Full wwPDB NMR Structure Validation Report (i)

Jun 12, 2024 – 12:30 PM EDT

PDB ID	:	2KT8
BMRB ID	:	16688
Title	:	Solution NMR structure of the CPE1231(468-535) protein from Clostridium perfringens, Northeast Structural Genomics Consortium Target CpR82B
Authors	:	Yang, Y.; Ramelot, T.A.; Lee, D.; Ciccosanti, C.; Hamilton, K.; Acton, T.B.; Xiao, R.; Everett, J.K.; Montelione, G.T.; Kennedy, M.A.; Northeast Structural Genomics Consortium (NESG)
Deposited on	:	2010-01-21

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:

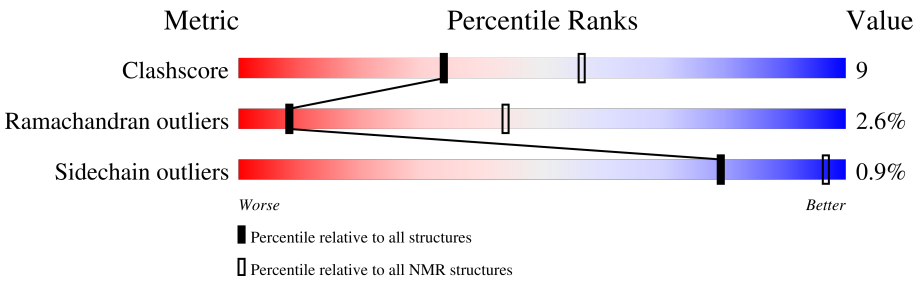
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson 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 is 97%.

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	76	75% 7% 18%

2 Ensemble composition and analysis (i)

This entry contains 20 models. Model 1 is the overall representative, medoid model (most similar to other models).

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:64 (62)	0.64	1

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 2 clusters and 1 single-model cluster was found.

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

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 1162 atoms, of which 575 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Probable surface protein.

Mol	Chain	Residues	Atoms					Trace
			Total	C	H	N	O	
1	A	76	1162	366	575	104	117	0

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	ALA	-	expression tag	UNP Q8XL11
A	69	LEU	-	expression tag	UNP Q8XL11
A	70	GLU	-	expression tag	UNP Q8XL11
A	71	HIS	-	expression tag	UNP Q8XL11
A	72	HIS	-	expression tag	UNP Q8XL11
A	73	HIS	-	expression tag	UNP Q8XL11
A	74	HIS	-	expression tag	UNP Q8XL11
A	75	HIS	-	expression tag	UNP Q8XL11
A	76	HIS	-	expression tag	UNP Q8XL11

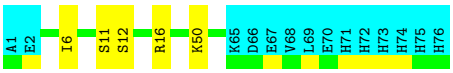
4 Residue-property plots (i)

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: Probable surface protein

Chain A:



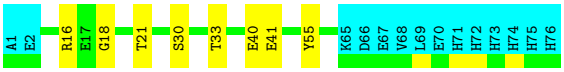
4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1 (medoid)

• Molecule 1: Probable surface protein

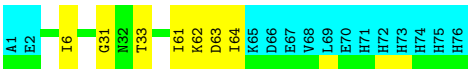
Chain A:



4.2.2 Score per residue for model 2

• Molecule 1: Probable surface protein

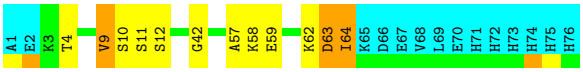
Chain A:



4.2.3 Score per residue for model 3

- Molecule 1: Probable surface protein

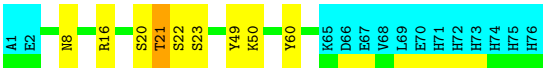
Chain A:



4.2.4 Score per residue for model 4

- Molecule 1: Probable surface protein

Chain A:



4.2.5 Score per residue for model 5

- Molecule 1: Probable surface protein

Chain A:

4.2.6 Score per residue for model 6

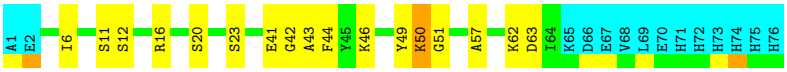
- Molecule 1: Probable surface protein

Chain A:

4.2.7 Score per residue for model 7

- Molecule 1: Probable surface protein

Chain A:



4.2.8 Score per residue for model 8

- Molecule 1: Probable surface protein

Chain A: 63% 17% • 18%

A1 E2 G18 A19 S20 S30 G31 N32 T33 K46 Y49 K50 G51 S52 H53 G54 Y55 E59 Y60 K65 D66 E67 V68 L69 E70 H71 H72 H73 H74 H75 H76

4.2.9 Score per residue for model 9

- Molecule 1: Probable surface protein

Chain A: 68% 11% • 18%

A1 E2 I6 S11 S12 G18 V38 G39 Y49 K50 G51 Y55 K65 D66 E67 V68 L69 E70 H71 H72 H73 H74 H75 H76

4.2.10 Score per residue for model 10

- Molecule 1: Probable surface protein

Chain A: 64% 16% • 18%

A1 E2 I6 V7 N8 R16 E17 G18 T21 S22 S23 Y45 K58 E59 Y60 I61 K62 D63 I64 K65 D66 E67 V68 L69 E70 H71 H72 H73 H74 H75 H76

4.2.11 Score per residue for model 11

- Molecule 1: Probable surface protein

Chain A: 59% 21% • 18%

A1 E2 I6 S11 S12 R16 E17 T21 I26 G31 N32 T33 Y49 K50 G51 Y60 I61 K62 D63 I64 K65 D66 E67 V68 L69 E70 H71 H72 H73 H74 H75 H76

4.2.12 Score per residue for model 12

- Molecule 1: Probable surface protein

Chain A: 74% 5% • 18%

A1 E2 I6 S11 S12 R16 T21 K50 K65 D66 E67 V68 L69 E70 H71 H72 H73 H74 H75 H76

4.2.13 Score per residue for model 13

- Molecule 1: Probable surface protein

Chain A: 72% 9% 18%

4.2.14 Score per residue for model 14

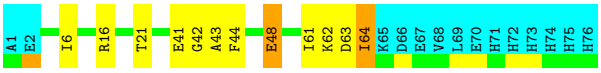
- Molecule 1: Probable surface protein

Chain A: 70% 11% • 18%

4.2.15 Score per residue for model 15

- Molecule 1: Probable surface protein

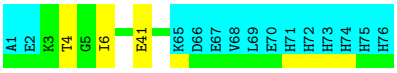
Chain A: 66% 13% • 18%



4.2.16 Score per residue for model 16

- Molecule 1: Probable surface protein

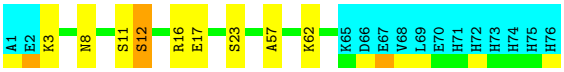
Chain A: 78% • 18%



4.2.17 Score per residue for model 17

- Molecule 1: Probable surface protein

Chain A: 70% 11% • 18%



4.2.18 Score per residue for model 18

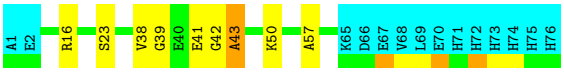
- Molecule 1: Probable surface protein

Chain A:

4.2.19 Score per residue for model 19

- Molecule 1: Probable surface protein

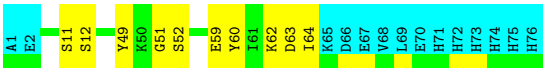
Chain A:



4.2.20 Score per residue for model 20

- Molecule 1: Probable surface protein

Chain A:



5 Refinement protocol and experimental data overview (i)

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

Of the 150 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
X-PLOR NIH	structure solution	2.20
CNS	refinement	1.2
PSVS	refinement	1.4
PdbStat	structure solution	5.1

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)	working_cs.cif
Number of chemical shift lists	1
Total number of shifts	912
Number of shifts mapped to atoms	912
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	97%

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	462	471	471	8±3
All	All	9240	9420	9420	168

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 9.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:6:ILE:N	1:A:6:ILE:HD12	0.71	2.01	12	11
1:A:16:ARG:NH2	1:A:20:SER:N	0.64	2.46	4	1
1:A:16:ARG:NH2	1:A:21:THR:N	0.63	2.46	4	1
1:A:45:TYR:CZ	1:A:58:LYS:NZ	0.63	2.67	10	1
1:A:42:GLY:O	1:A:43:ALA:HB2	0.62	1.95	19	1
1:A:46:LYS:NZ	1:A:53:HIS:ND1	0.61	2.48	5	1
1:A:16:ARG:HH21	1:A:20:SER:N	0.61	1.94	14	1
1:A:42:GLY:O	1:A:43:ALA:HB3	0.60	1.96	7	2
1:A:61:ILE:HD12	1:A:61:ILE:N	0.60	2.10	15	3
1:A:16:ARG:NH2	1:A:57:ALA:H	0.59	1.95	7	3
1:A:8:ASN:HD22	1:A:62:LYS:NZ	0.59	1.95	18	1
1:A:62:LYS:O	1:A:64:ILE:N	0.58	2.37	3	3
1:A:49:TYR:O	1:A:51:GLY:N	0.58	2.36	18	5
1:A:6:ILE:N	1:A:6:ILE:CD1	0.57	2.67	10	11

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:46:LYS:NZ	1:A:53:HIS:CD2	0.57	2.72	8	1
1:A:8:ASN:CB	1:A:62:LYS:NZ	0.57	2.68	18	2
1:A:16:ARG:NH2	1:A:21:THR:H	0.56	1.97	4	1
1:A:16:ARG:HH21	1:A:20:SER:H	0.56	1.42	4	1
1:A:61:ILE:N	1:A:61:ILE:HD12	0.56	2.13	6	2
1:A:16:ARG:NH2	1:A:57:ALA:N	0.56	2.53	19	3
1:A:38:VAL:HG23	1:A:39:GLY:N	0.55	2.16	5	3
1:A:16:ARG:NH2	1:A:20:SER:H	0.55	1.98	4	1
1:A:61:ILE:N	1:A:61:ILE:CD1	0.54	2.70	6	4
1:A:16:ARG:HH22	1:A:57:ALA:N	0.53	2.00	5	1
1:A:46:LYS:HZ3	1:A:53:HIS:CG	0.53	2.21	5	1
1:A:59:GLU:OE2	1:A:60:TYR:CE2	0.53	2.62	8	2
1:A:16:ARG:HH21	1:A:57:ALA:N	0.53	2.01	19	2
1:A:20:SER:O	1:A:22:SER:N	0.53	2.41	4	1
1:A:9:VAL:O	1:A:11:SER:N	0.53	2.41	3	2
1:A:58:LYS:O	1:A:60:TYR:N	0.53	2.42	6	2
1:A:8:ASN:ND2	1:A:62:LYS:NZ	0.52	2.57	18	1
1:A:41:GLU:O	1:A:43:ALA:N	0.52	2.43	19	1
1:A:61:ILE:CD1	1:A:61:ILE:N	0.51	2.73	2	1
1:A:59:GLU:OE2	1:A:60:TYR:CZ	0.51	2.62	8	1
1:A:41:GLU:OE1	1:A:41:GLU:N	0.51	2.43	15	1
1:A:17:GLU:N	1:A:23:SER:OG	0.51	2.42	17	1
1:A:16:ARG:NE	1:A:21:THR:O	0.51	2.43	12	2
1:A:42:GLY:O	1:A:43:ALA:CB	0.51	2.59	19	3
1:A:16:ARG:NH1	1:A:21:THR:O	0.50	2.45	11	1
1:A:11:SER:OG	1:A:12:SER:N	0.50	2.43	6	4
1:A:18:GLY:N	1:A:23:SER:OG	0.50	2.44	10	1
1:A:46:LYS:HZ3	1:A:53:HIS:CD2	0.50	2.25	8	1
1:A:20:SER:C	1:A:21:THR:HG1	0.49	2.11	4	1
1:A:62:LYS:O	1:A:63:ASP:CB	0.49	2.61	20	3
1:A:8:ASN:ND2	1:A:62:LYS:HZ2	0.49	2.05	18	1
1:A:58:LYS:C	1:A:60:TYR:N	0.48	2.67	6	2
1:A:18:GLY:O	1:A:55:TYR:CG	0.48	2.66	9	2
1:A:18:GLY:O	1:A:55:TYR:CD1	0.48	2.67	9	1
1:A:9:VAL:C	1:A:11:SER:N	0.47	2.67	3	1
1:A:38:VAL:CG2	1:A:39:GLY:N	0.47	2.78	5	2
1:A:19:ALA:H	1:A:55:TYR:CB	0.47	2.23	8	1
1:A:57:ALA:HB1	1:A:59:GLU:OE1	0.47	2.10	3	1
1:A:16:ARG:NH2	1:A:20:SER:C	0.47	2.68	14	1
1:A:42:GLY:O	1:A:44:PHE:CD2	0.46	2.68	15	1
1:A:42:GLY:O	1:A:58:LYS:NZ	0.46	2.48	3	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:9:VAL:HG22	1:A:11:SER:H	0.46	1.69	5	1
1:A:18:GLY:O	1:A:55:TYR:CD2	0.46	2.69	1	1
1:A:63:ASP:O	1:A:64:ILE:O	0.46	2.33	3	1
1:A:21:THR:O	1:A:22:SER:CB	0.46	2.62	5	1
1:A:21:THR:OG1	1:A:22:SER:N	0.46	2.48	4	1
1:A:29:LEU:HD21	1:A:49:TYR:CE1	0.45	2.46	13	1
1:A:16:ARG:HH22	1:A:57:ALA:H	0.45	1.55	5	1
1:A:6:ILE:HD13	1:A:63:ASP:O	0.45	2.11	10	1
1:A:58:LYS:C	1:A:60:TYR:H	0.45	2.15	6	1
1:A:16:ARG:NH1	1:A:44:PHE:CE1	0.45	2.85	14	1
1:A:40:GLU:CD	1:A:41:GLU:N	0.45	2.70	5	2
1:A:31:GLY:O	1:A:33:THR:N	0.45	2.49	6	2
1:A:31:GLY:C	1:A:33:THR:H	0.44	2.15	11	5
1:A:19:ALA:O	1:A:20:SER:O	0.44	2.35	8	1
1:A:11:SER:O	1:A:12:SER:O	0.44	2.34	9	3
1:A:49:TYR:O	1:A:50:LYS:C	0.44	2.56	9	2
1:A:60:TYR:C	1:A:61:ILE:HD12	0.44	2.32	11	2
1:A:31:GLY:C	1:A:33:THR:N	0.44	2.70	6	3
1:A:20:SER:OG	1:A:23:SER:OG	0.44	2.32	7	1
1:A:57:ALA:HB3	1:A:60:TYR:CE2	0.44	2.48	6	1
1:A:17:GLU:OE2	1:A:26:ILE:HD13	0.44	2.13	11	1
1:A:18:GLY:C	1:A:20:SER:N	0.44	2.71	5	1
1:A:46:LYS:NZ	1:A:53:HIS:CG	0.44	2.86	5	1
1:A:14:ASN:O	1:A:14:ASN:OD1	0.44	2.36	13	1
1:A:16:ARG:CZ	1:A:21:THR:O	0.43	2.66	15	2
1:A:8:ASN:OD1	1:A:62:LYS:NZ	0.43	2.48	17	1
1:A:41:GLU:OE1	1:A:41:GLU:O	0.43	2.36	16	3
1:A:45:TYR:CE2	1:A:58:LYS:NZ	0.43	2.83	10	1
1:A:8:ASN:OD1	1:A:60:TYR:O	0.42	2.36	4	1
1:A:30:SER:O	1:A:33:THR:OG1	0.42	2.36	1	2
1:A:21:THR:O	1:A:23:SER:N	0.42	2.51	4	1
1:A:8:ASN:HD22	1:A:62:LYS:HZ1	0.42	1.54	18	1
1:A:22:SER:O	1:A:23:SER:O	0.42	2.37	5	1
1:A:41:GLU:O	1:A:44:PHE:O	0.42	2.37	7	1
1:A:18:GLY:C	1:A:20:SER:H	0.42	2.17	5	1
1:A:18:GLY:O	1:A:19:ALA:C	0.41	2.59	8	1
1:A:48:GLU:OE1	1:A:53:HIS:CD2	0.41	2.73	18	1
1:A:49:TYR:CG	1:A:50:LYS:N	0.41	2.88	4	1
1:A:16:ARG:HH22	1:A:21:THR:H	0.41	1.57	4	1
1:A:49:TYR:CD2	1:A:51:GLY:N	0.40	2.88	20	1
1:A:63:ASP:O	1:A:64:ILE:C	0.40	2.60	20	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:48:GLU:CD	1:A:48:GLU:H	0.40	2.20	15	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	62/76 (82%)	55±2 (89±3%)	5±2 (9±3%)	2±1 (3±2%)	8	44
All	All	1240/1520 (82%)	1101 (89%)	107 (9%)	32 (3%)	8	44

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	50	LYS	8
1	A	64	ILE	4
1	A	12	SER	4
1	A	63	ASP	3
1	A	9	VAL	2
1	A	23	SER	2
1	A	59	GLU	2
1	A	10	SER	1
1	A	21	THR	1
1	A	11	SER	1
1	A	32	ASN	1
1	A	20	SER	1
1	A	43	ALA	1
1	A	52	SER	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	51/64 (80%)	51±1 (99±1%)	0±1 (1±1%)	79 97
All	All	1020/1280 (80%)	1011 (99%)	9 (1%)	79 97

All 7 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	4	THR	2
1	A	23	SER	2
1	A	16	ARG	1
1	A	22	SER	1
1	A	46	LYS	1
1	A	21	THR	1
1	A	48	GLU	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)

The completeness of assignment taking into account all chemical shift lists is 97% for the well-defined parts and 92% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *assigned_chem_shift_list_1*

7.1.1 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	912
Number of shifts mapped to atoms	912
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	2

7.1.2 Chemical shift referencing (i)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	76	-0.27 ± 0.12	None needed (< 0.5 ppm)
$^{13}C_{\beta}$	68	0.22 ± 0.14	None needed (< 0.5 ppm)
$^{13}C'$	75	0.13 ± 0.23	None needed (< 0.5 ppm)
^{15}N	75	0.37 ± 0.45	None needed (< 0.5 ppm)

7.1.3 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 97%, i.e. 770 atoms were assigned a chemical shift out of a possible 796. 0 out of 9 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	318/318 (100%)	132/132 (100%)	124/124 (100%)	62/62 (100%)
Sidechain	404/424 (95%)	272/277 (98%)	128/134 (96%)	4/13 (31%)

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	Total	^{1}H	^{13}C	^{15}N
Aromatic	48/54 (89%)	23/25 (92%)	23/27 (85%)	2/2 (100%)
Overall	770/796 (97%)	427/434 (98%)	275/285 (96%)	68/77 (88%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 92%, i.e. 912 atoms were assigned a chemical shift out of a possible 991. 0 out of 11 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	384/388 (99%)	158/160 (99%)	151/152 (99%)	75/76 (99%)
Sidechain	480/507 (95%)	323/330 (98%)	153/163 (94%)	4/14 (29%)
Aromatic	48/96 (50%)	23/49 (47%)	23/39 (59%)	2/8 (25%)
Overall	912/991 (92%)	504/539 (94%)	327/354 (92%)	81/98 (83%)

7.1.4 Statistically unusual chemical shifts (i)

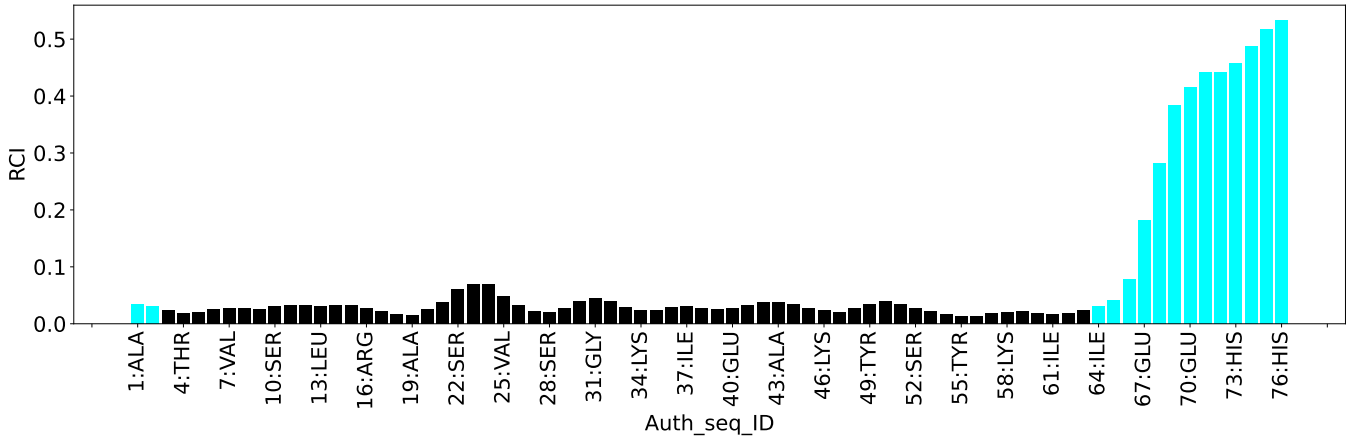
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, *ppm*	Expected range, *ppm*	Z-score
1	A	58	LYS	HG3	-0.41	0.04 – 2.67	-6.7
1	A	6	ILE	CD1	21.80	5.18 – 21.60	5.1

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.If well-defined core and ill-defined regions are not identified then it is shown as gray bars.

Random coil index (RCI) for chain A:


RCI
0.0
0.1
0.2
0.3
0.4
0.5
1:ALA
4:THR
7:VAL
10:SER
13:LEU
16:ARG
19:ALA
22:SER
25:VAL
28:SER
31:GLY
34:LYS
37:ILE
40:GLU
43:ALA
46:LYS
49:TYR
52:SER
55:TYR
58:LYS
61:ILE
64:ILE
67:GLU
70:GLU
73:HIS
76:HIS
Auth_seq_ID