entries in the PDB archive December 25th 2019) |
| RCI | : | v_1n_11_5_13_A (Berjanski et al., 2005) |
| PANAV | : | Wang et al. (2010) |
| ShiftChecker | : | 2.26 |
| Ideal geometry (proteins) | : | Engh & Huber (2001) |
| Ideal geometry (DNA, RNA) | : | Parkinson et al. (1996) |
| Validation Pipeline (wwPDB-VP) | : | 2.26 |

# 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
*SOLUTION NMR*

The overall completeness of chemical shifts assignment was not calculated.

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) | NMR archive (#Entries) |
|---|---|---|
| Clashscore | 158937 | 12864 |
| Ramachandran outliers | 154571 | 11451 |
| Sidechain outliers | 154315 | 11428 |

The table below summarises the geometric issues observed across the polymeric chains and their fit to the experimental data. The red, orange, yellow and green segments indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. A cyan segment indicates the fraction of residues that are not part of the well-defined cores, and 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%

| Mol | Chain | Length | Quality of chain |
|---|---|---|---|
| 1 | A | 97 | 9% 53% 13% • 24% |

# 2 Ensemble composition and analysis (i)

This entry contains 16 models. Model 10 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *lowest target function*.

The following residues are included in the computation of the global validation metrics.

| Well-defined (core) protein residues | | | |
|---|---|---|---|
| **Well-defined core** | **Residue range (total)** | **Backbone RMSD (Å)** | **Medoid model** |
| 1 | A:9-A:27, A:32-A:86 (74) | 0.25 | 10 |

Ill-defined regions of proteins are excluded from the global statistics.

Ligands and non-protein polymers are included in the analysis.

The models can be grouped into 4 clusters and 4 single-model clusters were found.

| Cluster number | Models |
|---|---|
| 1 | 2, 3, 10, 11 |
| 2 | 1, 4, 13, 14 |
| 3 | 6, 8 |
| 4 | 9, 12 |
| Single-model clusters | 5; 7; 15; 16 |

# 3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 1532 atoms, of which 752 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Protein yrbA.

| Mol | Chain | Residues | Atoms | | | | | | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | |
| 1 | A | 97 | 1532 | 489 | 752 | 142 | 144 | 5 | 0 |

There are 8 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|---|---|---|---|---|---|
| A | 90 | LEU | - | expression tag | UNP P0A9W6 |
| A | 91 | GLU | - | expression tag | UNP P0A9W6 |
| A | 92 | HIS | - | expression tag | UNP P0A9W6 |
| A | 93 | HIS | - | expression tag | UNP P0A9W6 |
| A | 94 | HIS | - | expression tag | UNP P0A9W6 |
| A | 95 | HIS | - | expression tag | UNP P0A9W6 |
| A | 96 | HIS | - | expression tag | UNP P0A9W6 |
| A | 97 | HIS | - | expression tag | UNP P0A9W6 |

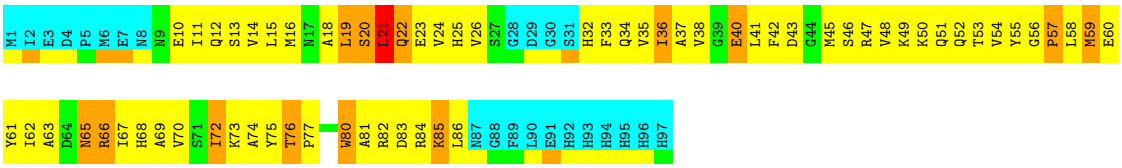
# 4 Residue-property plots (i)

## 4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-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. Stretches of 2 or more consecutive residues without any outliers are shown as green connectors. Residues which are classified as ill-defined in the NMR ensemble, are shown in cyan with an underline colour-coded according to the previous scheme. Residues which were present in the experimental sample, but not modelled in the final structure are shown in grey.

• Molecule 1: Protein yrbA

Chain A:

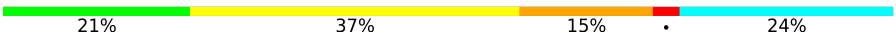



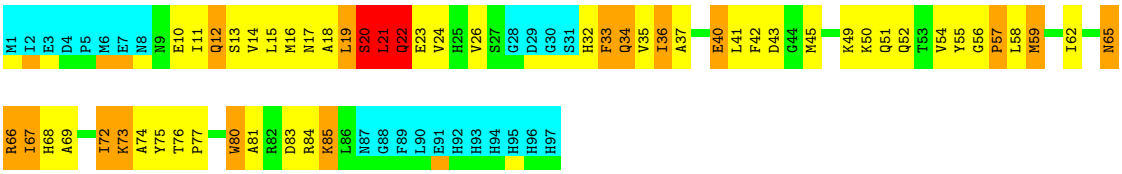

## 4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

### 4.2.1 Score per residue for model 1

• Molecule 1: Protein yrbA

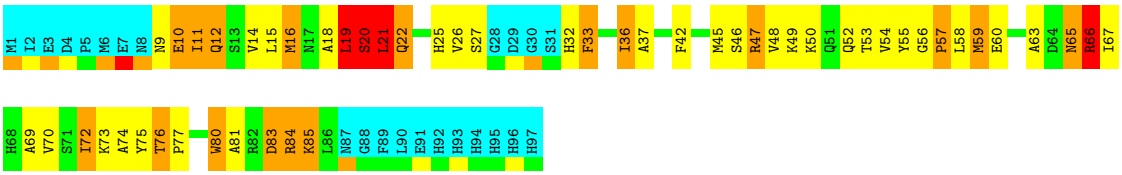
Chain A: 


### 4.2.2 Score per residue for model 2

• Molecule 1: Protein yrbA

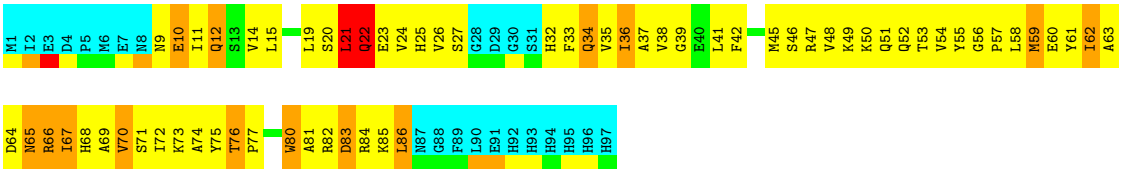
Chain A:




### 4.2.3 Score per residue for model 3

- Molecule 1: Protein yrbA

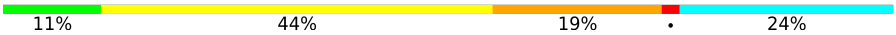
Chain A:




### 4.2.4 Score per residue for model 4

- Molecule 1: Protein yrbA

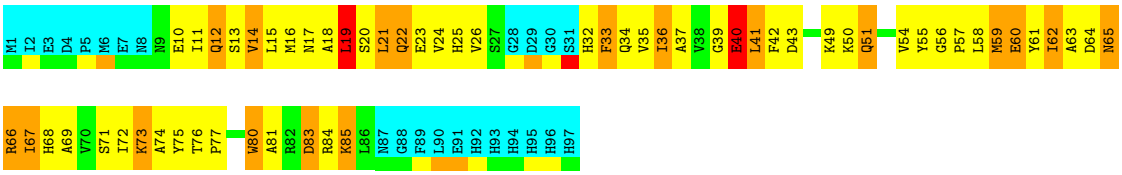
Chain A:



### 4.2.5 Score per residue for model 5

- Molecule 1: Protein yrbA

Chain A:




### 4.2.6 Score per residue for model 6

- Molecule 1: Protein yrbA

Chain A: 13% 45% 16% • 24%

M1 I2 E3 D4 P5 M6 E7 N8 N9 E10 I11 Q12 S13 V14 L15 M16 N17 A18 L19 S20 L21 Q22 E23 V24 H25 V26 S27 G28 D29 G30 S31 H32 F33 Q34 V35 I36 A37 V38 G39 E40 L41 F42 D43 G44 M45 S46 R47 V48 Q51 Q52 T53 V54 Y55 G56 P57 L58 M59 E60 Y61

I62 A63 D64 N65 R66 I67 H68 A69 V70 S71 I72 K73 A74 Y75 T76 P77 W80 A81 R82 D83 R84 K85 L86 N87 G88 F89 L90 E91 H92 H93 H94 H95 H96 H97

### 4.2.7 Score per residue for model 7

- Molecule 1: Protein yrbA

Chain A: 14% 44% 15% • 24%

M1 I2 E3 D4 P5 M6 E7 N8 N9 E10 I11 L15 A18 L19 S20 L21 Q22 H25 V26 S27 G28 D29 G30 S31 H32 F33 Q34 V35 I36 A37 V38 G39 E40 L41 F42 D43 S46 R47 V48 K49 K50 Q51 Q52 T53 V54 Y55 G56 P57 L58 M59 E60 Y61 I62 A63 D64 N65

R66 I67 H68 A69 V70 S71 I72 K73 A74 Y75 T76 P77 A78 E79 W80 A81 R82 D83 R84 K85 L86 N87 G88 F89 L90 E91 H92 H93 H94 H95 H96 H97

### 4.2.8 Score per residue for model 8

- Molecule 1: Protein yrbA

Chain A: 15% 41% 18% • 24%

M1 I2 E3 D4 P5 M6 E7 N8 N9 E10 I11 Q12 S13 V14 L15 M16 N17 A18 L19 S20 L21 Q22 E23 V24 H25 V26 S27 G28 D29 G30 S31 H32 V35 I36 A37 V38 G39 E40 L41 F42 D43 S46 R47 V48 K49 K50 Q51 Q52 T53 V54 Y55 G56 P57 L58 M59 E60 Y61 I62

A63 D64 N65 R66 I67 H68 A69 V70 S71 I72 K73 A74 Y75 T76 P77 W80 A81 R82 D83 R84 K85 L86 N87 G88 F89 L90 E91 H92 H93 H94 H95 H96 H97

### 4.2.9 Score per residue for model 9

- Molecule 1: Protein yrbA

Chain A: 15% 40% 19% • 24%

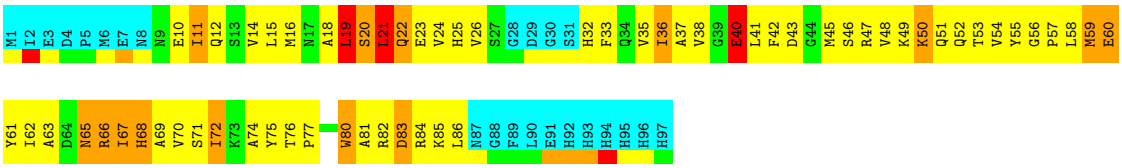
M1 I2 E3 D4 P5 M6 E7 N8 I11 Q12 S13 V14 L15 M16 N17 A18 L19 S20 L21 Q22 E23 V24 H25 V26 S27 G28 D29 G30 S31 H32 F33 Q34 V35 I36 A37 E40 L41 F42 D43 G44 M45 S46 R47 V48 K49 K50 Q51 Q52 T53 V54 Y55 G56 P57 L58 M59 E60 Y61 I62

A63 D64 N65 R66 I67 H68 A69 V70 S71 I72 K73 A74 Y75 T76 P77 A78 E79 W80 A81 R82 D83 R84 K85 L86 N87 G88 F89 L90 E91 H92 H93 H94 H95 H96 H97

### 4.2.10 Score per residue for model 10 (medoid)

- Molecule 1: Protein yrbA

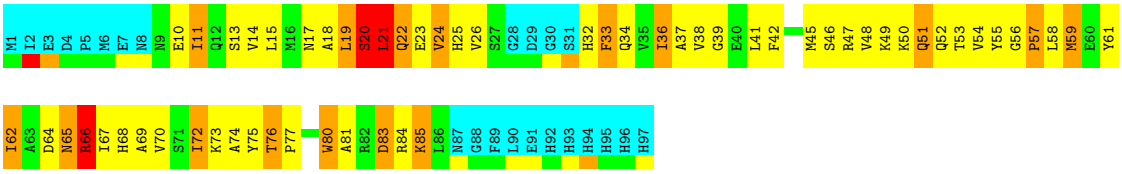
Chain A: 11% 47% 14% • 24%




### 4.2.11 Score per residue for model 11

- Molecule 1: Protein yrbA

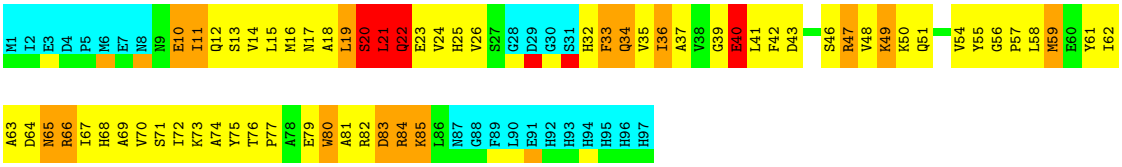
Chain A: 15% 41% 16% • 24%




### 4.2.12 Score per residue for model 12

- Molecule 1: Protein yrbA

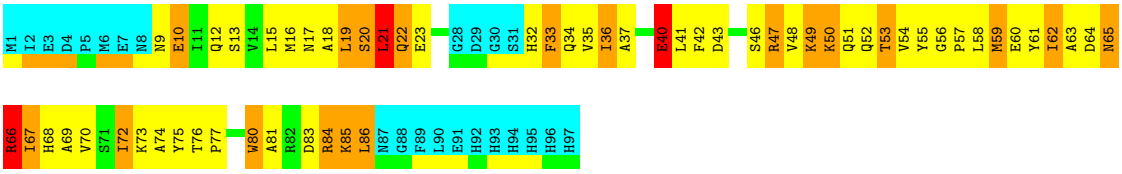
Chain A: 10% 46% 15% • 24%




### 4.2.13 Score per residue for model 13

- Molecule 1: Protein yrbA

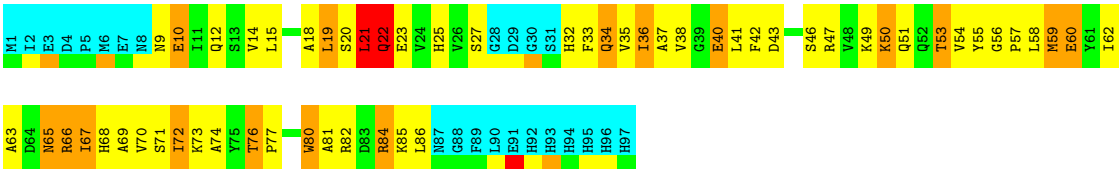
Chain A: 14% 39% 20% • 24%



### 4.2.14 Score per residue for model 14

- Molecule 1: Protein yrbA

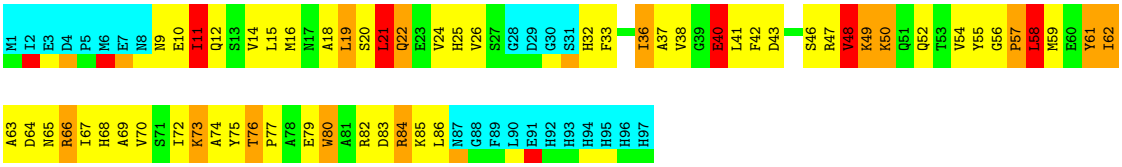
Chain A: 18% 40% 16% • 24%




### 4.2.15 Score per residue for model 15

- Molecule 1: Protein yrbA

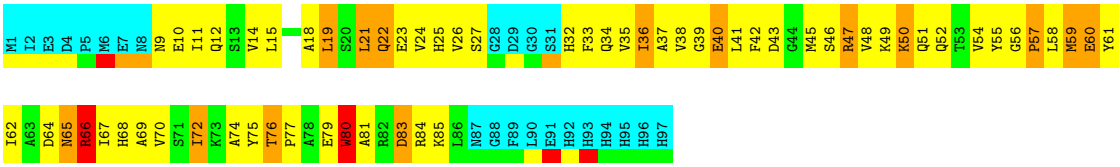
Chain A: 15% 42% 13% 5% 24%




### 4.2.16 Score per residue for model 16

- Molecule 1: Protein yrbA

Chain A: 12% 47% 14% • 24%



# 5 Refinement protocol and experimental data overview (i)

The models were refined using the following method: *torsion angle dynamics*.

Of the 100 calculated structures, 16 were deposited, based on the following criterion: *target function*.

The following table shows the software used for structure solution, optimisation and refinement.

| Software name | Classification | Version |
|---|---|---|
| HYPER | structure solution | 3.2 |
| DYANA | refinement | 1.5 |

No chemical shift data was provided.

# 6 Model quality (i)

## 6.1 Standard geometry (i)

There are no covalent bond-length or bond-angle outliers.

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no planarity outliers.

## 6.2 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 each 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 averaged over the ensemble.

| Mol | Chain | Non-H | H(model) | H(added) | Clashes |
|---|---|---|---|---|---|
| 1 | A | 593 | 597 | 597 | 73±8 |
| All | All | 9488 | 9552 | 9552 | 1165 |

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 61.

All unique clashes are listed below, sorted by their clash magnitude.

| Atom-1 | Atom-2 | Clash(Å) | Distance(Å) | Models | |
|---|---|---|---|---|---|
| | | | | Worst | Total |
| 1:A:15:LEU:HD21 | 1:A:37:ALA:HB2 | 1.06 | 1.22 | 12 | 5 |
| 1:A:14:VAL:HG11 | 1:A:61:TYR:CD2 | 0.97 | 1.95 | 3 | 3 |
| 1:A:15:LEU:HD11 | 1:A:37:ALA:HB2 | 0.96 | 1.34 | 14 | 13 |
| 1:A:14:VAL:HG11 | 1:A:61:TYR:CE2 | 0.95 | 1.97 | 12 | 2 |
| 1:A:55:TYR:CE1 | 1:A:62:ILE:HG21 | 0.95 | 1.96 | 12 | 8 |
| 1:A:36:ILE:HD12 | 1:A:80:TRP:CE2 | 0.94 | 1.97 | 15 | 16 |
| 1:A:14:VAL:HG21 | 1:A:61:TYR:CZ | 0.91 | 2.01 | 12 | 3 |
| 1:A:15:LEU:HD22 | 1:A:35:VAL:HG12 | 0.86 | 1.45 | 13 | 5 |
| 1:A:11:ILE:HG21 | 1:A:35:VAL:HG21 | 0.86 | 1.45 | 10 | 5 |
| 1:A:36:ILE:HG21 | 1:A:80:TRP:CD1 | 0.84 | 2.07 | 5 | 11 |
| 1:A:21:LEU:HD11 | 1:A:42:PHE:CD1 | 0.84 | 2.07 | 16 | 4 |
| 1:A:58:LEU:HD12 | 1:A:58:LEU:O | 0.82 | 1.73 | 1 | 13 |
| 1:A:25:HIS:CE1 | 1:A:38:VAL:HG21 | 0.81 | 2.09 | 3 | 10 |
| 1:A:18:ALA:HB1 | 1:A:57:PRO:HG2 | 0.80 | 1.53 | 9 | 13 |

*Continued on next page...*

*Continued from previous page...*

| Atom-1 | Atom-2 | Clash(Å) | Distance(Å) | Models | |
|---|---|---|---|---|---|
| | | | | Worst | Total |
| 1:A:15:LEU:HD22 | 1:A:35:VAL:CG1 | 0.80 | 2.06 | 5 | 5 |
| 1:A:19:LEU:HD11 | 1:A:54:VAL:HG22 | 0.80 | 1.52 | 16 | 2 |
| 1:A:12:GLN:CG | 1:A:24:VAL:HG21 | 0.80 | 2.07 | 3 | 7 |
| 1:A:50:LYS:O | 1:A:54:VAL:HG23 | 0.80 | 1.76 | 14 | 9 |
| 1:A:14:VAL:HG22 | 1:A:61:TYR:CE2 | 0.80 | 2.12 | 15 | 1 |
| 1:A:14:VAL:HG21 | 1:A:61:TYR:CE2 | 0.80 | 2.12 | 10 | 4 |
| 1:A:58:LEU:CD1 | 1:A:62:ILE:HD12 | 0.80 | 2.07 | 5 | 3 |
| 1:A:19:LEU:HD21 | 1:A:54:VAL:HG22 | 0.79 | 1.54 | 11 | 2 |
| 1:A:15:LEU:HD21 | 1:A:37:ALA:CB | 0.79 | 2.07 | 12 | 2 |
| 1:A:21:LEU:HD11 | 1:A:42:PHE:HB2 | 0.78 | 1.53 | 9 | 1 |
| 1:A:11:ILE:CG2 | 1:A:35:VAL:HG21 | 0.77 | 2.09 | 7 | 5 |
| 1:A:50:LYS:HD3 | 1:A:74:ALA:HB3 | 0.77 | 1.55 | 16 | 7 |
| 1:A:33:PHE:CE1 | 1:A:70:VAL:HG12 | 0.77 | 2.14 | 6 | 2 |
| 1:A:12:GLN:HG2 | 1:A:24:VAL:HG21 | 0.76 | 1.58 | 4 | 2 |
| 1:A:12:GLN:HG3 | 1:A:24:VAL:HG21 | 0.75 | 1.57 | 15 | 3 |
| 1:A:12:GLN:CD | 1:A:24:VAL:HG21 | 0.75 | 2.01 | 5 | 5 |
| 1:A:32:HIS:HA | 1:A:69:ALA:HB3 | 0.75 | 1.55 | 8 | 6 |
| 1:A:33:PHE:CZ | 1:A:70:VAL:HG12 | 0.74 | 2.17 | 16 | 5 |
| 1:A:12:GLN:OE1 | 1:A:24:VAL:HG21 | 0.73 | 1.83 | 9 | 2 |
| 1:A:32:HIS:CB | 1:A:69:ALA:HB3 | 0.73 | 2.14 | 11 | 16 |
| 1:A:12:GLN:CG | 1:A:24:VAL:HG11 | 0.73 | 2.13 | 9 | 2 |
| 1:A:35:VAL:HB | 1:A:72:ILE:HD12 | 0.72 | 1.61 | 3 | 1 |
| 1:A:26:VAL:HG12 | 1:A:35:VAL:HG22 | 0.72 | 1.61 | 6 | 3 |
| 1:A:36:ILE:HD12 | 1:A:80:TRP:CZ2 | 0.72 | 2.19 | 16 | 15 |
| 1:A:11:ILE:HG22 | 1:A:72:ILE:HD11 | 0.72 | 1.61 | 8 | 1 |
| 1:A:71:SER:O | 1:A:72:ILE:HD12 | 0.71 | 1.83 | 7 | 1 |
| 1:A:21:LEU:HD22 | 1:A:37:ALA:O | 0.71 | 1.84 | 9 | 3 |
| 1:A:58:LEU:HD12 | 1:A:62:ILE:HG13 | 0.70 | 1.63 | 8 | 1 |
| 1:A:19:LEU:CD1 | 1:A:42:PHE:CZ | 0.70 | 2.75 | 15 | 1 |
| 1:A:50:LYS:HD2 | 1:A:74:ALA:HB3 | 0.69 | 1.63 | 1 | 8 |
| 1:A:41:LEU:HD12 | 1:A:41:LEU:O | 0.69 | 1.87 | 5 | 3 |
| 1:A:15:LEU:HB2 | 1:A:72:ILE:HD11 | 0.69 | 1.64 | 14 | 1 |
| 1:A:70:VAL:HG23 | 1:A:70:VAL:O | 0.69 | 1.88 | 16 | 11 |
| 1:A:21:LEU:CD1 | 1:A:42:PHE:CD2 | 0.69 | 2.76 | 3 | 5 |
| 1:A:11:ILE:CG2 | 1:A:72:ILE:HD11 | 0.69 | 2.18 | 8 | 1 |
| 1:A:11:ILE:HD12 | 1:A:35:VAL:CG2 | 0.68 | 2.17 | 1 | 2 |
| 1:A:15:LEU:HD23 | 1:A:24:VAL:HG23 | 0.68 | 1.63 | 11 | 1 |
| 1:A:32:HIS:HB2 | 1:A:69:ALA:HB3 | 0.68 | 1.66 | 11 | 10 |
| 1:A:21:LEU:HD23 | 1:A:39:GLY:CA | 0.67 | 2.19 | 3 | 1 |
| 1:A:10:GLU:O | 1:A:14:VAL:HG23 | 0.67 | 1.89 | 6 | 3 |
| 1:A:26:VAL:HG23 | 1:A:26:VAL:O | 0.67 | 1.89 | 1 | 8 |

*Continued on next page...*

*Continued from previous page...*

| Atom-1 | Atom-2 | Clash(Å) | Distance(Å) | Models | |
|---|---|---|---|---|---|
| | | | | Worst | Total |
| 1:A:36:ILE:CG2 | 1:A:80:TRP:CD1 | 0.67 | 2.77 | 5 | 5 |
| 1:A:32:HIS:CA | 1:A:69:ALA:HB3 | 0.67 | 2.20 | 8 | 5 |
| 1:A:21:LEU:HD23 | 1:A:39:GLY:HA3 | 0.66 | 1.67 | 3 | 1 |
| 1:A:19:LEU:HD22 | 1:A:42:PHE:CZ | 0.66 | 2.25 | 10 | 3 |
| 1:A:19:LEU:O | 1:A:20:SER:CB | 0.65 | 2.44 | 8 | 4 |
| 1:A:33:PHE:N | 1:A:33:PHE:CD1 | 0.64 | 2.65 | 2 | 5 |
| 1:A:36:ILE:HD12 | 1:A:80:TRP:CD2 | 0.64 | 2.27 | 15 | 10 |
| 1:A:21:LEU:HD13 | 1:A:42:PHE:CD2 | 0.64 | 2.28 | 7 | 4 |
| 1:A:41:LEU:HD12 | 1:A:42:PHE:CE1 | 0.64 | 2.28 | 3 | 2 |
| 1:A:19:LEU:HD22 | 1:A:53:THR:CG2 | 0.64 | 2.23 | 14 | 1 |
| 1:A:36:ILE:CD1 | 1:A:80:TRP:CE2 | 0.64 | 2.81 | 4 | 15 |
| 1:A:50:LYS:CD | 1:A:74:ALA:HB3 | 0.63 | 2.23 | 8 | 6 |
| 1:A:19:LEU:HD11 | 1:A:54:VAL:CG2 | 0.62 | 2.24 | 3 | 1 |
| 1:A:42:PHE:CD2 | 1:A:74:ALA:HB1 | 0.62 | 2.29 | 7 | 1 |
| 1:A:15:LEU:HD23 | 1:A:24:VAL:CG2 | 0.62 | 2.24 | 11 | 1 |
| 1:A:19:LEU:HD12 | 1:A:42:PHE:CZ | 0.62 | 2.28 | 15 | 2 |
| 1:A:12:GLN:HG2 | 1:A:24:VAL:HG11 | 0.62 | 1.71 | 9 | 1 |
| 1:A:54:VAL:HG12 | 1:A:72:ILE:CG2 | 0.62 | 2.24 | 8 | 4 |
| 1:A:21:LEU:CD1 | 1:A:42:PHE:CD1 | 0.62 | 2.82 | 16 | 3 |
| 1:A:33:PHE:CZ | 1:A:70:VAL:CG1 | 0.62 | 2.82 | 16 | 3 |
| 1:A:21:LEU:HD21 | 1:A:42:PHE:HB2 | 0.61 | 1.72 | 5 | 1 |
| 1:A:19:LEU:HD12 | 1:A:20:SER:N | 0.61 | 2.10 | 12 | 1 |
| 1:A:58:LEU:HD12 | 1:A:62:ILE:HD12 | 0.61 | 1.72 | 10 | 2 |
| 1:A:81:ALA:O | 1:A:85:LYS:HB3 | 0.61 | 1.95 | 14 | 3 |
| 1:A:42:PHE:CD2 | 1:A:74:ALA:CB | 0.61 | 2.84 | 7 | 1 |
| 1:A:14:VAL:HG21 | 1:A:61:TYR:CG | 0.60 | 2.31 | 5 | 2 |
| 1:A:70:VAL:O | 1:A:70:VAL:CG2 | 0.60 | 2.49 | 15 | 9 |
| 1:A:83:ASP:HA | 1:A:86:LEU:HD12 | 0.60 | 1.73 | 7 | 1 |
| 1:A:34:GLN:OE1 | 1:A:80:TRP:CH2 | 0.60 | 2.55 | 5 | 1 |
| 1:A:19:LEU:HD23 | 1:A:42:PHE:HZ | 0.59 | 1.56 | 7 | 1 |
| 1:A:54:VAL:CG1 | 1:A:72:ILE:CG2 | 0.59 | 2.80 | 2 | 4 |
| 1:A:50:LYS:NZ | 1:A:75:TYR:CE1 | 0.59 | 2.70 | 8 | 3 |
| 1:A:55:TYR:CZ | 1:A:62:ILE:HG21 | 0.59 | 2.33 | 9 | 6 |
| 1:A:51:GLN:O | 1:A:55:TYR:CB | 0.58 | 2.52 | 6 | 11 |
| 1:A:75:TYR:CD1 | 1:A:79:GLU:CD | 0.58 | 2.76 | 9 | 2 |
| 1:A:81:ALA:O | 1:A:85:LYS:CB | 0.58 | 2.51 | 10 | 3 |
| 1:A:15:LEU:CD2 | 1:A:37:ALA:HB2 | 0.58 | 2.15 | 12 | 1 |
| 1:A:33:PHE:CE2 | 1:A:70:VAL:HG12 | 0.58 | 2.34 | 9 | 1 |
| 1:A:21:LEU:O | 1:A:22:GLN:CB | 0.58 | 2.52 | 2 | 9 |
| 1:A:37:ALA:HB3 | 1:A:74:ALA:HA | 0.58 | 1.74 | 4 | 5 |
| 1:A:25:HIS:ND1 | 1:A:38:VAL:CG2 | 0.57 | 2.67 | 3 | 1 |

*Continued on next page...*

*Continued from previous page...*

| Atom-1 | Atom-2 | Clash(Å) | Distance(Å) | Models | |
|---|---|---|---|---|---|
| | | | | Worst | Total |
| 1:A:19:LEU:HD23 | 1:A:42:PHE:CZ | 0.57 | 2.34 | 14 | 1 |
| 1:A:15:LEU:HD13 | 1:A:72:ILE:HG12 | 0.57 | 1.76 | 13 | 1 |
| 1:A:55:TYR:O | 1:A:59:MET:CB | 0.57 | 2.53 | 2 | 16 |
| 1:A:55:TYR:CE1 | 1:A:62:ILE:CG2 | 0.57 | 2.81 | 12 | 1 |
| 1:A:20:SER:O | 1:A:21:LEU:HD12 | 0.56 | 2.00 | 11 | 4 |
| 1:A:32:HIS:C | 1:A:33:PHE:CD1 | 0.56 | 2.79 | 14 | 2 |
| 1:A:80:TRP:O | 1:A:83:ASP:N | 0.56 | 2.39 | 5 | 11 |
| 1:A:25:HIS:ND1 | 1:A:38:VAL:HG21 | 0.56 | 2.15 | 3 | 5 |
| 1:A:55:TYR:CZ | 1:A:62:ILE:CG2 | 0.56 | 2.88 | 12 | 2 |
| 1:A:34:GLN:HG2 | 1:A:80:TRP:CZ2 | 0.56 | 2.35 | 4 | 3 |
| 1:A:54:VAL:O | 1:A:58:LEU:CD2 | 0.56 | 2.54 | 2 | 12 |
| 1:A:36:ILE:CG2 | 1:A:80:TRP:NE1 | 0.55 | 2.69 | 1 | 2 |
| 1:A:14:VAL:HG22 | 1:A:61:TYR:CZ | 0.55 | 2.35 | 15 | 1 |
| 1:A:14:VAL:HG21 | 1:A:61:TYR:CE1 | 0.55 | 2.37 | 12 | 1 |
| 1:A:41:LEU:HD12 | 1:A:41:LEU:C | 0.55 | 2.21 | 5 | 1 |
| 1:A:11:ILE:HD12 | 1:A:35:VAL:HG22 | 0.55 | 1.78 | 1 | 2 |
| 1:A:80:TRP:HA | 1:A:80:TRP:CE3 | 0.55 | 2.37 | 8 | 10 |
| 1:A:86:LEU:N | 1:A:86:LEU:CD2 | 0.55 | 2.70 | 13 | 1 |
| 1:A:40:GLU:O | 1:A:43:ASP:CB | 0.54 | 2.56 | 9 | 13 |
| 1:A:76:THR:CB | 1:A:77:PRO:CD | 0.54 | 2.85 | 16 | 16 |
| 1:A:40:GLU:O | 1:A:43:ASP:N | 0.54 | 2.40 | 7 | 13 |
| 1:A:11:ILE:HD13 | 1:A:11:ILE:N | 0.54 | 2.18 | 2 | 3 |
| 1:A:54:VAL:O | 1:A:58:LEU:CD1 | 0.54 | 2.56 | 15 | 1 |
| 1:A:58:LEU:CD2 | 1:A:72:ILE:HD13 | 0.54 | 2.32 | 1 | 1 |
| 1:A:81:ALA:O | 1:A:85:LYS:CG | 0.54 | 2.56 | 10 | 3 |
| 1:A:11:ILE:HG22 | 1:A:35:VAL:HG21 | 0.54 | 1.76 | 7 | 2 |
| 1:A:39:GLY:O | 1:A:40:GLU:CB | 0.54 | 2.54 | 12 | 5 |
| 1:A:67:ILE:CG2 | 1:A:68:HIS:CE1 | 0.54 | 2.90 | 16 | 1 |
| 1:A:65:ASN:O | 1:A:67:ILE:N | 0.53 | 2.41 | 16 | 16 |
| 1:A:65:ASN:ND2 | 1:A:70:VAL:CG1 | 0.53 | 2.71 | 4 | 1 |
| 1:A:55:TYR:O | 1:A:59:MET:N | 0.53 | 2.42 | 7 | 5 |
| 1:A:21:LEU:O | 1:A:22:GLN:HB2 | 0.53 | 2.04 | 3 | 12 |
| 1:A:36:ILE:CD1 | 1:A:80:TRP:CD2 | 0.53 | 2.92 | 3 | 13 |
| 1:A:14:VAL:CG2 | 1:A:61:TYR:CZ | 0.53 | 2.91 | 15 | 1 |
| 1:A:46:SER:O | 1:A:48:VAL:N | 0.53 | 2.42 | 16 | 11 |
| 1:A:86:LEU:N | 1:A:86:LEU:HD23 | 0.52 | 2.18 | 13 | 1 |
| 1:A:62:ILE:HD12 | 1:A:70:VAL:HG23 | 0.52 | 1.82 | 8 | 1 |
| 1:A:16:MET:O | 1:A:19:LEU:O | 0.52 | 2.27 | 2 | 5 |
| 1:A:58:LEU:O | 1:A:62:ILE:CG1 | 0.52 | 2.57 | 8 | 1 |
| 1:A:65:ASN:O | 1:A:68:HIS:N | 0.52 | 2.38 | 15 | 1 |
| 1:A:21:LEU:O | 1:A:22:GLN:CG | 0.52 | 2.58 | 9 | 6 |

*Continued on next page...*

*Continued from previous page...*

| Atom-1 | Atom-2 | Clash(Å) | Distance(Å) | Models | |
|---|---|---|---|---|---|
| | | | | Worst | Total |
| 1:A:34:GLN:HG2 | 1:A:80:TRP:CH2 | 0.52 | 2.40 | 4 | 1 |
| 1:A:19:LEU:HD23 | 1:A:53:THR:HG22 | 0.52 | 1.81 | 8 | 1 |
| 1:A:11:ILE:HA | 1:A:14:VAL:HG22 | 0.52 | 1.81 | 10 | 2 |
| 1:A:57:PRO:C | 1:A:59:MET:H | 0.52 | 2.09 | 15 | 1 |
| 1:A:19:LEU:CD1 | 1:A:53:THR:O | 0.51 | 2.58 | 9 | 2 |
| 1:A:39:GLY:O | 1:A:40:GLU:CG | 0.51 | 2.58 | 12 | 1 |
| 1:A:70:VAL:O | 1:A:70:VAL:HG22 | 0.51 | 2.04 | 4 | 1 |
| 1:A:34:GLN:OE1 | 1:A:35:VAL:C | 0.51 | 2.48 | 1 | 1 |
| 1:A:56:GLY:N | 1:A:57:PRO:CD | 0.51 | 2.73 | 6 | 16 |
| 1:A:19:LEU:HD22 | 1:A:42:PHE:HE2 | 0.51 | 1.64 | 8 | 1 |
| 1:A:62:ILE:HD12 | 1:A:70:VAL:CG2 | 0.51 | 2.36 | 8 | 1 |
| 1:A:55:TYR:CD2 | 1:A:59:MET:HG2 | 0.51 | 2.41 | 5 | 13 |
| 1:A:82:ARG:HA | 1:A:85:LYS:CE | 0.51 | 2.36 | 14 | 1 |
| 1:A:50:LYS:CE | 1:A:74:ALA:O | 0.51 | 2.58 | 15 | 1 |
| 1:A:82:ARG:O | 1:A:86:LEU:N | 0.51 | 2.44 | 8 | 4 |
| 1:A:65:ASN:O | 1:A:66:ARG:C | 0.51 | 2.49 | 15 | 16 |
| 1:A:18:ALA:O | 1:A:19:LEU:HD13 | 0.51 | 2.05 | 14 | 1 |
| 1:A:18:ALA:O | 1:A:19:LEU:CD1 | 0.50 | 2.59 | 14 | 1 |
| 1:A:81:ALA:O | 1:A:85:LYS:N | 0.50 | 2.42 | 16 | 10 |
| 1:A:19:LEU:HD11 | 1:A:42:PHE:CE2 | 0.50 | 2.42 | 11 | 1 |
| 1:A:55:TYR:O | 1:A:59:MET:CG | 0.50 | 2.59 | 4 | 7 |
| 1:A:58:LEU:CD1 | 1:A:62:ILE:CD1 | 0.50 | 2.89 | 10 | 2 |
| 1:A:50:LYS:HZ3 | 1:A:73:LYS:HA | 0.50 | 1.66 | 2 | 1 |
| 1:A:50:LYS:O | 1:A:54:VAL:CG2 | 0.50 | 2.60 | 5 | 4 |
| 1:A:54:VAL:CG1 | 1:A:72:ILE:HG23 | 0.50 | 2.36 | 6 | 3 |
| 1:A:21:LEU:CD1 | 1:A:42:PHE:CE2 | 0.50 | 2.95 | 3 | 1 |
| 1:A:55:TYR:OH | 1:A:62:ILE:CG2 | 0.50 | 2.60 | 6 | 3 |
| 1:A:20:SER:O | 1:A:21:LEU:CD1 | 0.50 | 2.60 | 11 | 5 |
| 1:A:48:VAL:O | 1:A:52:GLN:CB | 0.50 | 2.60 | 11 | 4 |
| 1:A:26:VAL:O | 1:A:26:VAL:CG2 | 0.50 | 2.60 | 1 | 3 |
| 1:A:11:ILE:HB | 1:A:35:VAL:HG21 | 0.50 | 1.83 | 12 | 2 |
| 1:A:48:VAL:HG13 | 1:A:49:LYS:H | 0.50 | 1.66 | 15 | 1 |
| 1:A:55:TYR:CE1 | 1:A:59:MET:HA | 0.49 | 2.43 | 11 | 5 |
| 1:A:34:GLN:OE1 | 1:A:71:SER:CB | 0.49 | 2.60 | 4 | 2 |
| 1:A:19:LEU:HD22 | 1:A:42:PHE:CE2 | 0.49 | 2.41 | 8 | 1 |
| 1:A:48:VAL:HG13 | 1:A:49:LYS:N | 0.49 | 2.22 | 12 | 2 |
| 1:A:14:VAL:O | 1:A:18:ALA:CB | 0.49 | 2.60 | 10 | 1 |
| 1:A:42:PHE:CD2 | 1:A:50:LYS:HG3 | 0.49 | 2.43 | 4 | 2 |
| 1:A:33:PHE:CD1 | 1:A:33:PHE:N | 0.49 | 2.81 | 14 | 2 |
| 1:A:50:LYS:NZ | 1:A:75:TYR:CD1 | 0.49 | 2.81 | 8 | 1 |
| 1:A:72:ILE:CG2 | 1:A:72:ILE:O | 0.49 | 2.60 | 10 | 4 |

*Continued on next page...*

*Continued from previous page...*

| Atom-1 | Atom-2 | Clash(Å) | Distance(Å) | Models | |
|---|---|---|---|---|---|
| | | | | Worst | Total |
| 1:A:50:LYS:CB | 1:A:50:LYS:NZ | 0.48 | 2.75 | 13 | 1 |
| 1:A:18:ALA:CB | 1:A:58:LEU:HD23 | 0.48 | 2.38 | 9 | 1 |
| 1:A:19:LEU:CD1 | 1:A:42:PHE:CE2 | 0.48 | 2.97 | 15 | 2 |
| 1:A:55:TYR:CE2 | 1:A:59:MET:HG2 | 0.48 | 2.44 | 12 | 3 |
| 1:A:9:ASN:O | 1:A:12:GLN:CB | 0.48 | 2.62 | 2 | 1 |
| 1:A:67:ILE:HG23 | 1:A:68:HIS:CE1 | 0.48 | 2.43 | 16 | 1 |
| 1:A:55:TYR:OH | 1:A:62:ILE:HG21 | 0.48 | 2.09 | 6 | 3 |
| 1:A:21:LEU:HD11 | 1:A:42:PHE:CD2 | 0.48 | 2.44 | 3 | 2 |
| 1:A:14:VAL:CG2 | 1:A:61:TYR:CE2 | 0.48 | 2.94 | 15 | 1 |
| 1:A:40:GLU:O | 1:A:41:LEU:C | 0.48 | 2.52 | 9 | 11 |
| 1:A:81:ALA:O | 1:A:85:LYS:CE | 0.48 | 2.62 | 7 | 1 |
| 1:A:19:LEU:CD1 | 1:A:20:SER:N | 0.47 | 2.77 | 12 | 1 |
| 1:A:74:ALA:O | 1:A:75:TYR:CD1 | 0.47 | 2.67 | 2 | 6 |
| 1:A:27:SER:O | 1:A:33:PHE:CB | 0.47 | 2.62 | 7 | 2 |
| 1:A:42:PHE:HD2 | 1:A:74:ALA:HB1 | 0.47 | 1.69 | 7 | 1 |
| 1:A:51:GLN:O | 1:A:55:TYR:HB2 | 0.47 | 2.09 | 12 | 9 |
| 1:A:67:ILE:N | 1:A:67:ILE:HD13 | 0.47 | 2.24 | 6 | 2 |
| 1:A:32:HIS:CG | 1:A:32:HIS:O | 0.47 | 2.67 | 3 | 6 |
| 1:A:58:LEU:HD22 | 1:A:72:ILE:HD13 | 0.47 | 1.85 | 1 | 1 |
| 1:A:58:LEU:CD1 | 1:A:62:ILE:HD13 | 0.47 | 2.40 | 9 | 1 |
| 1:A:66:ARG:O | 1:A:68:HIS:N | 0.47 | 2.48 | 6 | 10 |
| 1:A:9:ASN:O | 1:A:12:GLN:N | 0.47 | 2.48 | 14 | 3 |
| 1:A:65:ASN:O | 1:A:65:ASN:ND2 | 0.47 | 2.47 | 15 | 11 |
| 1:A:50:LYS:CD | 1:A:74:ALA:O | 0.47 | 2.62 | 8 | 2 |
| 1:A:26:VAL:HG13 | 1:A:26:VAL:O | 0.47 | 2.10 | 2 | 1 |
| 1:A:27:SER:O | 1:A:33:PHE:CA | 0.47 | 2.63 | 7 | 1 |
| 1:A:52:GLN:O | 1:A:55:TYR:N | 0.46 | 2.48 | 15 | 4 |
| 1:A:37:ALA:O | 1:A:75:TYR:O | 0.46 | 2.33 | 5 | 12 |
| 1:A:73:LYS:HB3 | 1:A:75:TYR:CE2 | 0.46 | 2.45 | 15 | 5 |
| 1:A:50:LYS:HE3 | 1:A:75:TYR:CE1 | 0.46 | 2.44 | 9 | 1 |
| 1:A:10:GLU:O | 1:A:12:GLN:N | 0.46 | 2.49 | 15 | 3 |
| 1:A:11:ILE:HD13 | 1:A:11:ILE:H | 0.46 | 1.70 | 2 | 2 |
| 1:A:48:VAL:O | 1:A:52:GLN:CG | 0.46 | 2.63 | 16 | 2 |
| 1:A:55:TYR:O | 1:A:59:MET:CA | 0.46 | 2.64 | 2 | 5 |
| 1:A:46:SER:O | 1:A:49:LYS:N | 0.46 | 2.49 | 12 | 4 |
| 1:A:48:VAL:CG1 | 1:A:49:LYS:N | 0.46 | 2.79 | 12 | 2 |
| 1:A:58:LEU:O | 1:A:58:LEU:CD1 | 0.46 | 2.57 | 1 | 6 |
| 1:A:46:SER:O | 1:A:47:ARG:C | 0.46 | 2.54 | 16 | 12 |
| 1:A:16:MET:CG | 1:A:20:SER:OG | 0.46 | 2.64 | 8 | 1 |
| 1:A:41:LEU:HD12 | 1:A:42:PHE:CD1 | 0.46 | 2.45 | 11 | 1 |
| 1:A:66:ARG:C | 1:A:68:HIS:N | 0.46 | 2.69 | 3 | 10 |

*Continued on next page...*

*Continued from previous page...*

| Atom-1 | Atom-2 | Clash(Å) | Distance(Å) | Models | |
|---|---|---|---|---|---|
| | | | | Worst | Total |
| 1:A:19:LEU:O | 1:A:20:SER:OG | 0.46 | 2.34 | 8 | 2 |
| 1:A:60:GLU:O | 1:A:63:ALA:N | 0.46 | 2.49 | 6 | 9 |
| 1:A:18:ALA:O | 1:A:19:LEU:CG | 0.46 | 2.64 | 5 | 1 |
| 1:A:66:ARG:O | 1:A:67:ILE:C | 0.46 | 2.55 | 5 | 14 |
| 1:A:42:PHE:CE1 | 1:A:45:MET:CE | 0.46 | 2.99 | 4 | 1 |
| 1:A:60:GLU:O | 1:A:63:ALA:HB3 | 0.46 | 2.11 | 14 | 2 |
| 1:A:80:TRP:O | 1:A:84:ARG:HB2 | 0.46 | 2.10 | 14 | 1 |
| 1:A:73:LYS:HG2 | 1:A:75:TYR:CE2 | 0.46 | 2.46 | 1 | 1 |
| 1:A:10:GLU:C | 1:A:12:GLN:N | 0.46 | 2.69 | 13 | 3 |
| 1:A:19:LEU:CD1 | 1:A:53:THR:HG22 | 0.46 | 2.41 | 4 | 1 |
| 1:A:55:TYR:CE1 | 1:A:59:MET:HG2 | 0.46 | 2.46 | 7 | 3 |
| 1:A:46:SER:C | 1:A:48:VAL:N | 0.45 | 2.68 | 16 | 9 |
| 1:A:21:LEU:HD11 | 1:A:42:PHE:CG | 0.45 | 2.44 | 16 | 2 |
| 1:A:42:PHE:CE1 | 1:A:45:MET:HE1 | 0.45 | 2.46 | 4 | 1 |
| 1:A:55:TYR:CD1 | 1:A:59:MET:HG2 | 0.45 | 2.46 | 4 | 2 |
| 1:A:50:LYS:HE2 | 1:A:75:TYR:CE1 | 0.45 | 2.45 | 15 | 1 |
| 1:A:76:THR:CB | 1:A:77:PRO:HD2 | 0.45 | 2.42 | 15 | 11 |
| 1:A:58:LEU:CD1 | 1:A:58:LEU:O | 0.45 | 2.64 | 15 | 1 |
| 1:A:24:VAL:O | 1:A:25:HIS:ND1 | 0.45 | 2.49 | 15 | 2 |
| 1:A:58:LEU:C | 1:A:58:LEU:HD12 | 0.45 | 2.32 | 15 | 1 |
| 1:A:55:TYR:CG | 1:A:59:MET:HG2 | 0.45 | 2.47 | 4 | 1 |
| 1:A:62:ILE:O | 1:A:65:ASN:N | 0.45 | 2.50 | 4 | 5 |
| 1:A:10:GLU:O | 1:A:11:ILE:C | 0.45 | 2.55 | 15 | 1 |
| 1:A:34:GLN:OE1 | 1:A:36:ILE:N | 0.45 | 2.50 | 16 | 2 |
| 1:A:10:GLU:O | 1:A:13:SER:N | 0.45 | 2.50 | 4 | 1 |
| 1:A:72:ILE:O | 1:A:73:LYS:CD | 0.45 | 2.64 | 9 | 1 |
| 1:A:65:ASN:C | 1:A:67:ILE:N | 0.45 | 2.70 | 4 | 14 |
| 1:A:13:SER:O | 1:A:17:ASN:ND2 | 0.45 | 2.49 | 9 | 7 |
| 1:A:48:VAL:O | 1:A:50:LYS:N | 0.45 | 2.50 | 15 | 1 |
| 1:A:50:LYS:CG | 1:A:74:ALA:HB3 | 0.45 | 2.42 | 3 | 1 |
| 1:A:21:LEU:CD1 | 1:A:74:ALA:HB1 | 0.45 | 2.42 | 9 | 1 |
| 1:A:21:LEU:HD13 | 1:A:42:PHE:CE2 | 0.44 | 2.46 | 3 | 1 |
| 1:A:48:VAL:O | 1:A:51:GLN:N | 0.44 | 2.49 | 3 | 2 |
| 1:A:25:HIS:HB2 | 1:A:36:ILE:HG22 | 0.44 | 1.88 | 4 | 1 |
| 1:A:14:VAL:CG1 | 1:A:61:TYR:CD2 | 0.44 | 2.89 | 12 | 1 |
| 1:A:42:PHE:O | 1:A:50:LYS:NZ | 0.44 | 2.50 | 5 | 1 |
| 1:A:58:LEU:O | 1:A:62:ILE:HD13 | 0.44 | 2.11 | 15 | 1 |
| 1:A:19:LEU:C | 1:A:20:SER:OG | 0.44 | 2.55 | 2 | 1 |
| 1:A:79:GLU:CG | 1:A:83:ASP:OD1 | 0.44 | 2.65 | 15 | 1 |
| 1:A:33:PHE:CE1 | 1:A:70:VAL:HB | 0.44 | 2.47 | 3 | 2 |
| 1:A:48:VAL:C | 1:A:50:LYS:N | 0.44 | 2.70 | 15 | 2 |

*Continued on next page...*

*Continued from previous page...*

| Atom-1 | Atom-2 | Clash(Å) | Distance(Å) | Models | |
|---|---|---|---|---|---|
| | | | | Worst | Total |
| 1:A:19:LEU:HD12 | 1:A:19:LEU:O | 0.44 | 2.13 | 11 | 1 |
| 1:A:54:VAL:HG11 | 1:A:72:ILE:CG2 | 0.44 | 2.40 | 2 | 1 |
| 1:A:34:GLN:OE1 | 1:A:71:SER:C | 0.44 | 2.56 | 12 | 2 |
| 1:A:53:THR:O | 1:A:57:PRO:CD | 0.44 | 2.66 | 14 | 3 |
| 1:A:60:GLU:CG | 1:A:61:TYR:N | 0.44 | 2.80 | 4 | 1 |
| 1:A:19:LEU:O | 1:A:20:SER:HB2 | 0.44 | 2.13 | 8 | 1 |
| 1:A:10:GLU:O | 1:A:14:VAL:CG2 | 0.44 | 2.66 | 14 | 1 |
| 1:A:34:GLN:OE1 | 1:A:80:TRP:CZ2 | 0.44 | 2.71 | 13 | 1 |
| 1:A:82:ARG:O | 1:A:86:LEU:HG | 0.44 | 2.13 | 14 | 1 |
| 1:A:75:TYR:CD1 | 1:A:79:GLU:HG2 | 0.44 | 2.48 | 7 | 1 |
| 1:A:21:LEU:HD11 | 1:A:41:LEU:HB3 | 0.44 | 1.90 | 11 | 1 |
| 1:A:15:LEU:HD12 | 1:A:15:LEU:O | 0.44 | 2.13 | 12 | 1 |
| 1:A:58:LEU:HD13 | 1:A:62:ILE:HD12 | 0.44 | 1.87 | 12 | 1 |
| 1:A:80:TRP:O | 1:A:81:ALA:C | 0.44 | 2.56 | 11 | 9 |
| 1:A:48:VAL:O | 1:A:49:LYS:C | 0.44 | 2.57 | 15 | 1 |
| 1:A:55:TYR:HE1 | 1:A:62:ILE:HG21 | 0.43 | 1.72 | 8 | 1 |
| 1:A:85:LYS:C | 1:A:86:LEU:HD23 | 0.43 | 2.33 | 13 | 1 |
| 1:A:75:TYR:CG | 1:A:79:GLU:HG2 | 0.43 | 2.48 | 7 | 1 |
| 1:A:63:ALA:O | 1:A:66:ARG:CB | 0.43 | 2.66 | 9 | 2 |
| 1:A:11:ILE:HD12 | 1:A:33:PHE:CZ | 0.43 | 2.49 | 15 | 1 |
| 1:A:80:TRP:O | 1:A:80:TRP:HE3 | 0.43 | 1.97 | 7 | 1 |
| 1:A:40:GLU:O | 1:A:43:ASP:CG | 0.43 | 2.57 | 6 | 4 |
| 1:A:67:ILE:HG13 | 1:A:68:HIS:CE1 | 0.43 | 2.48 | 4 | 1 |
| 1:A:67:ILE:HG23 | 1:A:68:HIS:CG | 0.43 | 2.49 | 16 | 2 |
| 1:A:36:ILE:HA | 1:A:73:LYS:O | 0.43 | 2.14 | 1 | 3 |
| 1:A:60:GLU:O | 1:A:61:TYR:C | 0.43 | 2.58 | 16 | 3 |
| 1:A:18:ALA:HB1 | 1:A:57:PRO:CG | 0.43 | 2.36 | 9 | 1 |
| 1:A:19:LEU:HD12 | 1:A:20:SER:O | 0.43 | 2.14 | 11 | 1 |
| 1:A:85:LYS:C | 1:A:86:LEU:CD2 | 0.43 | 2.87 | 13 | 1 |
| 1:A:21:LEU:CD1 | 1:A:41:LEU:HB3 | 0.42 | 2.44 | 3 | 2 |
| 1:A:55:TYR:CZ | 1:A:59:MET:HG2 | 0.42 | 2.49 | 4 | 2 |
| 1:A:65:ASN:ND2 | 1:A:70:VAL:HG12 | 0.42 | 2.29 | 4 | 1 |
| 1:A:21:LEU:O | 1:A:22:GLN:CD | 0.42 | 2.58 | 8 | 1 |
| 1:A:34:GLN:CG | 1:A:80:TRP:CZ2 | 0.42 | 3.02 | 11 | 1 |
| 1:A:32:HIS:O | 1:A:32:HIS:CG | 0.42 | 2.72 | 7 | 2 |
| 1:A:58:LEU:HD11 | 1:A:72:ILE:HG21 | 0.42 | 1.90 | 9 | 1 |
| 1:A:11:ILE:O | 1:A:15:LEU:CB | 0.42 | 2.67 | 11 | 3 |
| 1:A:15:LEU:O | 1:A:19:LEU:O | 0.42 | 2.37 | 15 | 1 |
| 1:A:34:GLN:CD | 1:A:34:GLN:C | 0.42 | 2.78 | 16 | 1 |
| 1:A:15:LEU:HD22 | 1:A:35:VAL:HG13 | 0.42 | 1.88 | 5 | 1 |
| 1:A:80:TRP:CZ3 | 1:A:84:ARG:HD2 | 0.42 | 2.49 | 2 | 1 |

*Continued on next page...*

*Continued from previous page...*

| Atom-1 | Atom-2 | Clash(Å) | Distance(Å) | Models | |
|---|---|---|---|---|---|
| | | | | Worst | Total |
| 1:A:50:LYS:NZ | 1:A:74:ALA:O | 0.42 | 2.51 | 5 | 2 |
| 1:A:19:LEU:HD12 | 1:A:53:THR:O | 0.42 | 2.14 | 10 | 1 |
| 1:A:32:HIS:O | 1:A:32:HIS:CD2 | 0.42 | 2.73 | 11 | 1 |
| 1:A:15:LEU:HD13 | 1:A:72:ILE:CD1 | 0.42 | 2.44 | 2 | 1 |
| 1:A:51:GLN:O | 1:A:55:TYR:HB3 | 0.42 | 2.15 | 9 | 4 |
| 1:A:64:ASP:C | 1:A:66:ARG:N | 0.42 | 2.72 | 15 | 1 |
| 1:A:11:ILE:HD12 | 1:A:35:VAL:HG21 | 0.42 | 1.89 | 1 | 1 |
| 1:A:82:ARG:HD3 | 1:A:86:LEU:HD11 | 0.42 | 1.91 | 7 | 1 |
| 1:A:18:ALA:HB2 | 1:A:58:LEU:HB3 | 0.42 | 1.90 | 15 | 1 |
| 1:A:57:PRO:C | 1:A:59:MET:N | 0.42 | 2.72 | 15 | 1 |
| 1:A:13:SER:O | 1:A:17:ASN:CB | 0.42 | 2.68 | 6 | 2 |
| 1:A:72:ILE:O | 1:A:72:ILE:CG2 | 0.42 | 2.68 | 16 | 1 |
| 1:A:66:ARG:O | 1:A:68:HIS:O | 0.41 | 2.38 | 16 | 4 |
| 1:A:19:LEU:HD13 | 1:A:42:PHE:CZ | 0.41 | 2.50 | 16 | 1 |
| 1:A:41:LEU:HG | 1:A:42:PHE:CD1 | 0.41 | 2.50 | 6 | 1 |
| 1:A:57:PRO:O | 1:A:59:MET:N | 0.41 | 2.48 | 15 | 1 |
| 1:A:34:GLN:HG3 | 1:A:35:VAL:N | 0.41 | 2.31 | 5 | 2 |
| 1:A:58:LEU:HD12 | 1:A:62:ILE:CD1 | 0.41 | 2.45 | 10 | 1 |
| 1:A:67:ILE:HG23 | 1:A:68:HIS:CD2 | 0.41 | 2.49 | 16 | 1 |
| 1:A:58:LEU:HD21 | 1:A:72:ILE:HG21 | 0.41 | 1.91 | 7 | 1 |
| 1:A:86:LEU:HD23 | 1:A:86:LEU:HA | 0.41 | 1.78 | 8 | 2 |
| 1:A:13:SER:O | 1:A:17:ASN:CG | 0.41 | 2.59 | 12 | 2 |
| 1:A:51:GLN:CD | 1:A:72:ILE:O | 0.41 | 2.59 | 13 | 1 |
| 1:A:36:ILE:HB | 1:A:80:TRP:NE1 | 0.41 | 2.31 | 1 | 4 |
| 1:A:12:GLN:O | 1:A:16:MET:SD | 0.41 | 2.78 | 12 | 1 |
| 1:A:62:ILE:O | 1:A:63:ALA:C | 0.41 | 2.59 | 15 | 2 |
| 1:A:34:GLN:HA | 1:A:71:SER:CB | 0.41 | 2.46 | 7 | 1 |
| 1:A:11:ILE:HA | 1:A:14:VAL:CG2 | 0.41 | 2.46 | 16 | 3 |
| 1:A:23:GLU:CB | 1:A:38:VAL:HB | 0.41 | 2.46 | 10 | 2 |
| 1:A:22:GLN:CB | 1:A:39:GLY:HA2 | 0.41 | 2.45 | 11 | 1 |
| 1:A:62:ILE:CG2 | 1:A:63:ALA:N | 0.40 | 2.84 | 5 | 1 |
| 1:A:64:ASP:O | 1:A:65:ASN:C | 0.40 | 2.59 | 15 | 1 |
| 1:A:54:VAL:HG12 | 1:A:58:LEU:HD21 | 0.40 | 1.93 | 4 | 1 |
| 1:A:19:LEU:O | 1:A:19:LEU:CG | 0.40 | 2.68 | 11 | 1 |
| 1:A:19:LEU:HD13 | 1:A:42:PHE:HZ | 0.40 | 1.76 | 4 | 1 |
| 1:A:65:ASN:ND2 | 1:A:65:ASN:O | 0.40 | 2.52 | 4 | 1 |
| 1:A:80:TRP:CE3 | 1:A:80:TRP:CA | 0.40 | 3.05 | 6 | 1 |
| 1:A:76:THR:HG23 | 1:A:79:GLU:OE1 | 0.40 | 2.16 | 12 | 1 |
| 1:A:20:SER:O | 1:A:21:LEU:HB2 | 0.40 | 2.16 | 1 | 1 |
| 1:A:54:VAL:O | 1:A:58:LEU:HD23 | 0.40 | 2.16 | 3 | 1 |
| 1:A:42:PHE:CD2 | 1:A:45:MET:SD | 0.40 | 3.15 | 6 | 1 |

*Continued on next page...*

*Continued from previous page...*

| Atom-1 | Atom-2 | Clash(Å) | Distance(Å) | Models | |
|---|---|---|---|---|---|
| | | | | Worst | Total |
| 1:A:50:LYS:O | 1:A:51:GLN:C | 0.40 | 2.60 | 7 | 1 |
| 1:A:22:GLN:HB2 | 1:A:39:GLY:CA | 0.40 | 2.46 | 12 | 1 |
| 1:A:9:ASN:O | 1:A:9:ASN:ND2 | 0.40 | 2.55 | 14 | 1 |

## 6.3 Torsion angles (i)

### 6.3.1 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 PDB entries followed by that with respect to all NMR entries. 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 | 74/97 (76%) | 49±3 (66±4%) | 18±3 (25±3%) | 7±1 (9±1%) | 1 12 |
| All | All | 1184/1552 (76%) | 784 (66%) | 293 (25%) | 107 (9%) | 1 12 |

All 15 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

| Mol | Chain | Res | Type | Models (Total) |
|---|---|---|---|---|
| 1 | A | 22 | GLN | 16 |
| 1 | A | 66 | ARG | 16 |
| 1 | A | 21 | LEU | 14 |
| 1 | A | 40 | GLU | 13 |
| 1 | A | 20 | SER | 10 |
| 1 | A | 57 | PRO | 9 |
| 1 | A | 19 | LEU | 8 |
| 1 | A | 47 | ARG | 8 |
| 1 | A | 67 | ILE | 7 |
| 1 | A | 10 | GLU | 1 |
| 1 | A | 86 | LEU | 1 |
| 1 | A | 11 | ILE | 1 |
| 1 | A | 48 | VAL | 1 |
| 1 | A | 58 | LEU | 1 |
| 1 | A | 80 | TRP | 1 |

### 6.3.2 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 PDB entries followed by that with respect to all NMR entries. 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 | 64/84 (76%) | 43±3 (67±5%) | 21±3 (33±5%) | 1 12 |
| All | All | 1024/1344 (76%) | 690 (67%) | 334 (33%) | 1 12 |

All 46 unique residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

| Mol | Chain | Res | Type | Models (Total) |
|---|---|---|---|---|
| 1 | A | 36 | ILE | 16 |
| 1 | A | 80 | TRP | 16 |
| 1 | A | 84 | ARG | 16 |
| 1 | A | 21 | LEU | 15 |
| 1 | A | 59 | MET | 15 |
| 1 | A | 65 | ASN | 15 |
| 1 | A | 72 | ILE | 15 |
| 1 | A | 49 | LYS | 13 |
| 1 | A | 85 | LYS | 13 |
| 1 | A | 10 | GLU | 12 |
| 1 | A | 20 | SER | 12 |
| 1 | A | 19 | LEU | 11 |
| 1 | A | 62 | ILE | 10 |
| 1 | A | 73 | LYS | 10 |
| 1 | A | 23 | GLU | 9 |
| 1 | A | 83 | ASP | 9 |
| 1 | A | 16 | MET | 8 |
| 1 | A | 33 | PHE | 8 |
| 1 | A | 11 | ILE | 8 |
| 1 | A | 76 | THR | 8 |
| 1 | A | 45 | MET | 7 |
| 1 | A | 64 | ASP | 7 |
| 1 | A | 60 | GLU | 7 |
| 1 | A | 22 | GLN | 6 |
| 1 | A | 53 | THR | 6 |
| 1 | A | 34 | GLN | 5 |
| 1 | A | 27 | SER | 5 |
| 1 | A | 40 | GLU | 5 |
| 1 | A | 50 | LYS | 5 |

*Continued on next page...*

*Continued from previous page...*

| Mol | Chain | Res | Type | Models (Total) |
|---|---|---|---|---|
| 1 | A | 12 | GLN | 4 |
| 1 | A | 14 | VAL | 4 |
| 1 | A | 51 | GLN | 4 |
| 1 | A | 25 | HIS | 4 |
| 1 | A | 66 | ARG | 4 |
| 1 | A | 61 | TYR | 4 |
| 1 | A | 82 | ARG | 4 |
| 1 | A | 71 | SER | 3 |
| 1 | A | 70 | VAL | 2 |
| 1 | A | 24 | VAL | 2 |
| 1 | A | 26 | VAL | 1 |
| 1 | A | 41 | LEU | 1 |
| 1 | A | 52 | GLN | 1 |
| 1 | A | 68 | HIS | 1 |
| 1 | A | 86 | LEU | 1 |
| 1 | A | 48 | VAL | 1 |
| 1 | A | 58 | LEU | 1 |

### 6.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

## 6.5 Carbohydrates (i)

There are no monosaccharides in this entry.

## 6.6 Ligand geometry (i)

There are no ligands in this entry.

## 6.7 Other polymers (i)

There are no such molecules in this entry.

## 6.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

# 7 Chemical shift validation (i)

No chemical shift data were provided