



# Full wwPDB NMR Structure Validation Report ⓘ

Feb 12, 2017 – 10:04 pm GMT

PDB ID : 2HH8  
Title : Solution NMR structure of the ydfO protein from Escherichia coli. Northeast Structural Genomics target ER251.  
Authors : Rossi, P.; Cort, J.R.; Ho, C.K.; Janjua, H.; Cunningham, K.; Ma, L.-C.; Xiao, R.; Liu, J.; Baran, M.; Swapna, G.V.T.; Acton, T.B.; Rost, B.; Kennedy, M.A.; Montelione, G.T.; Northeast Structural Genomics Consortium (NESG)  
Deposited on : 2006-06-28

This is a Full wwPDB NMR Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<http://wwpdb.org/validation/2016/NMRValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

---

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

Cyrange	:	Kirchner and Güntert (2011)
NmrClust	:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	trunk28760
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	recalc28949

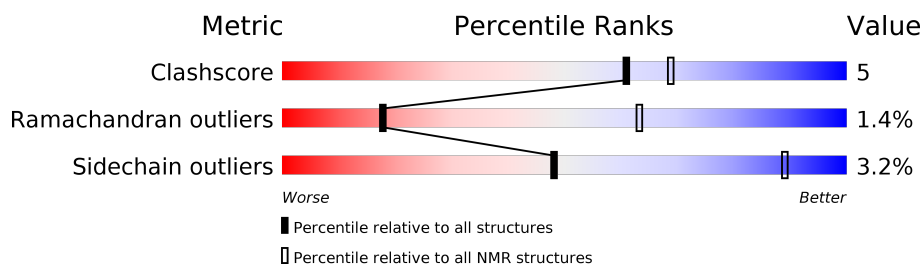
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*SOLUTION NMR*

The overall completeness of chemical shifts assignment is 87%.

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	125131	11601
Ramachandran outliers	121729	10391
Sidechain outliers	121581	10367

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  $\geq 3$ , 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  $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	149	

## 2 Ensemble composition and analysis

This entry contains 20 models. Model 18 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 energy*.

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:7-A:62, A:67-A:133 (123)	0.53	18

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 3 clusters and 2 single-model clusters were found.

Cluster number	Models
1	3, 5, 6, 7, 8, 9, 10, 12, 14, 15, 18, 20
2	1, 4, 16, 19
3	2, 17
Single-model clusters	11; 13

### 3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 2195 atoms, of which 1100 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Hypothetical protein ydfO.

Mol	Chain	Residues	Atoms					Trace
1	A	127	Total	C	H	N	O	0
			2195	708	1100	192	195	

There are 14 discrepancies between the modelled and reference sequences:

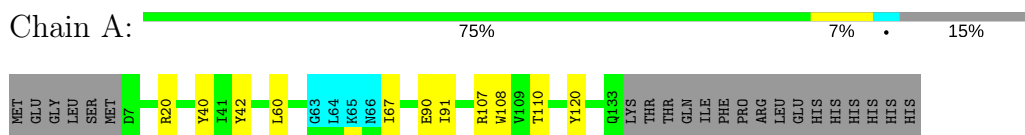
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	CLONING ARTIFACT	UNP P76156
A	2	GLU	-	CLONING ARTIFACT	UNP P76156
A	3	GLY	-	CLONING ARTIFACT	UNP P76156
A	4	LEU	-	CLONING ARTIFACT	UNP P76156
A	5	SER	-	CLONING ARTIFACT	UNP P76156
A	139	PHE	LEU	CLONING ARTIFACT	UNP P76156
A	142	LEU	-	CLONING ARTIFACT	UNP P76156
A	143	GLU	-	CLONING ARTIFACT	UNP P76156
A	144	HIS	-	EXPRESSION TAG	UNP P76156
A	145	HIS	-	EXPRESSION TAG	UNP P76156
A	146	HIS	-	EXPRESSION TAG	UNP P76156
A	147	HIS	-	EXPRESSION TAG	UNP P76156
A	148	HIS	-	EXPRESSION TAG	UNP P76156
A	149	HIS	-	EXPRESSION TAG	UNP P76156

## 4 Residue-property plots [i](#)

### 4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA and DNA 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: Hypothetical protein ydfO

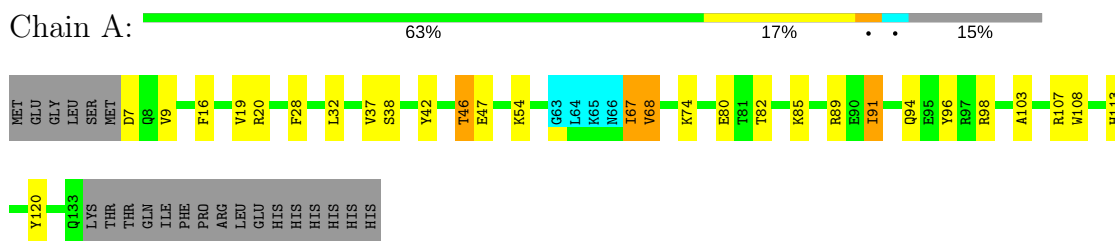


### 4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

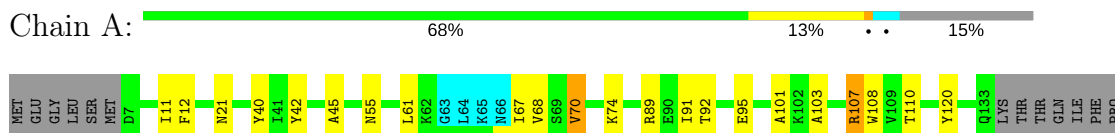
#### 4.2.1 Score per residue for model 1

- Molecule 1: Hypothetical protein ydfO



#### 4.2.2 Score per residue for model 2

- Molecule 1: Hypothetical protein ydfO



ARG  
LEU  
GLU  
HIS  
HIS  
HIS  
HIS  
HIS

### 4.2.3 Score per residue for model 3

- Molecule 1: Hypothetical protein ydfO

Chain A: 

MET GLU GLY LEU SER MET D7 F12 Y40 Y41 Y42 L61 K62 G63 L64 K65 N66 K74 D75 R76 E80 T92 E95 R107 W108 V109 T110 R117 Y118 Y119 Y120 T121 F122 D123 N124 L127 F128 G133 LYS THR THR GLN ILE PHE PRO ARG LEU GLU HIS

HIS  
HIS  
HIS  
HIS  
HIS

### 4.2.4 Score per residue for model 4

- Molecule 1: Hypothetical protein ydfO

Chain A: 

MET GLU GLY LEU SER MET D7 I11 I15 R20 F28 L32 K33 V37 Y42 N48 V49 K54 L60 G63 L64 K65 N66 T82 I91 F92 F93 Q94 E95 Y96 R97 R98 R107 W108 M111 I112 H113 E114 Y120 Q133 LYS THR THR

GLN  
ILE  
PHE  
PRO  
ARG  
LEU  
GLU  
HIS  
HIS  
HIS  
HIS  
HIS

### 4.2.5 Score per residue for model 5

- Molecule 1: Hypothetical protein ydfO

Chain A: 

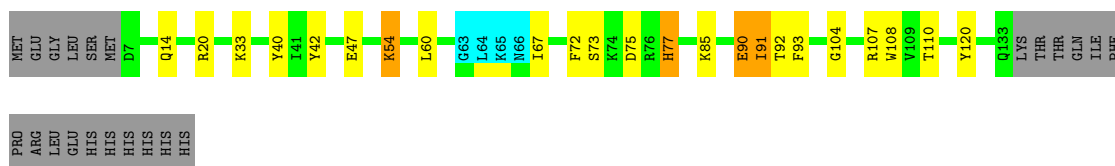
MET GLU GLY LEU SER MET D7 K18 V19 R20 N21 D22 L23 N24 Q26 W27 F28 L32 Y42 T46 N55 L60 G63 L64 K65 N66 V70 K85 I91 F92 R98 A101 R107 W108 Y120 T121 L127 Q133 LYS THR THR GLN ILE PHE

PRO  
ARG  
LEU  
GLU  
HIS  
HIS  
HIS  
HIS  
HIS

### 4.2.6 Score per residue for model 6

- Molecule 1: Hypothetical protein ydfO

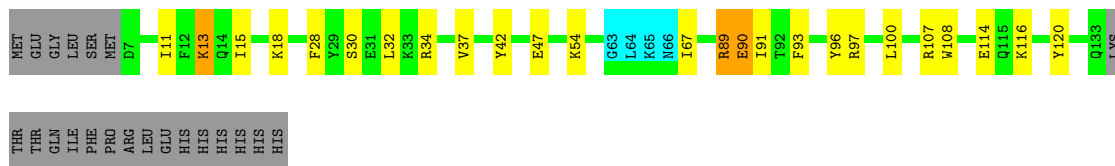
Chain A: 



#### 4.2.7 Score per residue for model 7

- Molecule 1: Hypothetical protein ydfO

Chain A: 66% 15% 15%



#### 4.2.8 Score per residue for model 8

- Molecule 1: Hypothetical protein ydfO

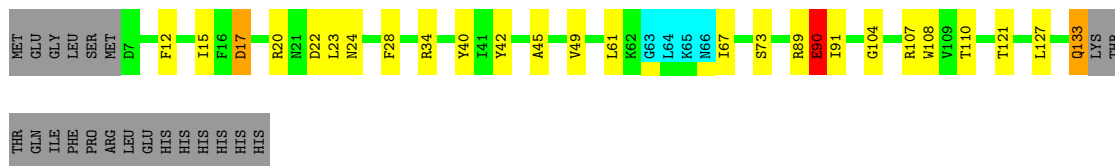
Chain A: 72% 10% 15%



#### 4.2.9 Score per residue for model 9

- Molecule 1: Hypothetical protein ydfO

Chain A: 65% 15% 15%



#### 4.2.10 Score per residue for model 10

- Molecule 1: Hypothetical protein ydfO

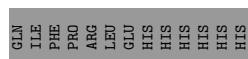
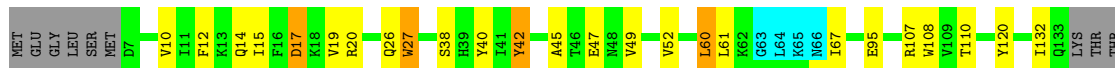
Chain A: 71% 11% 15%



#### 4.2.11 Score per residue for model 11

- Molecule 1: Hypothetical protein ydfO

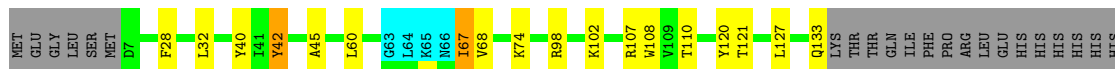
Chain A: 66% 14% 15%



#### 4.2.12 Score per residue for model 12

- Molecule 1: Hypothetical protein ydfO

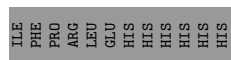
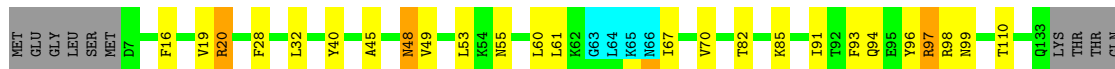
Chain A: 70% 11% 15%



#### 4.2.13 Score per residue for model 13

- Molecule 1: Hypothetical protein ydfO

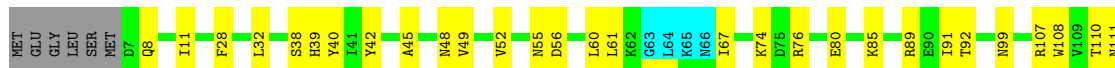
Chain A: 66% 15% 15%



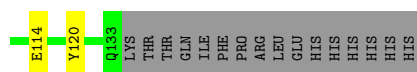
#### 4.2.14 Score per residue for model 14

- Molecule 1: Hypothetical protein ydfO

Chain A: 62% 21% 15%

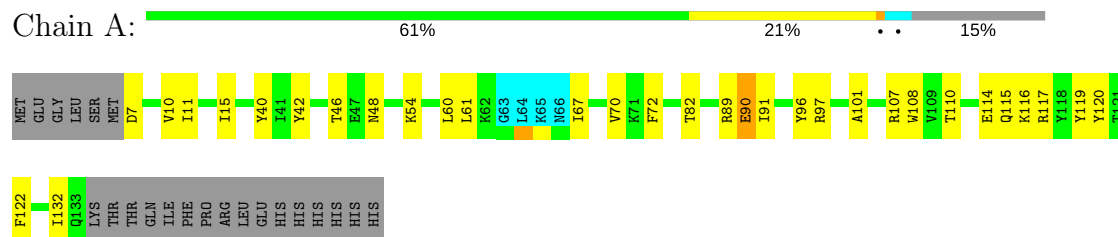






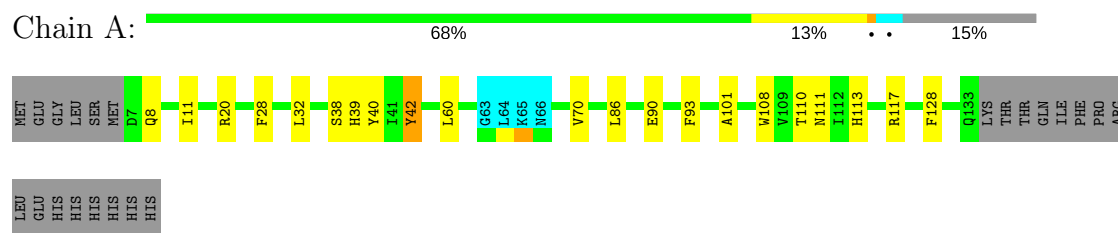
#### 4.2.15 Score per residue for model 15

- Molecule 1: Hypothetical protein ydfO



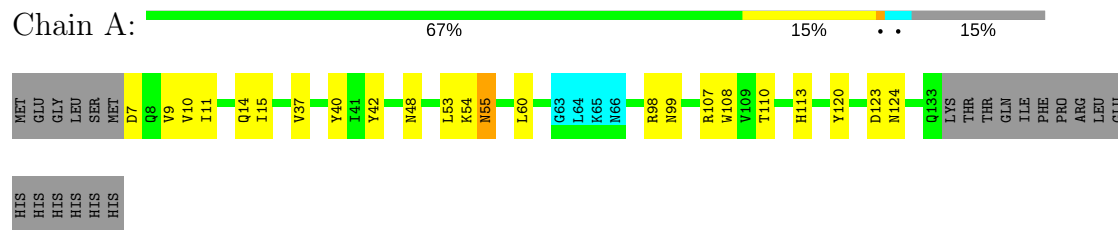
#### 4.2.16 Score per residue for model 16

- Molecule 1: Hypothetical protein ydfO



#### 4.2.17 Score per residue for model 17

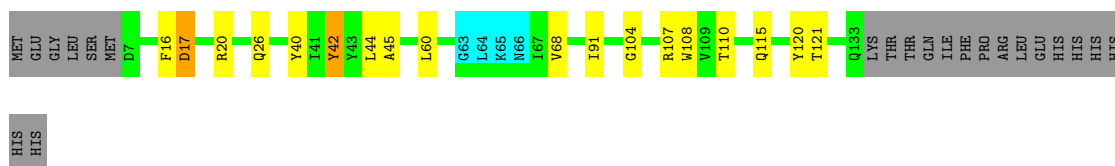
- Molecule 1: Hypothetical protein ydfO



#### 4.2.18 Score per residue for model 18 (medoid)

- Molecule 1: Hypothetical protein ydfO

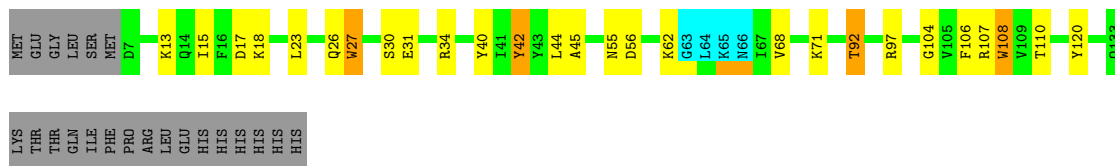




#### 4.2.19 Score per residue for model 19

- Molecule 1: Hypothetical protein ydfO

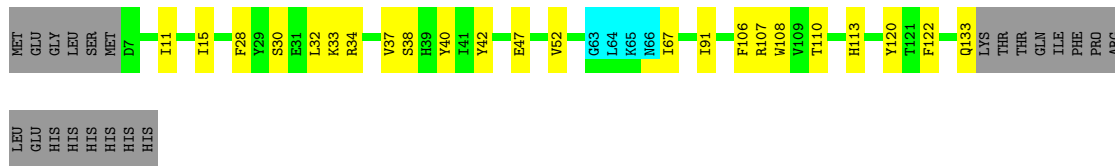
Chain A: 64% 15% 15%



#### 4.2.20 Score per residue for model 20

- Molecule 1: Hypothetical protein ydfO

Chain A: 67% 15% 15%



## 5 Refinement protocol and experimental data overview

The models were refined using the following method: *Noesy assignments made with iterative method using CS, 3J, Hyper (dihedral), and Dyana for simulated annealing MD. Converged structures are further refined using NIH-xplor followed by CNS in explicit water shell (Nielges) . Full lenght sequence was carried through the refinement protocol, the disordered regions and hexHIS tag are not reported. Structure based on 1885 constraints, 788 long range, 142 dihedral constraints and 114 H-bond constraints..*

Of the 100 calculated structures, 20 were deposited, based on the following criterion: *structures with the lowest energy.*

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

Software name	Classification	Version
DYANA	structure solution	1.2
X-PLOR	refinement	2.11.2
AutoStructure	structure solution	2.1.1
Hyper	structure solution	2.1
PSVS	refinement	1.3
CNS	refinement	1.1
Procheck NMR	refinement	3.51
MolProbity	refinement	3.01

The following table shows chemical shift validation statistics as aggregates over all chemical shift files. Detailed validation can be found in section 7 of this report.

Chemical shift file(s)	BMRB entry 7274
Number of chemical shift lists	1
Total number of shifts	1861
Number of shifts mapped to atoms	1861
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	87%

No validations of the models with respect to experimental NMR restraints is performed at this time.

## 6 Model quality

### 6.1 Standard geometry

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

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	1066	1067	1061	11±2
All	All	21320	21340	21220	226

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 5.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:107:ARG:HB3	1:A:120:TYR:HB2	0.87	1.44	20	7
1:A:107:ARG:HB2	1:A:120:TYR:HB2	0.85	1.47	5	10
1:A:42:TYR:HB3	1:A:108:TRP:HB3	0.79	1.52	7	18
1:A:18:LYS:HE2	1:A:18:LYS:HA	0.73	1.58	5	1
1:A:121:THR:HB	1:A:127:LEU:HD11	0.67	1.66	9	5
1:A:45:ALA:HA	1:A:67:ILE:O	0.64	1.92	2	4
1:A:60:LEU:H	1:A:60:LEU:HD23	0.63	1.54	13	5
1:A:40:TYR:CE1	1:A:110:THR:HB	0.63	2.29	17	8
1:A:92:THR:HB	1:A:95:GLU:OE1	0.61	1.95	2	1
1:A:38:SER:HA	1:A:113:HIS:HB2	0.61	1.72	1	2
1:A:45:ALA:HA	1:A:68:VAL:HG12	0.60	1.72	18	1
1:A:40:TYR:CE2	1:A:110:THR:HB	0.60	2.31	18	6
1:A:85:LYS:HE2	1:A:91:ILE:HG21	0.59	1.75	5	3
1:A:37:VAL:HB	1:A:54:LYS:HB2	0.57	1.75	1	2

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:85:LYS:HE3	1:A:91:ILE:HD13	0.57	1.77	13	1
1:A:85:LYS:HD2	1:A:91:ILE:HD13	0.56	1.78	6	1
1:A:15:ILE:HG22	1:A:28:PHE:HD1	0.56	1.61	9	1
1:A:110:THR:HG23	1:A:117:ARG:HG2	0.55	1.78	16	1
1:A:60:LEU:HD23	1:A:60:LEU:H	0.55	1.59	10	2
1:A:133:GLN:HE21	1:A:133:GLN:HA	0.54	1.63	9	1
1:A:70:VAL:HA	1:A:101:ALA:O	0.54	2.02	15	4
1:A:89:ARG:O	1:A:90:GLU:HB3	0.54	2.02	9	2
1:A:74:LYS:HA	1:A:103:ALA:O	0.53	2.03	2	2
1:A:22:ASP:HB3	1:A:24:ASN:OD1	0.52	2.04	5	1
1:A:15:ILE:HA	1:A:27:TRP:HZ2	0.52	1.63	19	1
1:A:16:PHE:O	1:A:20:ARG:HG3	0.52	2.05	18	3
1:A:86:LEU:O	1:A:90:GLU:HA	0.52	2.05	8	2
1:A:13:LYS:O	1:A:17:ASP:HB2	0.51	2.04	19	1
1:A:49:VAL:HB	1:A:61:LEU:HB2	0.51	1.82	9	1
1:A:17:ASP:HA	1:A:20:ARG:HE	0.51	1.66	18	1
1:A:19:VAL:HB	1:A:27:TRP:HE1	0.51	1.66	11	1
1:A:47:GLU:HG3	1:A:67:ILE:HD13	0.50	1.83	6	1
1:A:42:TYR:HB3	1:A:108:TRP:CD1	0.50	2.41	19	1
1:A:44:LEU:HD11	1:A:108:TRP:HB2	0.50	1.84	18	1
1:A:48:ASN:HA	1:A:61:LEU:O	0.50	2.06	14	3
1:A:89:ARG:HD2	1:A:90:GLU:HG2	0.49	1.84	7	1
1:A:28:PHE:O	1:A:32:LEU:HG	0.49	2.07	20	9
1:A:15:ILE:HA	1:A:27:TRP:CZ2	0.49	2.43	11	2
1:A:30:SER:O	1:A:34:ARG:HG3	0.49	2.08	7	3
1:A:123:ASP:O	1:A:124:ASN:HB3	0.49	2.08	3	1
1:A:89:ARG:CD	1:A:90:GLU:HG2	0.48	2.38	7	1
1:A:12:PHE:HB3	1:A:61:LEU:HD11	0.48	1.86	11	4
1:A:80:GLU:HG2	1:A:128:PHE:CE1	0.48	2.44	3	1
1:A:17:ASP:HA	1:A:20:ARG:HD3	0.48	1.85	9	1
1:A:20:ARG:HA	1:A:93:PHE:HB3	0.47	1.85	6	4
1:A:117:ARG:HD2	1:A:119:TYR:OH	0.47	2.09	15	1
1:A:98:ARG:HA	1:A:98:ARG:HE	0.47	1.69	10	1
1:A:16:PHE:HA	1:A:19:VAL:HG12	0.47	1.86	13	2
1:A:94:GLN:O	1:A:97:ARG:HG3	0.47	2.10	13	1
1:A:39:HIS:HB3	1:A:111:ASN:HA	0.47	1.85	14	2
1:A:44:LEU:CD2	1:A:97:ARG:HG3	0.47	2.40	19	1
1:A:115:GLN:HE21	1:A:132:ILE:HD11	0.47	1.68	15	1
1:A:10:VAL:O	1:A:14:GLN:HG3	0.47	2.10	17	1
1:A:7:ASP:OD2	1:A:9:VAL:HB	0.47	2.10	17	2
1:A:47:GLU:HB2	1:A:67:ILE:HD13	0.47	1.86	20	1

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:17:ASP:HA	1:A:20:ARG:NE	0.46	2.25	18	1
1:A:44:LEU:HG	1:A:108:TRP:NE1	0.46	2.26	19	1
1:A:114:GLU:HB3	1:A:116:LYS:HE2	0.46	1.85	15	1
1:A:72:PHE:HA	1:A:122:PHE:CZ	0.46	2.46	15	1
1:A:98:ARG:O	1:A:102:LYS:HG2	0.46	2.09	12	1
1:A:82:THR:HG22	1:A:96:TYR:CD1	0.46	2.46	4	4
1:A:12:PHE:HB2	1:A:61:LEU:HD21	0.46	1.87	8	1
1:A:54:LYS:O	1:A:55:ASN:HB2	0.46	2.11	17	1
1:A:10:VAL:O	1:A:14:GLN:HG2	0.46	2.11	11	1
1:A:85:LYS:HD3	1:A:91:ILE:HD13	0.46	1.87	1	1
1:A:73:SER:O	1:A:104:GLY:HA3	0.46	2.11	6	3
1:A:19:VAL:O	1:A:23:LEU:HD23	0.45	2.10	5	1
1:A:76:ARG:O	1:A:80:GLU:HG3	0.45	2.11	3	2
1:A:123:ASP:O	1:A:124:ASN:HB2	0.45	2.12	17	1
1:A:49:VAL:O	1:A:60:LEU:HA	0.45	2.11	4	4
1:A:104:GLY:O	1:A:121:THR:HA	0.45	2.11	18	1
1:A:38:SER:HB3	1:A:52:VAL:O	0.45	2.11	11	1
1:A:107:ARG:CB	1:A:120:TYR:HB2	0.45	2.42	4	1
1:A:26:GLN:HE21	1:A:26:GLN:HA	0.45	1.71	5	1
1:A:94:GLN:O	1:A:98:ARG:HG3	0.45	2.12	4	2
1:A:70:VAL:HA	1:A:101:ALA:HB1	0.45	1.89	2	1
1:A:67:ILE:HG22	1:A:68:VAL:HG23	0.44	1.89	1	1
1:A:7:ASP:HB2	1:A:10:VAL:HG23	0.44	1.89	15	1
1:A:96:TYR:O	1:A:100:LEU:HD13	0.44	2.11	7	1
1:A:8:GLN:HA	1:A:11:ILE:HD13	0.44	1.89	16	2
1:A:11:ILE:O	1:A:15:ILE:HG13	0.44	2.13	15	5
1:A:33:LYS:HD3	1:A:112:ILE:HG23	0.44	1.89	4	1
1:A:108:TRP:H	1:A:108:TRP:HD1	0.44	1.56	19	1
1:A:94:GLN:O	1:A:98:ARG:HG2	0.44	2.13	1	1
1:A:71:LYS:O	1:A:104:GLY:HA2	0.43	2.13	19	1
1:A:89:ARG:HG3	1:A:90:GLU:OE2	0.43	2.13	9	1
1:A:60:LEU:H	1:A:60:LEU:CD1	0.43	2.26	11	1
1:A:111:ASN:HB3	1:A:114:GLU:HB2	0.43	1.90	4	1
1:A:89:ARG:NE	1:A:89:ARG:HA	0.43	2.28	1	1
1:A:93:PHE:O	1:A:97:ARG:HG3	0.43	2.13	7	1
1:A:47:GLU:OE2	1:A:67:ILE:HG13	0.43	2.13	11	1
1:A:74:LYS:HB2	1:A:127:LEU:HD21	0.43	1.89	3	1
1:A:11:ILE:HD12	1:A:11:ILE:H	0.43	1.73	2	1
1:A:106:PHE:HB3	1:A:122:PHE:HA	0.43	1.90	20	1
1:A:44:LEU:HD22	1:A:97:ARG:HB3	0.43	1.91	10	1
1:A:38:SER:HB2	1:A:52:VAL:O	0.42	2.14	14	2

*Continued on next page...*

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:37:VAL:O	1:A:113:HIS:HB2	0.42	2.14	20	2
1:A:111:ASN:HB2	1:A:114:GLU:HB2	0.42	1.92	14	1
1:A:89:ARG:O	1:A:90:GLU:HG3	0.42	2.15	15	1
1:A:33:LYS:O	1:A:33:LYS:HD3	0.42	2.14	20	1
1:A:55:ASN:O	1:A:56:ASP:HB3	0.42	2.15	14	2
1:A:117:ARG:HD3	1:A:119:TYR:OH	0.42	2.14	3	1
1:A:75:ASP:OD1	1:A:77:HIS:HB3	0.42	2.15	6	1
1:A:20:ARG:HA	1:A:93:PHE:CB	0.41	2.45	6	1
1:A:47:GLU:HG2	1:A:67:ILE:HD13	0.41	1.91	7	1
1:A:72:PHE:HA	1:A:122:PHE:HZ	0.41	1.75	15	1
1:A:37:VAL:HG21	1:A:54:LYS:HD3	0.41	1.90	4	1
1:A:45:ALA:HB3	1:A:106:PHE:CE1	0.41	2.51	19	1
1:A:46:THR:HG23	1:A:67:ILE:HG12	0.41	1.91	1	1
1:A:114:GLU:O	1:A:116:LYS:HG3	0.41	2.15	7	1
1:A:23:LEU:HD11	1:A:92:THR:HA	0.41	1.92	19	1
1:A:17:ASP:HA	1:A:20:ARG:CD	0.41	2.46	11	1
1:A:45:ALA:HB2	1:A:70:VAL:HG23	0.40	1.93	13	1
1:A:108:TRP:CD1	1:A:108:TRP:C	0.40	2.95	10	1
1:A:93:PHE:CE2	1:A:97:ARG:HD3	0.40	2.51	10	1
1:A:13:LYS:HD2	1:A:13:LYS:O	0.40	2.17	7	1
1:A:45:ALA:O	1:A:67:ILE:HA	0.40	2.17	14	1
1:A:22:ASP:O	1:A:23:LEU:HB2	0.40	2.17	9	1

## 6.3 Torsion angles

### 6.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	121/149 (81%)	109±2 (90±2%)	10±2 (9±2%)	2±1 (1±1%)	18	63
All	All	2420/2980 (81%)	2179 (90%)	206 (9%)	35 (1%)	18	63

All 11 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	91	ILE	12
1	A	68	VAL	5
1	A	55	ASN	4
1	A	90	GLU	4
1	A	54	LYS	2
1	A	67	ILE	2
1	A	53	LEU	2
1	A	70	VAL	1
1	A	46	THR	1
1	A	45	ALA	1
1	A	132	ILE	1

### 6.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	119/143 (83%)	115±2 (97±1%)	4±2 (3±1%)	48 89
All	All	2380/2860 (83%)	2303 (97%)	77 (3%)	48 89

All 36 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	42	TYR	6
1	A	26	GLN	5
1	A	99	ASN	4
1	A	17	ASP	4
1	A	48	ASN	4
1	A	133	GLN	4
1	A	92	THR	4
1	A	27	TRP	3
1	A	95	GLU	3
1	A	60	LEU	3
1	A	89	ARG	3
1	A	98	ARG	3
1	A	74	LYS	2
1	A	18	LYS	2
1	A	20	ARG	2

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Res	Type	Models (Total)
1	A	107	ARG	2
1	A	24	ASN	2
1	A	97	ARG	2
1	A	90	GLU	2
1	A	115	GLN	1
1	A	14	GLN	1
1	A	108	TRP	1
1	A	130	GLU	1
1	A	77	HIS	1
1	A	46	THR	1
1	A	72	PHE	1
1	A	54	LYS	1
1	A	21	ASN	1
1	A	80	GLU	1
1	A	31	GLU	1
1	A	128	PHE	1
1	A	33	LYS	1
1	A	34	ARG	1
1	A	13	LYS	1
1	A	123	ASP	1
1	A	62	LYS	1

### 6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

### 6.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

### 6.6 Ligand geometry ⓘ

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

The completeness of assignment taking into account all chemical shift lists is 87% for the well-defined parts and 87% for the entire structure.

### 7.1 Chemical shift list 1

File name: BMRB entry 7274

Chemical shift list name: *assigned\_chem\_shift\_list\_1*

#### 7.1.1 Bookkeeping

The following table shows the results of parsing the chemical shift list and reports the number of nuclei with statistically unusual chemical shifts.

Total number of shifts	1861
Number of shifts mapped to atoms	1861
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	7

#### 7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	143	$-0.25 \pm 0.12$	None needed ( $< 0.5$ ppm)
$^{13}\text{C}_\beta$	141	$0.42 \pm 0.18$	None needed ( $< 0.5$ ppm)
$^{13}\text{C}'$	143	$-0.03 \pm 0.13$	None needed ( $< 0.5$ ppm)
$^{15}\text{N}$	142	$0.24 \pm 0.26$	None needed ( $< 0.5$ ppm)

#### 7.1.3 Completeness of resonance assignments

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 87%, i.e. 1470 atoms were assigned a chemical shift out of a possible 1693. 22 out of 22 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^1\text{H}$	$^{13}\text{C}$	$^{15}\text{N}$
Backbone	615/615 (100%)	246/246 (100%)	246/246 (100%)	123/123 (100%)
Sidechain	693/870 (80%)	408/508 (80%)	264/311 (85%)	21/51 (41%)

*Continued on next page...*

*Continued from previous page...*

	<b>Total</b>	<b><sup>1</sup>H</b>	<b><sup>13</sup>C</b>	<b><sup>15</sup>N</b>
Aromatic	162/208 (78%)	83/108 (77%)	77/88 (88%)	2/12 (17%)
Overall	1470/1693 (87%)	737/862 (85%)	587/645 (91%)	146/186 (78%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 87%, i.e. 1511 atoms were assigned a chemical shift out of a possible 1742. 23 out of 23 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	<b>Total</b>	<b><sup>1</sup>H</b>	<b><sup>13</sup>C</b>	<b><sup>15</sup>N</b>
Backbone	635/635 (100%)	254/254 (100%)	254/254 (100%)	127/127 (100%)
Sidechain	714/899 (79%)	419/525 (80%)	273/321 (85%)	22/53 (42%)
Aromatic	162/208 (78%)	83/108 (77%)	77/88 (88%)	2/12 (17%)
Overall	1511/1742 (87%)	756/887 (85%)	604/663 (91%)	151/192 (79%)

#### 7.1.4 Statistically unusual chemical shifts ⓘ

The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

Mol	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	20	ARG	NE	108.80	92.63 – 76.73	15.2
1	A	19	VAL	HG23	-0.70	2.20 – -0.60	-5.3
1	A	19	VAL	HG21	-0.70	2.20 – -0.60	-5.3
1	A	19	VAL	HG22	-0.70	2.20 – -0.60	-5.3
1	A	19	VAL	HG11	-0.51	2.13 – -0.47	-5.2
1	A	19	VAL	HG13	-0.51	2.13 – -0.47	-5.2
1	A	19	VAL	HG12	-0.51	2.13 – -0.47	-5.2

#### 7.1.5 Random Coil Index (RCI) plots ⓘ

The image below reports *random coil index* values for the protein chains in the structure. The height of each bar gives a probability of a given residue to be disordered, as predicted from the available chemical shifts and the amino acid sequence. A value above 0.2 is an indication of significant predicted disorder. The colour of the bar shows whether the residue is in the well-defined core (black) or in the ill-defined residue ranges (cyan), as described in section 2 on ensemble composition.

Random coil index (RCI) for chain A:

