



Full wwPDB NMR Structure Validation Report ⓘ

Apr 26, 2016 – 04:07 PM BST

PDB ID : 1MM4
Title : Solution NMR structure of the outer membrane enzyme PagP in DPC micelles
Authors : Hwang, P.M.; Choy, W.-Y.; Lo, E.I.; Chen, L.; Forman-Kay, J.D.; Raetz, C.R.H.; Prive, G.G.; Bishop, R.E.; Kay, L.E.
Deposited on : 2002-09-03

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
<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
Mogul : unknown
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
ShiftChecker : rb-20027457
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20027457

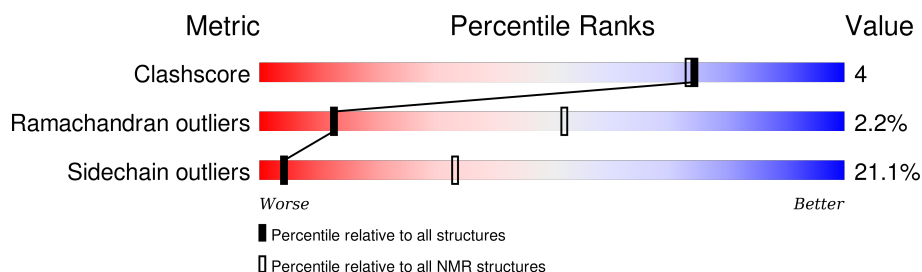
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 38%.

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	114402	11133
Ramachandran outliers	111179	9975
Sidechain outliers	111093	9958

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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	170	

2 Ensemble composition and analysis ⓘ

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, 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:3-A:19 (17)	0.40	5
2	A:21-A:30, A:52-A:163 (122)	1.30	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 2 single-model clusters were found.

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

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 2768 atoms, of which 1330 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called CrcA protein.

Mol	Chain	Residues	Atoms						Trace
1	A	170	Total	C	H	N	O	S	0
			2768	937	1330	247	249	5	

There are 9 discrepancies between the modelled and reference sequences:

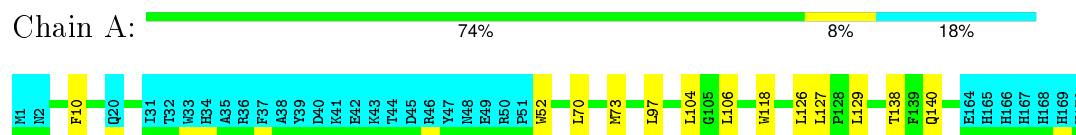
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	EXPRESSION TAG	UNP P37001
A	163	LEU	-	EXPRESSION TAG	UNP P37001
A	164	GLU	-	EXPRESSION TAG	UNP P37001
A	165	HIS	-	EXPRESSION TAG	UNP P37001
A	166	HIS	-	EXPRESSION TAG	UNP P37001
A	167	HIS	-	EXPRESSION TAG	UNP P37001
A	168	HIS	-	EXPRESSION TAG	UNP P37001
A	169	HIS	-	EXPRESSION TAG	UNP P37001
A	170	HIS	-	EXPRESSION TAG	UNP P37001

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: CrcA protein

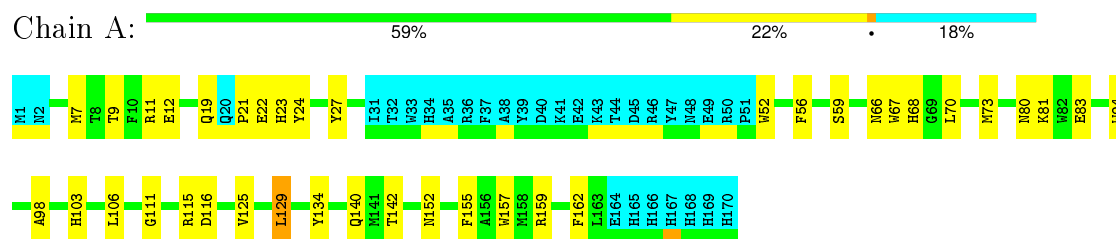


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

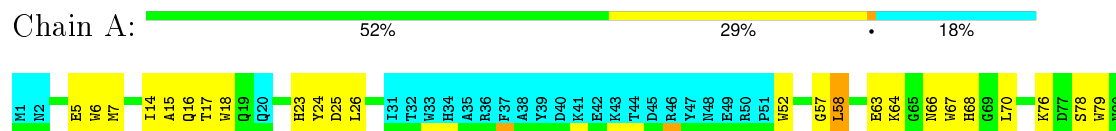
4.2.1 Score per residue for model 1

- Molecule 1: CrcA protein



4.2.2 Score per residue for model 2

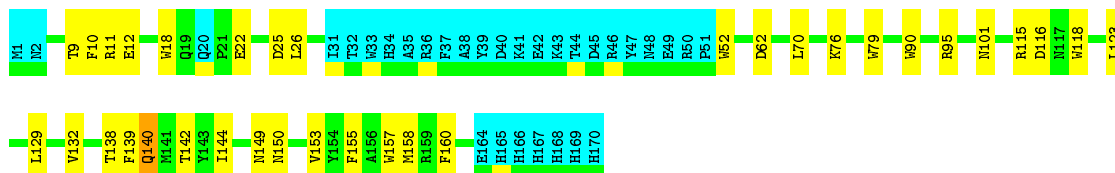
- Molecule 1: CrcA protein





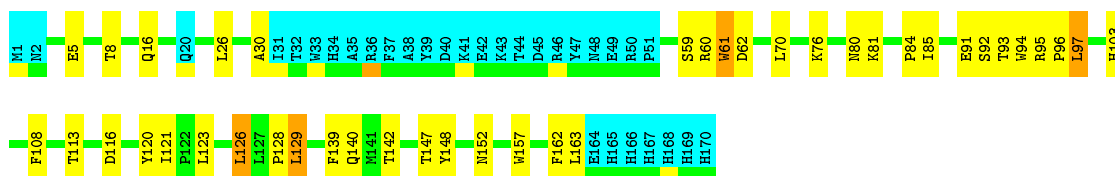
4.2.3 Score per residue for model 3

- Molecule 1: CrcA protein



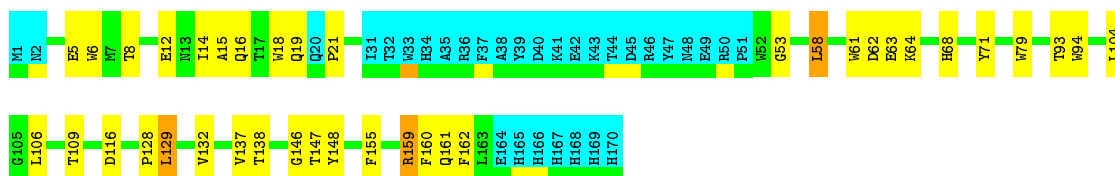
4.2.4 Score per residue for model 4

- Molecule 1: CrcA protein



4.2.5 Score per residue for model 5

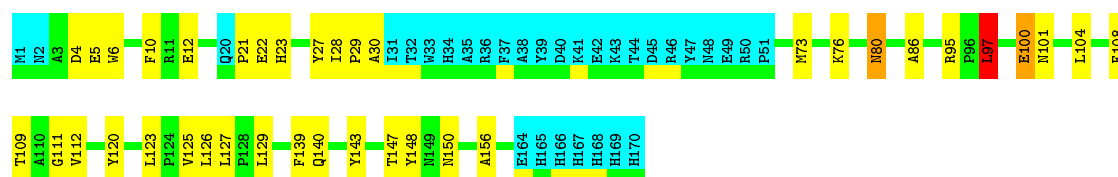
- Molecule 1: CrcA protein



4.2.6 Score per residue for model 6

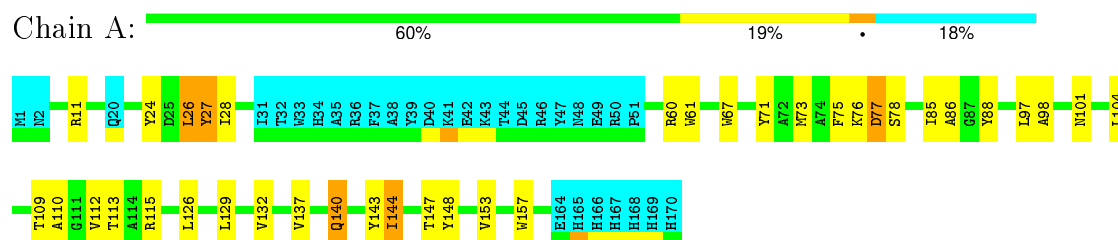
- Molecule 1: CrcA protein





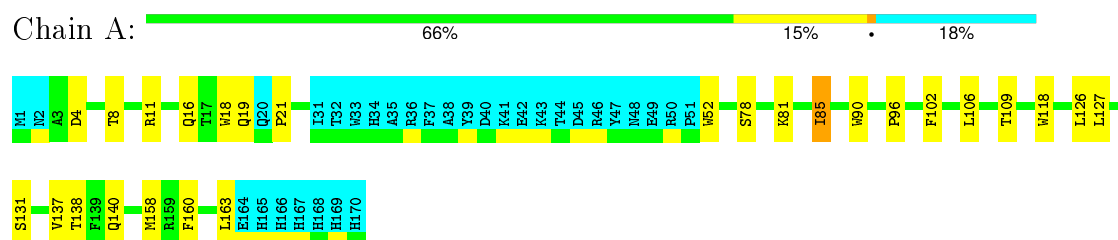
4.2.7 Score per residue for model 7

- Molecule 1: CrcA protein



4.2.8 Score per residue for model 8

- Molecule 1: CrcA protein



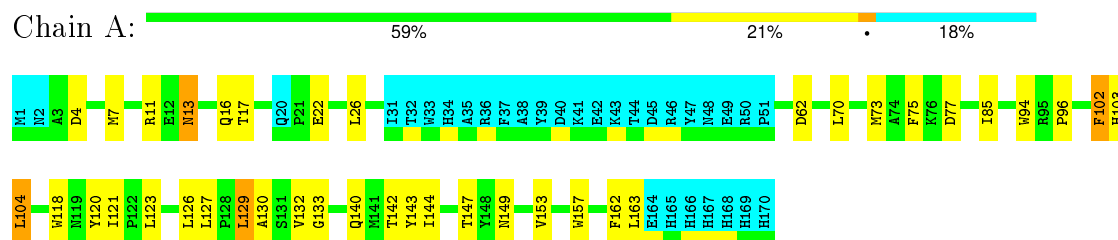
4.2.9 Score per residue for model 9

- Molecule 1: CrcA protein



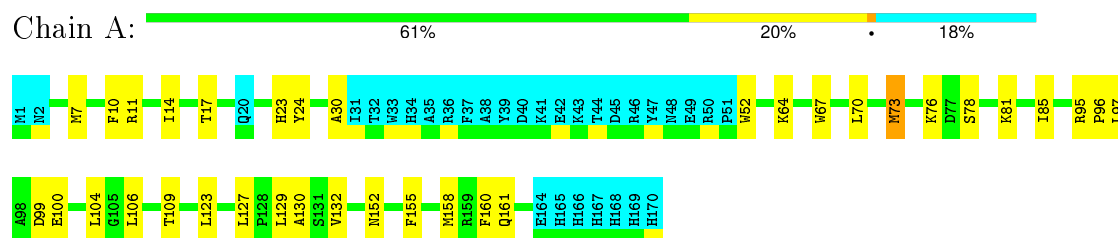
4.2.10 Score per residue for model 10

- Molecule 1: CrcA protein



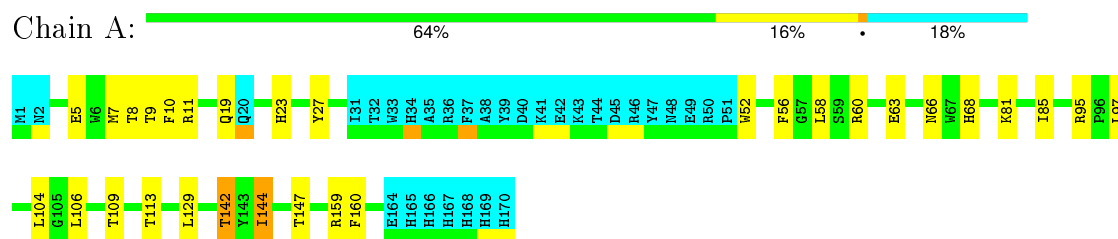
4.2.11 Score per residue for model 11

- Molecule 1: CrcA protein



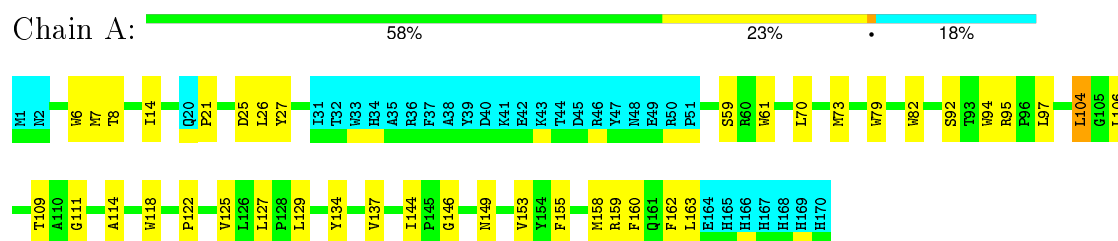
4.2.12 Score per residue for model 12

- Molecule 1: CrcA protein



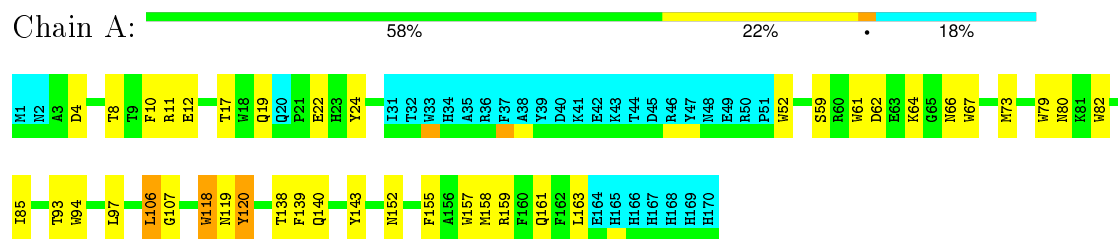
4.2.13 Score per residue for model 13

- Molecule 1: CrcA protein



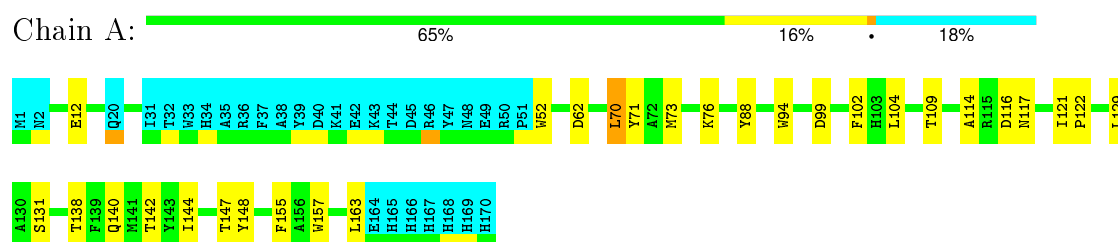
4.2.14 Score per residue for model 14

- Molecule 1: CrcA protein



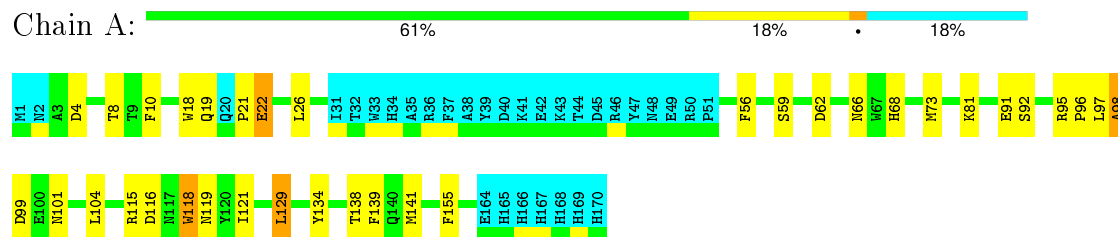
4.2.15 Score per residue for model 15

- Molecule 1: CrcA protein



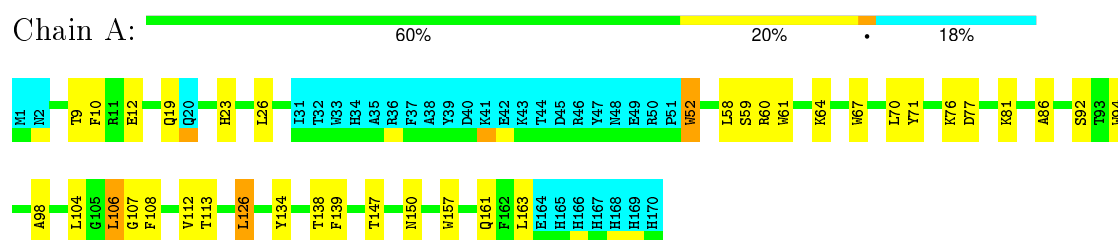
4.2.16 Score per residue for model 16

- Molecule 1: CrcA protein



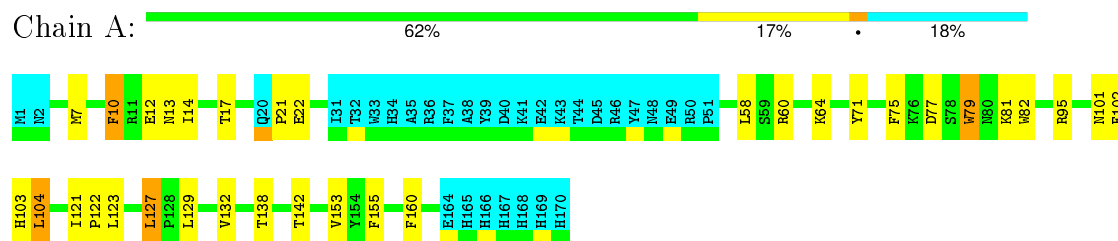
4.2.17 Score per residue for model 17 (medoid)

- Molecule 1: CrcA protein



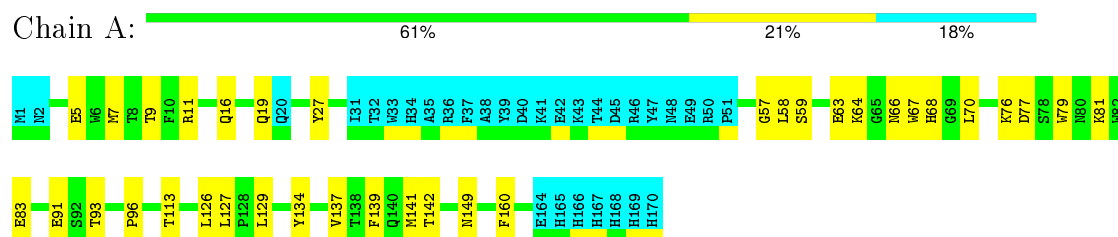
4.2.18 Score per residue for model 18

- Molecule 1: CrcA protein



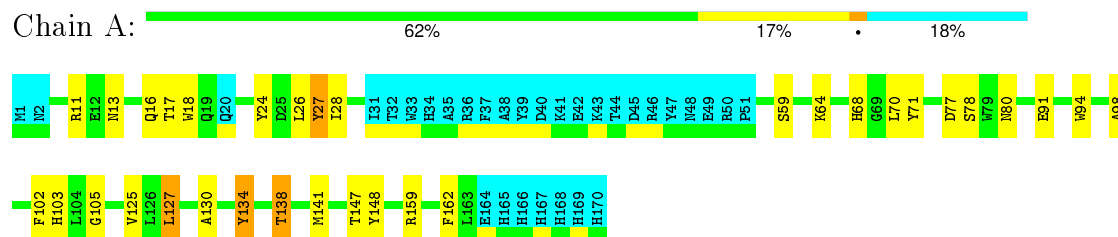
4.2.19 Score per residue for model 19

- Molecule 1: CrcA protein



4.2.20 Score per residue for model 20

- Molecule 1: CrcA protein



5 Refinement protocol and experimental data overview

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

Of the 250 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
CNS	structure solution	1.0
CNS	refinement	1.0

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 5557
Number of chemical shift lists	2
Total number of shifts	1471
Number of shifts mapped to atoms	1471
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	38%

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	1152	1068	1052	9±3
All	All	23040	21360	21040	176

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 4.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:144:ILE:HD12	1:A:153:VAL:HG23	0.81	1.52	3	1
1:A:106:LEU:HD23	1:A:130:ALA:HB2	0.79	1.55	11	1
1:A:26:LEU:HD23	1:A:28:ILE:HD11	0.77	1.55	7	1
1:A:134:TYR:O	1:A:138:THR:HG23	0.74	1.82	20	1
1:A:4:ASP:O	1:A:8:THR:HG23	0.70	1.86	8	2
1:A:144:ILE:HD11	1:A:155:PHE:CE1	0.69	2.23	13	1
1:A:121:ILE:HD12	1:A:122:PRO:O	0.68	1.88	15	2
1:A:111:GLY:O	1:A:125:VAL:HG22	0.68	1.87	13	3
1:A:84:PRO:O	1:A:85:ILE:HD13	0.65	1.90	4	1
1:A:132:VAL:HG13	1:A:139:PHE:HB2	0.65	1.69	3	1
1:A:129:LEU:CD1	1:A:142:THR:HG23	0.64	2.23	19	1
1:A:104:LEU:HG	1:A:132:VAL:HG12	0.63	1.70	10	1
1:A:109:THR:OG1	1:A:129:LEU:HD13	0.63	1.93	11	1
1:A:129:LEU:CD2	1:A:142:THR:HG22	0.62	2.24	2	1

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:109:THR:HG22	1:A:129:LEU:HD22	0.62	1.72	13	1
1:A:129:LEU:N	1:A:129:LEU:HD13	0.60	2.12	5	2
1:A:129:LEU:HD13	1:A:129:LEU:N	0.60	2.12	16	1
1:A:127:LEU:HD12	1:A:129:LEU:HD11	0.59	1.75	18	1
1:A:70:LEU:HD13	1:A:71:TYR:N	0.59	2.13	15	1
1:A:129:LEU:CG	1:A:142:THR:HG22	0.59	2.28	2	1
1:A:125:VAL:O	1:A:127:LEU:HD23	0.58	1.99	20	1
1:A:104:LEU:HA	1:A:132:VAL:HG12	0.58	1.74	7	1
1:A:128:PRO:C	1:A:129:LEU:HD13	0.58	2.19	5	2
1:A:26:LEU:HD12	1:A:162:PHE:CE1	0.58	2.33	20	1
1:A:144:ILE:CD1	1:A:153:VAL:HG23	0.58	2.26	3	1
1:A:28:ILE:N	1:A:28:ILE:HD13	0.58	2.14	9	1
1:A:144:ILE:HD13	1:A:144:ILE:N	0.57	2.14	7	1
1:A:104:LEU:O	1:A:104:LEU:HD12	0.57	1.99	12	1
1:A:121:ILE:HG23	1:A:121:ILE:O	0.57	2.00	10	1
1:A:144:ILE:HG23	1:A:144:ILE:O	0.56	2.00	15	1
1:A:120:TYR:CD2	1:A:121:ILE:HG23	0.55	2.36	4	1
1:A:70:LEU:HD12	1:A:70:LEU:O	0.55	2.00	20	2
1:A:10:PHE:O	1:A:14:ILE:HG22	0.55	2.02	11	1
1:A:129:LEU:HG	1:A:142:THR:HG22	0.55	1.77	2	1
1:A:114:ALA:HB2	1:A:122:PRO:HB3	0.55	1.77	13	2
1:A:129:LEU:HD21	1:A:142:THR:HG22	0.54	1.79	2	1
1:A:129:LEU:HD21	1:A:140:GLN:HG2	0.54	1.78	3	1
1:A:127:LEU:HD22	1:A:144:ILE:HG22	0.54	1.78	10	1
1:A:86:ALA:HB3	1:A:112:VAL:HG23	0.54	1.78	7	3
1:A:58:LEU:HD12	1:A:70:LEU:HD13	0.54	1.79	17	1
1:A:129:LEU:HB3	1:A:142:THR:HG23	0.54	1.79	12	1
1:A:105:GLY:O	1:A:130:ALA:HB1	0.54	2.03	20	1
1:A:97:LEU:O	1:A:97:LEU:HD23	0.54	2.02	4	1
1:A:137:VAL:HG12	1:A:160:PHE:CE2	0.53	2.38	19	1
1:A:139:PHE:CZ	1:A:156:ALA:HB1	0.53	2.38	6	1
1:A:144:ILE:HD13	1:A:144:ILE:H	0.53	1.64	7	1
1:A:106:LEU:CD2	1:A:130:ALA:HB2	0.53	2.31	11	1
1:A:144:ILE:O	1:A:144:ILE:HG23	0.52	2.04	12	1
1:A:104:LEU:HB3	1:A:132:VAL:HG23	0.52	1.82	5	1
1:A:115:ARG:NH2	1:A:123:LEU:HD22	0.52	2.19	3	1
1:A:129:LEU:HD21	1:A:140:GLN:CG	0.52	2.33	3	1
1:A:109:THR:OG1	1:A:129:LEU:HD21	0.52	2.04	15	1
1:A:88:TYR:O	1:A:110:ALA:HB3	0.52	2.05	2	1
1:A:21:PRO:HB3	1:A:58:LEU:HD11	0.52	1.81	5	1
1:A:104:LEU:N	1:A:104:LEU:HD23	0.52	2.20	13	1

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:13:ASN:O	1:A:17:THR:HG23	0.51	2.05	10	2
1:A:153:VAL:O	1:A:153:VAL:HG23	0.51	2.05	13	2
1:A:137:VAL:HG13	1:A:137:VAL:O	0.51	2.06	7	2
1:A:153:VAL:O	1:A:153:VAL:HG13	0.51	2.06	7	1
1:A:13:ASN:O	1:A:17:THR:HG22	0.51	2.06	20	1
1:A:108:PHE:HB3	1:A:126:LEU:HD21	0.51	1.82	17	1
1:A:28:ILE:HD13	1:A:28:ILE:H	0.51	1.65	9	1
1:A:129:LEU:C	1:A:129:LEU:HD22	0.50	2.26	10	1
1:A:70:LEU:HD11	1:A:88:TYR:CE2	0.50	2.41	9	1
1:A:110:ALA:HB2	1:A:126:LEU:HD23	0.50	1.82	7	1
1:A:85:ILE:HD13	1:A:85:ILE:C	0.49	2.28	8	1
1:A:57:GLY:C	1:A:58:LEU:HD12	0.49	2.28	19	1
1:A:106:LEU:HD23	1:A:130:ALA:CB	0.49	2.35	11	1
1:A:73:MET:HB2	1:A:85:ILE:HD11	0.49	1.84	11	1
1:A:97:LEU:HD23	1:A:97:LEU:O	0.49	2.07	11	1
1:A:106:LEU:HD13	1:A:107:GLY:N	0.48	2.23	17	2
1:A:104:LEU:HG	1:A:132:VAL:HG23	0.48	1.84	11	1
1:A:73:MET:HB3	1:A:85:ILE:HD12	0.48	1.85	14	1
1:A:73:MET:HB3	1:A:85:ILE:HD11	0.48	1.85	10	1
1:A:127:LEU:N	1:A:127:LEU:HD23	0.48	2.24	18	1
1:A:126:LEU:C	1:A:127:LEU:HD12	0.48	2.28	6	1
1:A:104:LEU:HG	1:A:132:VAL:HG13	0.48	1.83	18	1
1:A:5:GLU:O	1:A:9:THR:HG23	0.48	2.09	12	2
1:A:143:TYR:CZ	1:A:153:VAL:HG23	0.48	2.44	10	1
1:A:26:LEU:HD22	1:A:28:ILE:HG23	0.48	1.85	20	1
1:A:138:THR:HG23	1:A:159:ARG:HB3	0.48	1.85	5	1
1:A:21:PRO:CB	1:A:58:LEU:HD11	0.47	2.39	5	1
1:A:70:LEU:HD23	1:A:71:TYR:N	0.47	2.25	17	1
1:A:129:LEU:HD22	1:A:130:ALA:N	0.47	2.23	10	1
1:A:126:LEU:N	1:A:126:LEU:HD23	0.47	2.25	4	1
1:A:129:LEU:N	1:A:129:LEU:HD23	0.46	2.24	13	1
1:A:73:MET:CB	1:A:85:ILE:HD11	0.46	2.40	10	1
1:A:61:TRP:CZ2	1:A:67:TRP:CZ2	0.46	3.03	17	1
1:A:129:LEU:HD21	1:A:140:GLN:HB3	0.46	1.85	1	1
1:A:27:TYR:O	1:A:28:ILE:HG23	0.46	2.10	6	1
1:A:10:PHE:CD2	1:A:14:ILE:HD11	0.46	2.46	18	1
1:A:85:ILE:O	1:A:85:ILE:HG23	0.46	2.10	8	1
1:A:70:LEU:N	1:A:70:LEU:HD12	0.46	2.26	2	2
1:A:96:PRO:HB2	1:A:97:LEU:HD12	0.45	1.87	16	1
1:A:119:ASN:HB3	1:A:121:ILE:HD12	0.45	1.88	16	1
1:A:115:ARG:HH21	1:A:123:LEU:HD22	0.45	1.71	3	1

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:85:ILE:HG23	1:A:85:ILE:O	0.45	2.10	12	2
1:A:25:ASP:C	1:A:26:LEU:HD12	0.45	2.31	13	1
1:A:104:LEU:C	1:A:104:LEU:HD23	0.45	2.32	2	1
1:A:82:TRP:N	1:A:82:TRP:CD1	0.45	2.84	14	1
1:A:71:TYR:OH	1:A:109:THR:HG21	0.45	2.11	5	1
1:A:27:TYR:CE2	1:A:71:TYR:CE2	0.45	3.04	20	1
1:A:134:TYR:O	1:A:137:VAL:HG22	0.45	2.12	13	1
1:A:113:THR:HG23	1:A:123:LEU:HD23	0.45	1.88	4	1
1:A:129:LEU:HD21	1:A:140:GLN:HG3	0.45	1.88	7	1
1:A:108:PHE:N	1:A:108:PHE:CD1	0.45	2.85	4	1
1:A:147:THR:HG22	1:A:148:TYR:CD2	0.45	2.47	15	1
1:A:129:LEU:HG	1:A:142:THR:HG23	0.45	1.89	19	1
1:A:75:PHE:CD2	1:A:85:ILE:HD11	0.45	2.47	7	1
1:A:57:GLY:O	1:A:58:LEU:HD22	0.44	2.13	2	1
1:A:143:TYR:CD1	1:A:144:ILE:N	0.44	2.85	7	1
1:A:109:THR:OG1	1:A:129:LEU:HD22	0.44	2.11	2	1
1:A:68:HIS:CE1	1:A:70:LEU:HD11	0.44	2.47	19	1
1:A:95:ARG:HB2	1:A:98:ALA:HB2	0.44	1.90	16	1
1:A:70:LEU:HD13	1:A:71:TYR:H	0.44	1.73	15	1
1:A:70:LEU:HD23	1:A:88:TYR:CE2	0.43	2.48	15	1
1:A:126:LEU:C	1:A:126:LEU:HD23	0.43	2.33	10	1
1:A:127:LEU:O	1:A:129:LEU:HD12	0.43	2.13	19	2
1:A:27:TYR:CD2	1:A:73:MET:CE	0.43	3.01	7	1
1:A:56:PHE:N	1:A:56:PHE:CD1	0.43	2.87	16	2
1:A:14:ILE:HG23	1:A:15:ALA:N	0.43	2.29	2	2
1:A:120:TYR:CD1	1:A:120:TYR:N	0.43	2.87	4	1
1:A:127:LEU:HD13	1:A:142:THR:CG2	0.43	2.44	10	1
1:A:129:LEU:HD11	1:A:140:GLN:NE2	0.42	2.29	6	1
1:A:97:LEU:N	1:A:97:LEU:HD12	0.42	2.29	7	1
1:A:129:LEU:N	1:A:129:LEU:CD1	0.42	2.82	4	1
1:A:129:LEU:CG	1:A:142:THR:HG23	0.42	2.45	19	1
1:A:23:HIS:O	1:A:58:LEU:HD13	0.42	2.14	2	1
1:A:125:VAL:HG12	1:A:126:LEU:N	0.42	2.29	2	1
1:A:27:TYR:CE1	1:A:71:TYR:CZ	0.42	3.07	7	1
1:A:28:ILE:N	1:A:28:ILE:CD1	0.42	2.82	9	1
1:A:147:THR:HG23	1:A:147:THR:O	0.42	2.13	5	1
1:A:144:ILE:CD1	1:A:144:ILE:N	0.42	2.82	7	1
1:A:27:TYR:CE2	1:A:71:TYR:CD2	0.42	3.08	20	1
1:A:71:TYR:N	1:A:71:TYR:CD1	0.42	2.88	18	1
1:A:127:LEU:HD22	1:A:144:ILE:CG2	0.42	2.45	13	1
1:A:134:TYR:CD1	1:A:134:TYR:N	0.42	2.87	9	1

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:79:TRP:CD1	1:A:79:TRP:N	0.42	2.88	3	1
1:A:58:LEU:HD23	1:A:58:LEU:N	0.41	2.30	12	1
1:A:23:HIS:O	1:A:58:LEU:HD23	0.41	2.16	17	1
1:A:91:GLU:OE2	1:A:129:LEU:HD23	0.41	2.15	4	1
1:A:75:PHE:N	1:A:75:PHE:CD1	0.41	2.88	10	1
1:A:85:ILE:HD12	1:A:113:THR:OG1	0.41	2.15	4	1
1:A:129:LEU:CD1	1:A:129:LEU:N	0.41	2.82	10	1
1:A:26:LEU:CD2	1:A:28:ILE:HG23	0.41	2.46	20	1
1:A:58:LEU:H	1:A:58:LEU:HD23	0.41	1.76	12	1
1:A:97:LEU:O	1:A:97:LEU:HD13	0.41	2.16	6	1
1:A:5:GLU:HA	1:A:8:THR:HG22	0.41	1.93	12	1
1:A:82:TRP:CD1	1:A:82:TRP:O	0.40	2.74	2	1
1:A:109:THR:OG1	1:A:129:LEU:HD11	0.40	2.16	5	1
1:A:61:TRP:N	1:A:61:TRP:CD1	0.40	2.88	4	1
1:A:102:PHE:CD1	1:A:133:GLY:O	0.40	2.74	10	1
1:A:28:ILE:O	1:A:28:ILE:HD12	0.40	2.15	20	1
1:A:137:VAL:O	1:A:137:VAL:HG23	0.40	2.17	8	1
1:A:88:TYR:N	1:A:88:TYR:CD1	0.40	2.89	7	1
1:A:148:TYR:O	1:A:148:TYR:CD1	0.40	2.74	5	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	139/170 (82%)	124±3 (89±2%)	12±2 (8±2%)	3±2 (2±1%)	13	52
All	All	2780/3400 (82%)	2483 (89%)	236 (8%)	61 (2%)	13	52

All 23 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	98	ALA	7
1	A	80	ASN	6
1	A	96	PRO	5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Models (Total)
1	A	21	PRO	5
1	A	118	TRP	4
1	A	149	ASN	4
1	A	22	GLU	4
1	A	146	GLY	4
1	A	152	ASN	3
1	A	101	ASN	3
1	A	97	LEU	2
1	A	116	ASP	2
1	A	52	TRP	2
1	A	100	GLU	1
1	A	79	TRP	1
1	A	77	ASP	1
1	A	81	LYS	1
1	A	122	PRO	1
1	A	29	PRO	1
1	A	119	ASN	1
1	A	53	GLY	1
1	A	120	TYR	1
1	A	148	TYR	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	113/142 (80%)	89±4 (79±3%)	24±4 (21±3%)	4	33
All	All	2260/2840 (80%)	1784 (79%)	476 (21%)	4	33

All 94 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	11	ARG	10
1	A	76	LYS	10
1	A	81	LYS	9
1	A	157	TRP	9
1	A	138	THR	9

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Models (Total)
1	A	12	GLU	9
1	A	7	MET	9
1	A	19	GLN	9
1	A	155	PHE	9
1	A	94	TRP	9
1	A	52	TRP	9
1	A	160	PHE	8
1	A	140	GLN	8
1	A	10	PHE	8
1	A	59	SER	8
1	A	95	ARG	8
1	A	64	LYS	8
1	A	62	ASP	8
1	A	106	LEU	8
1	A	18	TRP	7
1	A	79	TRP	7
1	A	104	LEU	7
1	A	147	THR	7
1	A	159	ARG	7
1	A	16	GLN	7
1	A	163	LEU	7
1	A	67	TRP	7
1	A	26	LEU	7
1	A	27	TYR	6
1	A	77	ASP	6
1	A	68	HIS	6
1	A	103	HIS	6
1	A	66	ASN	6
1	A	118	TRP	6
1	A	129	LEU	6
1	A	142	THR	6
1	A	73	MET	6
1	A	158	MET	6
1	A	70	LEU	6
1	A	24	TYR	6
1	A	60	ARG	5
1	A	126	LEU	5
1	A	78	SER	5
1	A	97	LEU	5
1	A	116	ASP	5
1	A	102	PHE	5
1	A	139	PHE	5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Models (Total)
1	A	134	TYR	5
1	A	123	LEU	5
1	A	61	TRP	5
1	A	120	TYR	5
1	A	162	PHE	5
1	A	4	ASP	4
1	A	93	THR	4
1	A	115	ARG	4
1	A	92	SER	4
1	A	99	ASP	4
1	A	5	GLU	4
1	A	113	THR	4
1	A	6	TRP	4
1	A	161	GLN	4
1	A	141	MET	4
1	A	109	THR	4
1	A	22	GLU	4
1	A	8	THR	4
1	A	23	HIS	4
1	A	63	GLU	4
1	A	9	THR	3
1	A	150	ASN	3
1	A	83	GLU	3
1	A	152	ASN	3
1	A	91	GLU	3
1	A	58	LEU	3
1	A	127	LEU	3
1	A	148	TYR	3
1	A	17	THR	3
1	A	131	SER	3
1	A	144	ILE	2
1	A	82	TRP	2
1	A	100	GLU	2
1	A	25	ASP	2
1	A	56	PHE	2
1	A	101	ASN	2
1	A	90	TRP	2
1	A	143	TYR	2
1	A	80	ASN	2
1	A	75	PHE	1
1	A	13	ASN	1
1	A	117	ASN	1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Models (Total)
1	A	85	ILE	1
1	A	14	ILE	1
1	A	108	PHE	1
1	A	119	ASN	1
1	A	28	ILE	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 carbohydrates 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

The completeness of assignment taking into account all chemical shift lists is 38% for the well-defined parts and 35% for the entire structure.

7.1 Chemical shift list 1

File name: BMRB entry 5557

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	726
Number of shifts mapped to atoms	726
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	160	0.47 ± 0.09	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	144	0.48 ± 0.12	None needed (< 0.5 ppm)
$^{13}\text{C}'$	136	0.70 ± 0.11	Should be applied
^{15}N	143	-0.29 ± 0.29	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 35%, i.e. 618 atoms were assigned a chemical shift out of a possible 1744. 0 out of 16 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	498/677 (74%)	122/269 (45%)	254/278 (91%)	122/130 (94%)
Sidechain	120/758 (16%)	0/449 (0%)	120/278 (43%)	0/31 (0%)

Continued on next page...

Continued from previous page...

	Total	¹ H	¹³ C	¹⁵ N
Aromatic	0/309 (0%)	0/159 (0%)	0/133 (0%)	0/17 (0%)
Overall	618/1744 (35%)	122/877 (14%)	374/689 (54%)	122/178 (69%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 33%, i.e. 726 atoms were assigned a chemical shift out of a possible 2194. 0 out of 16 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	582/830 (70%)	143/330 (43%)	296/340 (87%)	143/160 (89%)
Sidechain	144/962 (15%)	0/572 (0%)	144/345 (42%)	0/45 (0%)
Aromatic	0/402 (0%)	0/206 (0%)	0/164 (0%)	0/32 (0%)
Overall	726/2194 (33%)	143/1108 (13%)	440/849 (52%)	143/237 (60%)

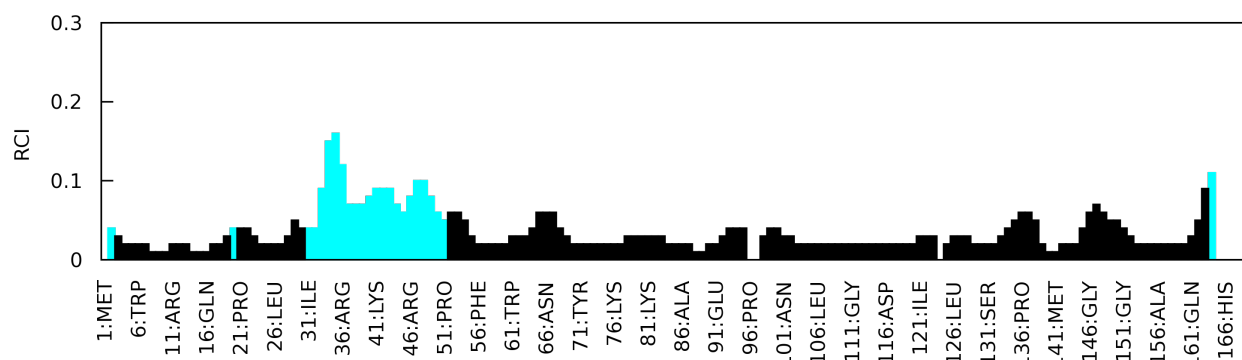
7.1.4 Statistically unusual chemical shifts [i](#)

There are no statistically unusual chemical shifts.

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

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:



7.2 Chemical shift list 2

File name: BMRB entry 5557

Chemical shift list name: *assigned_chem_shift_list_2*

7.2.1 Bookkeeping [i](#)

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	745
Number of shifts mapped to atoms	745
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

7.2.2 Chemical shift referencing [i](#)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	159	0.62 ± 0.15	Should be applied
$^{13}\text{C}_\beta$	139	0.41 ± 0.10	None needed (< 0.5 ppm)
$^{13}\text{C}'$	151	0.73 ± 0.16	Should be applied
^{15}N	148	-0.12 ± 0.23	None needed (< 0.5 ppm)

7.2.3 Completeness of resonance assignments [i](#)

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 36%, i.e. 630 atoms were assigned a chemical shift out of a possible 1744. 0 out of 16 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	515/677 (76%)	126/269 (47%)	263/278 (95%)	126/130 (97%)
Sidechain	115/758 (15%)	0/449 (0%)	115/278 (41%)	0/31 (0%)
Aromatic	0/309 (0%)	0/159 (0%)	0/133 (0%)	0/17 (0%)
Overall	630/1744 (36%)	126/877 (14%)	378/689 (55%)	126/178 (71%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 34%, i.e. 745 atoms were assigned a chemical shift out of a possible 2194. 0 out of 16 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	606/830 (73%)	148/330 (45%)	310/340 (91%)	148/160 (92%)

Continued on next page...

Continued from previous page...

	Total	¹ H	¹³ C	¹⁵ N
Sidechain	139/962 (14%)	0/572 (0%)	139/345 (40%)	0/45 (0%)
Aromatic	0/402 (0%)	0/206 (0%)	0/164 (0%)	0/32 (0%)
Overall	745/2194 (34%)	148/1108 (13%)	449/849 (53%)	148/237 (62%)

7.2.4 Statistically unusual chemical shifts [i](#)

There are no statistically unusual chemical shifts.

7.2.5 Random Coil Index (RCI) plots [i](#)

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:

