Full wwPDB NMR Structure Validation Report (i)

Jun 12, 2024 – 04:12 PM EDT

PDB ID	:	1HKY
Title	:	Solution structure of a PAN module from Eimeria tenella
Authors	:	Brown, P.J.; Mulvey, D.; Potts, J.R.; Tomley, F.M.; Campbell, I.D.
Deposited on	:	2002-10-03

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

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

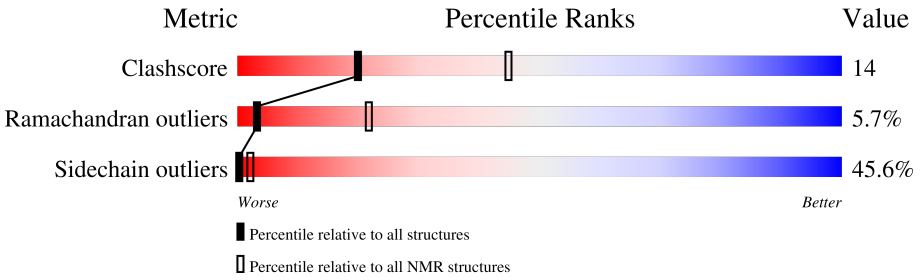
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

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	86	28% 35% 7% 30%

2 Ensemble composition and analysis (i)

This entry contains 20 models. Model 17 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative.

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:18-A:77 (60)	0.70	17

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 3 single-model clusters were found.

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

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 1265 atoms, of which 623 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called MICRONEME PROTEIN 5 PRECURSOR.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	86	1265	392	623	110	134	6	0

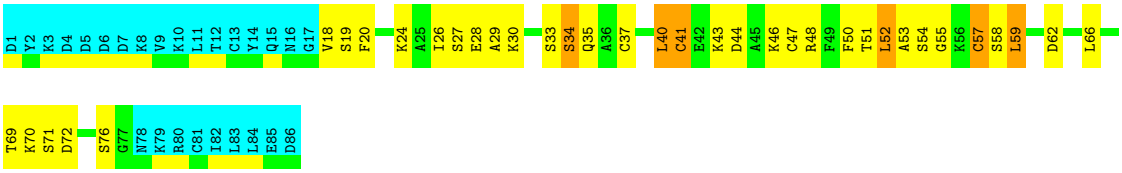
4 Residue-property plots (i)

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: MICRONEME PROTEIN 5 PRECURSOR

Chain A: 28% 35% 7% 30%



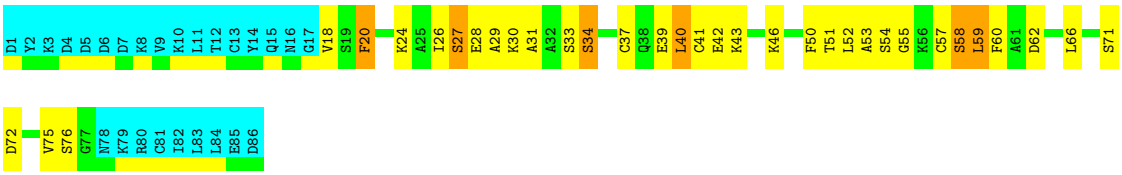
4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

• Molecule 1: MICRONEME PROTEIN 5 PRECURSOR

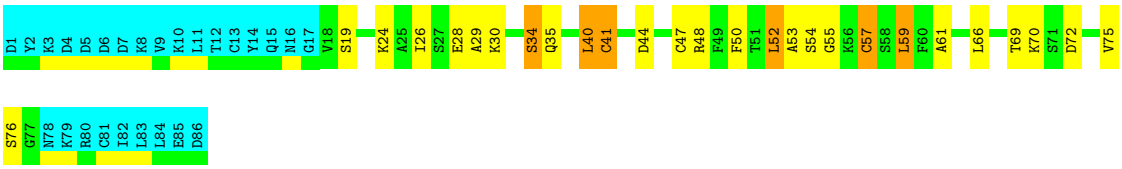
Chain A: 30% 33% 7% 30%



4.2.2 Score per residue for model 2

• Molecule 1: MICRONEME PROTEIN 5 PRECURSOR

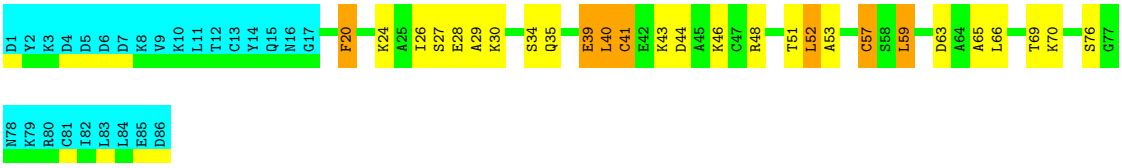
Chain A: 38% 24% 7% 30%



4.2.3 Score per residue for model 3

- Molecule 1: MICRONEME PROTEIN 5 PRECURSOR

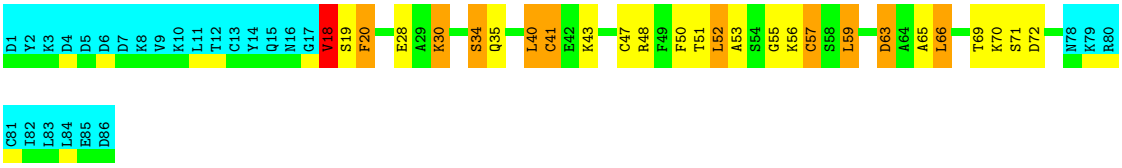
Chain A: 38% 23% 8% 30%



4.2.4 Score per residue for model 4

- Molecule 1: MICRONEME PROTEIN 5 PRECURSOR

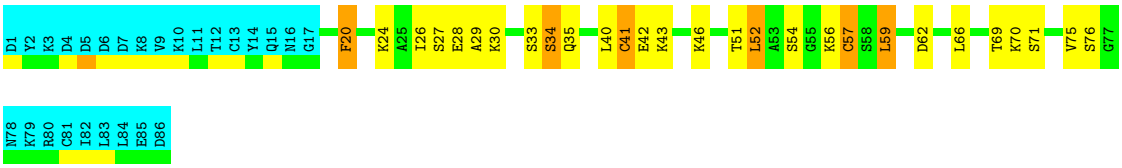
Chain A: 38% 19% 12% • 30%



4.2.5 Score per residue for model 5

- Molecule 1: MICRONEME PROTEIN 5 PRECURSOR

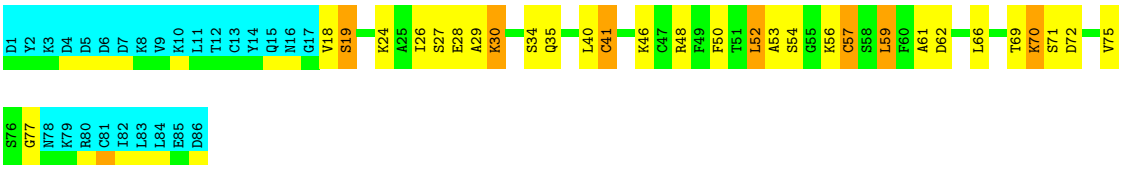
Chain A: 37% 26% 7% 30%



4.2.6 Score per residue for model 6

- Molecule 1: MICRONEME PROTEIN 5 PRECURSOR

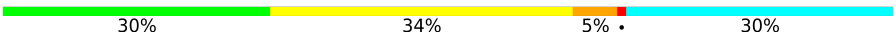
Chain A: 35% 27% 8% 30%

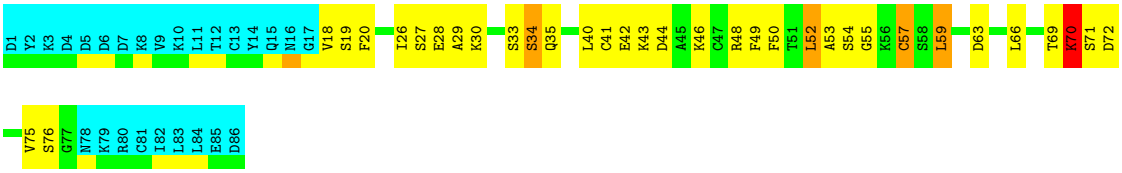


4.2.7 Score per residue for model 7

- Molecule 1: MICRONEME PROTEIN 5 PRECURSOR

Chain A:

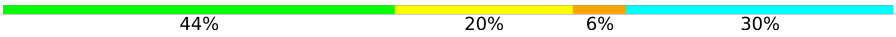


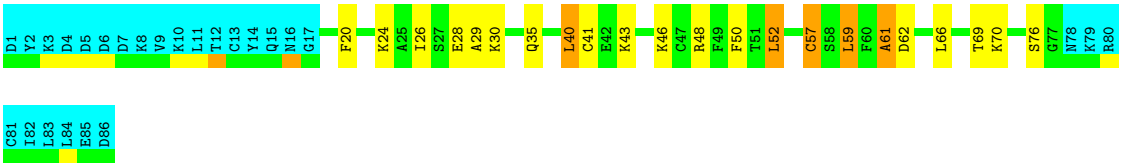


4.2.8 Score per residue for model 8

- Molecule 1: MICRONEME PROTEIN 5 PRECURSOR

Chain A:

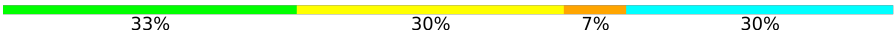


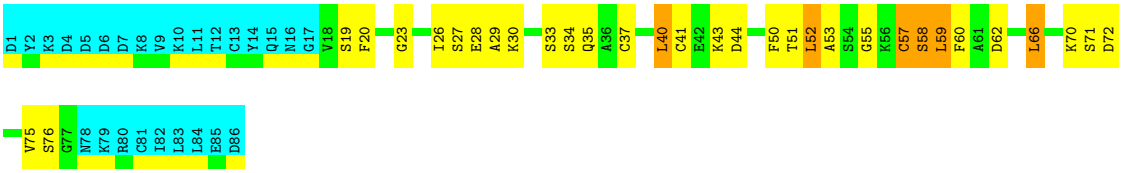


4.2.9 Score per residue for model 9

- Molecule 1: MICRONEME PROTEIN 5 PRECURSOR

Chain A:

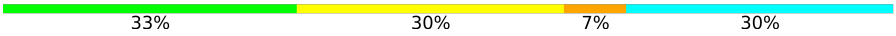


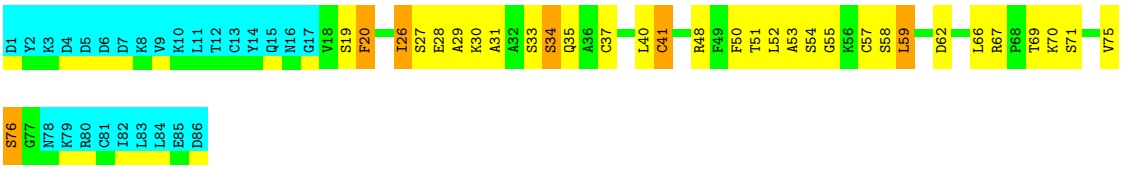


4.2.10 Score per residue for model 10

- Molecule 1: MICRONEME PROTEIN 5 PRECURSOR

Chain A:

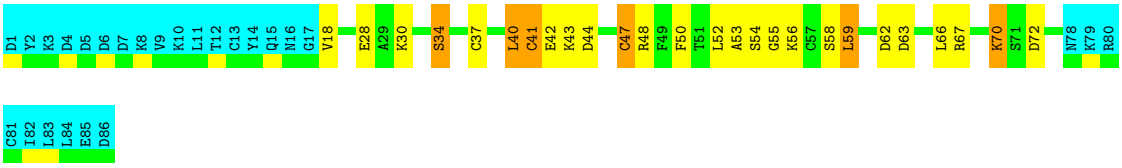




4.2.11 Score per residue for model 11

- Molecule 1: MICRONEME PROTEIN 5 PRECURSOR

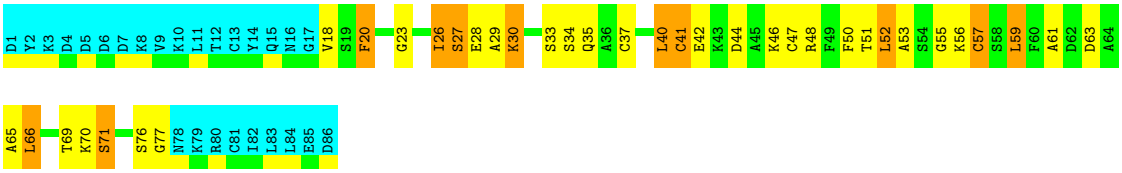
Chain A: 40% 23% 7% 30%



4.2.12 Score per residue for model 12

- Molecule 1: MICRONEME PROTEIN 5 PRECURSOR

Chain A: 28% 29% 13% 30%



4.2.13 Score per residue for model 13

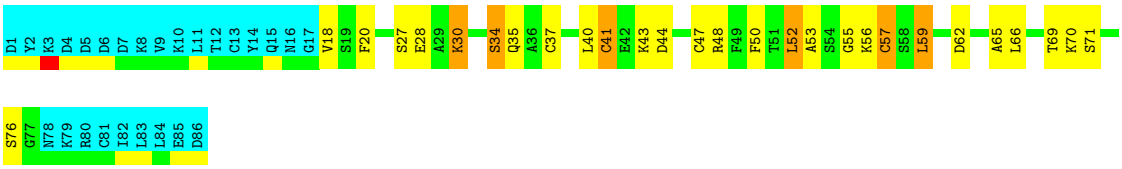
- Molecule 1: MICRONEME PROTEIN 5 PRECURSOR

Chain A: 31% 29% 9% 30%

4.2.14 Score per residue for model 14

- Molecule 1: MICRONEME PROTEIN 5 PRECURSOR

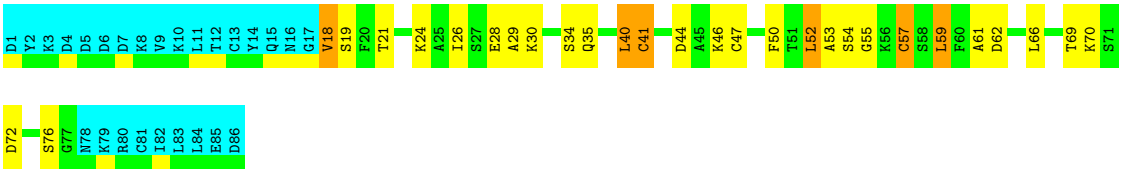
Chain A: 37% 26% 7% 30%



4.2.15 Score per residue for model 15

- Molecule 1: MICRONEME PROTEIN 5 PRECURSOR

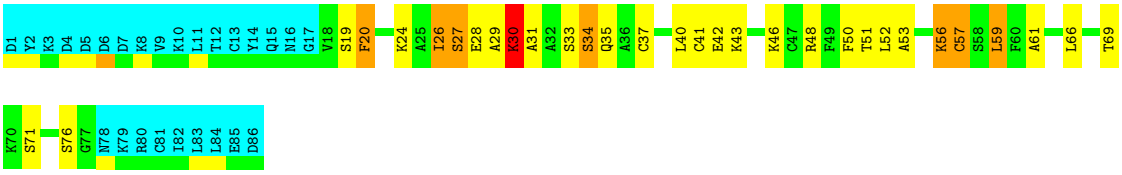
Chain A: 36% 27% 7% 30%



4.2.16 Score per residue for model 16

- Molecule 1: MICRONEME PROTEIN 5 PRECURSOR

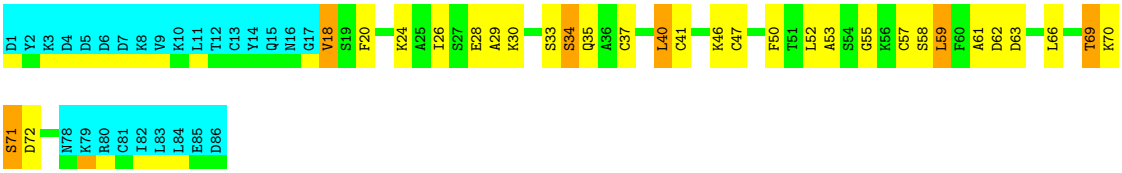
Chain A: 34% 27% 8% • 30%



4.2.17 Score per residue for model 17 (medoid)

- Molecule 1: MICRONEME PROTEIN 5 PRECURSOR

Chain A: 35% 28% 7% 30%



4.2.18 Score per residue for model 18

- Molecule 1: MICRONEME PROTEIN 5 PRECURSOR

Chain A: 31% 30% 8% 30%

D1 Y2 K3 D4 D5 D6 D7 K8 V9 K10 L11 T12 C13 Y14 Q15 N16 G17 V18 S19 F20 I26 S27 E28 A29 S34 Q35 A36 C37 C41 E42 K43 C47 R48 F49 F50 T51 L52 A53 S54 G55 K56 C57 S58 L59 F60 D63 A64 A65 L66 R67 P68 T69 K70 S71 D72

G73 A74 V75 S76 G77 N78 K79 R80 C81 I82 L83 L84 E85 D86

4.2.19 Score per residue for model 19

- Molecule 1: MICRONEME PROTEIN 5 PRECURSOR

Chain A: 26% 30% 13% • 30%

D1 Y2 K3 D4 D5 D6 D7 K8 V9 K10 L11 T12 C13 Y14 Q15 N16 G17 V18 S19 F20 K24 A25 I26 S27 E28 A31 A32 S33 S34 Q35 A36 C37 Q38 E39 L40 C41 E42 K43 D44 A45 K46 C47 R48 F49 F50 T51 L52 A53 S54 G55 K56 C57 S58 L59 F60 A61 D62

L66 T69 K70 S71 D72 G73 A74 V75 S76 G77 N78 K79 R80 C81 I82 L83 L84 E85 D86

4.2.20 Score per residue for model 20

- Molecule 1: MICRONEME PROTEIN 5 PRECURSOR

Chain A: 27% 35% 8% 30%

D1 Y2 K3 D4 D5 D6 D7 K8 V9 K10 L11 T12 C13 Y14 Q15 N16 G17 V18 S19 K24 A25 I26 S27 E28 A29 K30 A31 A32 S33 S34 Q35 A36 C37 L40 C41 D44 A45 K46 C47 R48 F49 F50 T51 L52 A53 S54 G55 K56 C57 S58 L59 D62 D63 A64 A65 L66

R67 P68 T69 K70 S71 D72 V75 S76 G77 N78 K79 R80 C81 I82 L83 L84 E85 D86

5 Refinement protocol and experimental data overview (i)

The models were refined using the following method: *simulated annealing*.

Of the 250 calculated structures, 20 were deposited, based on the following criterion: *LOW ENERGY AND LEAST RESTRAINT VIOLATIONS*.

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

Software name	Classification	Version
X-PLOR3.8	refinement	
XPLOR3.8	structure solution	

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	426	417	417	12±3
All	All	8520	8340	8340	233

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 14.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:52:LEU:HA	1:A:57:CYS:HA	0.66	1.67	14	17
1:A:52:LEU:HD12	1:A:57:CYS:HB2	0.65	1.67	5	8
1:A:30:LYS:HA	1:A:56:LYS:HA	0.65	1.68	14	3
1:A:69:THR:HG22	1:A:70:LYS:HG3	0.64	1.68	7	1
1:A:20:PHE:HB2	1:A:51:THR:HG21	0.63	1.68	1	8
1:A:47:CYS:HB2	1:A:59:LEU:HD13	0.62	1.71	12	2
1:A:50:PHE:HA	1:A:59:LEU:HA	0.61	1.72	10	18
1:A:27:SER:HB3	1:A:59:LEU:HD11	0.61	1.72	12	3
1:A:51:THR:HG23	1:A:76:SER:HB3	0.60	1.73	10	6
1:A:26:ILE:HD11	1:A:59:LEU:HD12	0.60	1.73	18	8
1:A:26:ILE:HD13	1:A:46:LYS:HB3	0.60	1.73	3	2
1:A:19:SER:HB3	1:A:70:LYS:HB2	0.60	1.73	18	1
1:A:34:SER:HA	1:A:52:LEU:HD13	0.59	1.74	9	8
1:A:63:ASP:HA	1:A:66:LEU:HD21	0.59	1.74	4	1

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:18:VAL:HA	1:A:71:SER:HB3	0.58	1.73	13	1
1:A:29:ALA:HB2	1:A:40:LEU:HG	0.58	1.75	16	1
1:A:21:THR:HG22	1:A:69:THR:HG22	0.57	1.74	15	1
1:A:18:VAL:HB	1:A:74:ALA:HB3	0.57	1.76	18	1
1:A:34:SER:N	1:A:52:LEU:HD22	0.56	2.15	1	7
1:A:37:CYS:HA	1:A:40:LEU:HD23	0.55	1.76	19	1
1:A:41:CYS:HB2	1:A:59:LEU:HD22	0.55	1.77	5	6
1:A:18:VAL:HG22	1:A:71:SER:HB3	0.54	1.79	12	1
1:A:40:LEU:O	1:A:40:LEU:HD22	0.54	2.02	20	9
1:A:52:LEU:HG	1:A:53:ALA:N	0.54	2.17	11	18
1:A:18:VAL:HB	1:A:71:SER:HB2	0.53	1.80	19	1
1:A:52:LEU:HG	1:A:54:SER:H	0.52	1.64	10	2
1:A:27:SER:O	1:A:59:LEU:HG	0.51	2.05	10	11
1:A:41:CYS:SG	1:A:59:LEU:HB3	0.51	2.46	11	5
1:A:34:SER:HA	1:A:37:CYS:SG	0.50	2.45	16	3
1:A:37:CYS:SG	1:A:52:LEU:HD13	0.50	2.46	17	6
1:A:29:ALA:HB3	1:A:57:CYS:HB2	0.50	1.84	18	4
1:A:26:ILE:HD13	1:A:26:ILE:H	0.50	1.67	12	2
1:A:31:ALA:HB3	1:A:57:CYS:SG	0.49	2.47	10	5
1:A:18:VAL:HG23	1:A:70:LYS:C	0.49	2.28	6	1
1:A:29:ALA:O	1:A:57:CYS:HB3	0.48	2.09	6	10
1:A:40:LEU:HD11	1:A:59:LEU:HD21	0.48	1.84	14	1
1:A:29:ALA:HB3	1:A:57:CYS:SG	0.47	2.49	20	2
1:A:52:LEU:HG	1:A:53:ALA:H	0.47	1.70	15	3
1:A:58:SER:HB3	1:A:60:PHE:CE1	0.47	2.45	19	3
1:A:30:LYS:HA	1:A:56:LYS:HG3	0.47	1.86	16	1
1:A:41:CYS:SG	1:A:59:LEU:HD22	0.46	2.51	15	1
1:A:44:ASP:HB3	1:A:47:CYS:HB3	0.45	1.86	19	2
1:A:46:LYS:O	1:A:61:ALA:HB2	0.45	2.11	17	2
1:A:51:THR:HB	1:A:60:PHE:HE1	0.45	1.71	9	2
1:A:37:CYS:O	1:A:41:CYS:HB2	0.45	2.11	14	3
1:A:26:ILE:HG13	1:A:59:LEU:O	0.45	2.11	19	1
1:A:41:CYS:HB2	1:A:59:LEU:HD13	0.44	1.89	18	1
1:A:30:LYS:HG2	1:A:56:LYS:HG3	0.44	1.87	4	1
1:A:20:PHE:HD2	1:A:51:THR:HG1	0.44	1.56	5	1
1:A:23:GLY:HA3	1:A:66:LEU:HB3	0.44	1.89	9	2
1:A:57:CYS:SG	1:A:59:LEU:HD23	0.43	2.52	9	1
1:A:37:CYS:O	1:A:40:LEU:HD23	0.43	2.13	9	3
1:A:69:THR:HG23	1:A:70:LYS:H	0.43	1.74	19	1
1:A:18:VAL:HB	1:A:71:SER:HA	0.42	1.91	17	1
1:A:37:CYS:HA	1:A:40:LEU:CD2	0.42	2.44	14	1

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:51:THR:N	1:A:58:SER:O	0.42	2.53	18	5
1:A:26:ILE:HD12	1:A:27:SER:HB2	0.42	1.91	19	1
1:A:29:ALA:HB2	1:A:40:LEU:HD13	0.42	1.92	12	1
1:A:59:LEU:N	1:A:59:LEU:HD23	0.42	2.30	11	1
1:A:18:VAL:HG23	1:A:19:SER:N	0.41	2.30	15	2
1:A:60:PHE:CG	1:A:66:LEU:HD21	0.41	2.50	18	1
1:A:39:GLU:HG2	1:A:40:LEU:N	0.41	2.30	3	1
1:A:18:VAL:HG21	1:A:69:THR:H	0.41	1.75	19	1
1:A:51:THR:HB	1:A:60:PHE:HE2	0.41	1.75	1	1
1:A:20:PHE:CD2	1:A:66:LEU:HD23	0.41	2.51	18	1
1:A:58:SER:HB3	1:A:60:PHE:CE2	0.41	2.51	1	1
1:A:27:SER:CB	1:A:59:LEU:HD11	0.40	2.43	12	1
1:A:26:ILE:HD13	1:A:59:LEU:O	0.40	2.15	16	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	60/86 (70%)	47±2 (78±3%)	10±2 (16±3%)	3±1 (6±2%)	3	22
All	All	1200/1720 (70%)	941 (78%)	191 (16%)	68 (6%)	3	22

All 14 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	55	GLY	15
1	A	30	LYS	12
1	A	69	THR	9
1	A	61	ALA	7
1	A	18	VAL	7
1	A	65	ALA	5
1	A	70	LYS	4
1	A	19	SER	2
1	A	64	ALA	2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Models (Total)
1	A	66	LEU	1
1	A	71	SER	1
1	A	62	ASP	1
1	A	72	ASP	1
1	A	73	GLY	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	44/69 (64%)	24±3 (54±6%)	20±3 (46±6%)	0 2
All	All	880/1380 (64%)	479 (54%)	401 (46%)	0 2

All 37 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	28	GLU	20
1	A	41	CYS	20
1	A	59	LEU	20
1	A	66	LEU	18
1	A	35	GLN	18
1	A	40	LEU	17
1	A	34	SER	16
1	A	20	PHE	15
1	A	48	ARG	15
1	A	57	CYS	14
1	A	70	LYS	14
1	A	52	LEU	13
1	A	76	SER	13
1	A	43	LYS	12
1	A	62	ASP	12
1	A	71	SER	12
1	A	24	LYS	11
1	A	33	SER	11
1	A	72	ASP	11
1	A	44	ASP	10

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Models (Total)
1	A	54	SER	9
1	A	75	VAL	9
1	A	47	CYS	9
1	A	69	THR	9
1	A	63	ASP	9
1	A	30	LYS	8
1	A	42	GLU	8
1	A	46	LYS	8
1	A	26	ILE	7
1	A	58	SER	7
1	A	19	SER	7
1	A	18	VAL	4
1	A	56	LYS	4
1	A	67	ARG	4
1	A	27	SER	3
1	A	39	GLU	3
1	A	49	PHE	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