



Full wwPDB NMR Structure Validation Report ⓘ

Jun 3, 2023 – 04:20 AM EDT

PDB ID : 5KQJ
BMRB ID : 30133
Title : Solution Structure of Antibiotic-Resistance Factor ANT(2'')-Ia Reveals Substrate-Regulated Conformation Dynamics
Authors : Bacot-Davis, V.R.; Berghuis, A.M.
Deposited on : 2016-07-06

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 ⓘ 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 ⓘ](#)) 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
BMRB Restraints Analysis : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.33

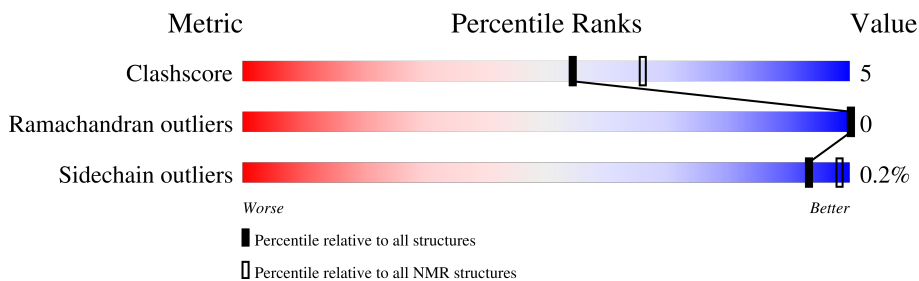
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 81%.

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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	185	

2 Ensemble composition and analysis

This entry contains 15 models. Model 6 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:9-A:128 (120)	1.01	6
2	A:145-A:180 (36)	0.34	7

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. No single-model clusters were found.

Cluster number	Models
1	1, 2, 3, 4, 5, 6, 7, 8, 9, 10
2	11, 12, 13, 14, 15

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 2857 atoms, of which 1379 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called 2''-aminoglycoside nucleotidyltransferase.

Mol	Chain	Residues	Atoms					Trace	
			Total	C	H	N	O		S
1	A	185	2857	937	1379	257	277	7	0

There are 8 discrepancies between the modelled and reference sequences:

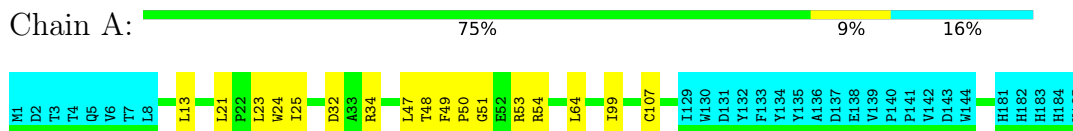
Chain	Residue	Modelled	Actual	Comment	Reference
A	178	LEU	-	expression tag	UNP P0AE05
A	179	GLU	-	expression tag	UNP P0AE05
A	180	HIS	-	expression tag	UNP P0AE05
A	181	HIS	-	expression tag	UNP P0AE05
A	182	HIS	-	expression tag	UNP P0AE05
A	183	HIS	-	expression tag	UNP P0AE05
A	184	HIS	-	expression tag	UNP P0AE05
A	185	HIS	-	expression tag	UNP P0AE05

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: 2'-aminoglycoside nucleotidyltransferase

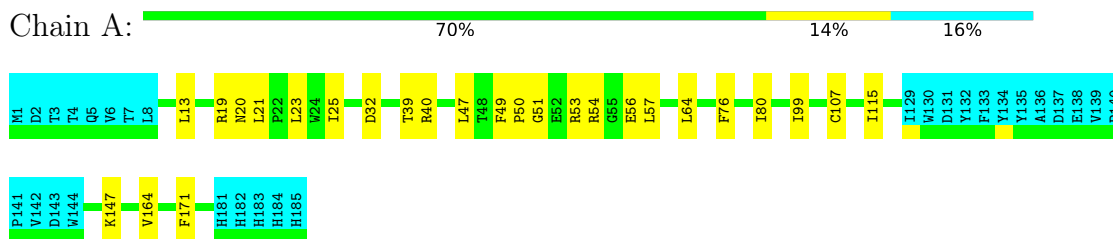


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

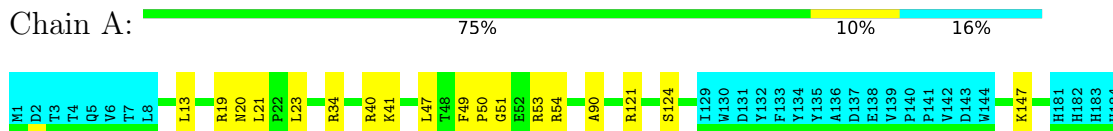
4.2.1 Score per residue for model 1

- Molecule 1: 2'-aminoglycoside nucleotidyltransferase



4.2.2 Score per residue for model 2

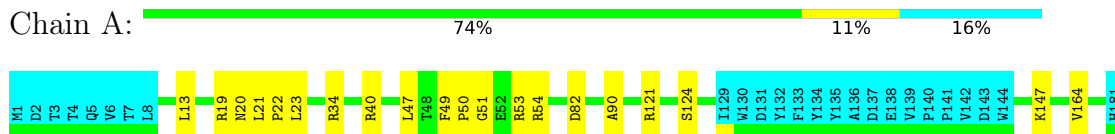
- Molecule 1: 2'-aminoglycoside nucleotidyltransferase



H185

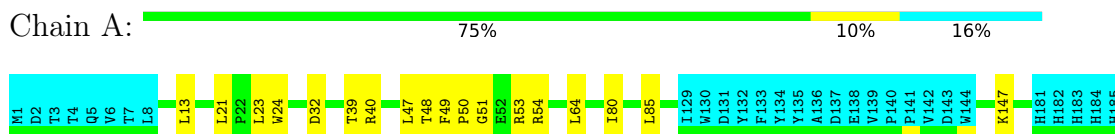
4.2.3 Score per residue for model 3

- Molecule 1: 2'-aminoglycoside nucleotidyltransferase

H182
H183
H184
H185

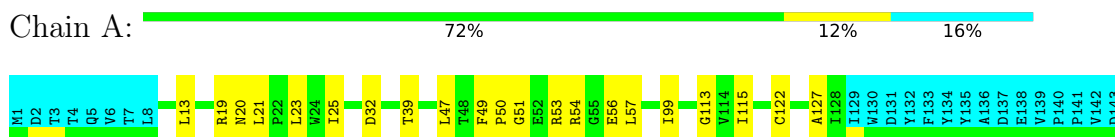
4.2.4 Score per residue for model 4

- Molecule 1: 2'-aminoglycoside nucleotidyltransferase



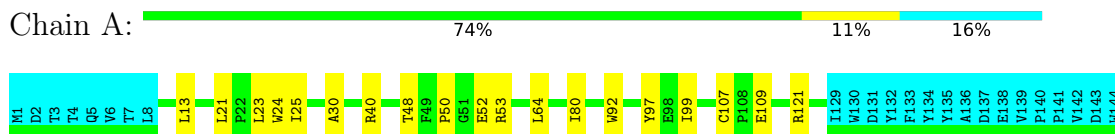
4.2.5 Score per residue for model 5

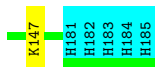
- Molecule 1: 2'-aminoglycoside nucleotidyltransferase

W144
V164
H181
H182
H183
H184
H185

4.2.6 Score per residue for model 6 (medoid)

- Molecule 1: 2'-aminoglycoside nucleotidyltransferase





4.2.7 Score per residue for model 7

- Molecule 1: 2''-aminoglycoside nucleotidyltransferase

Chain A: 75% 10% 16%



4.2.8 Score per residue for model 8

- Molecule 1: 2''-aminoglycoside nucleotidyltransferase

Chain A: 74% 10% 16%



4.2.9 Score per residue for model 9

- Molecule 1: 2''-aminoglycoside nucleotidyltransferase

Chain A: 74% 10% 16%



4.2.10 Score per residue for model 10

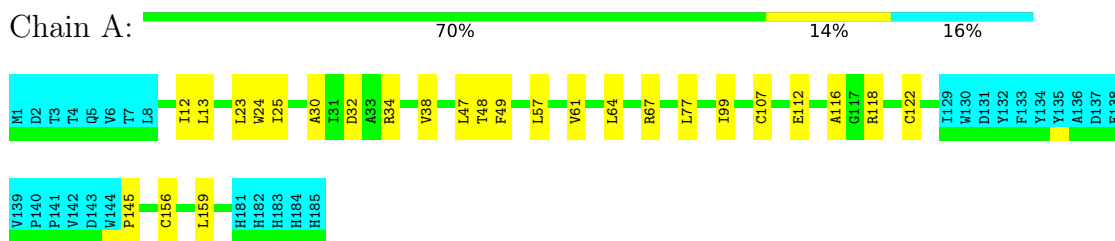
- Molecule 1: 2''-aminoglycoside nucleotidyltransferase

Chain A: 75% 9% 16%



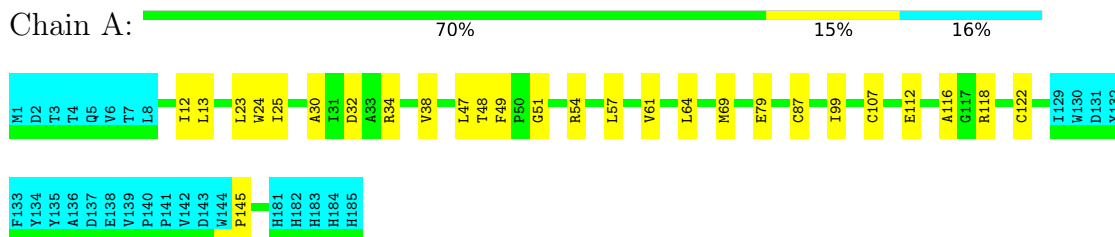
4.2.11 Score per residue for model 11

- Molecule 1: 2''-aminoglycoside nucleotidyltransferase



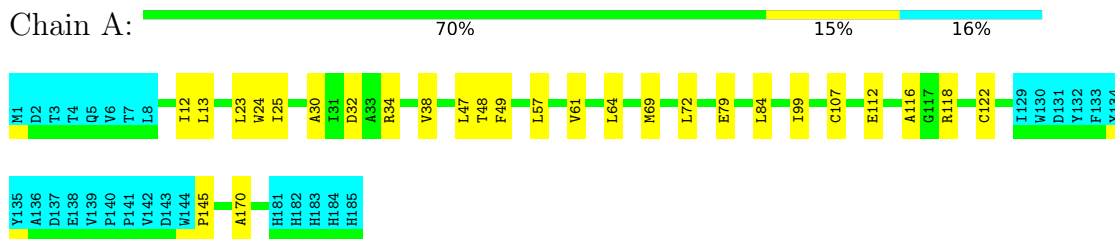
4.2.12 Score per residue for model 12

- Molecule 1: 2''-aminoglycoside nucleotidyltransferase



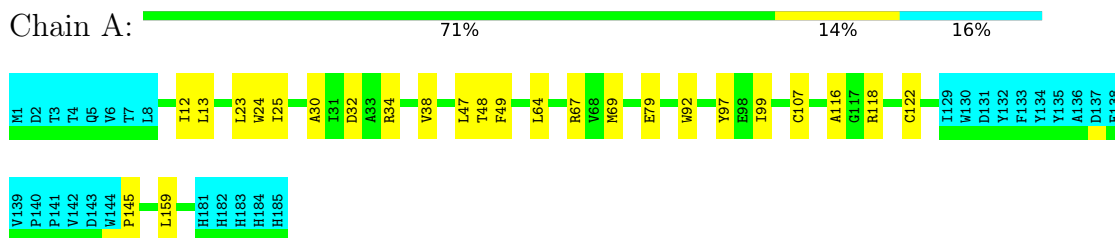
4.2.13 Score per residue for model 13

- Molecule 1: 2''-aminoglycoside nucleotidyltransferase



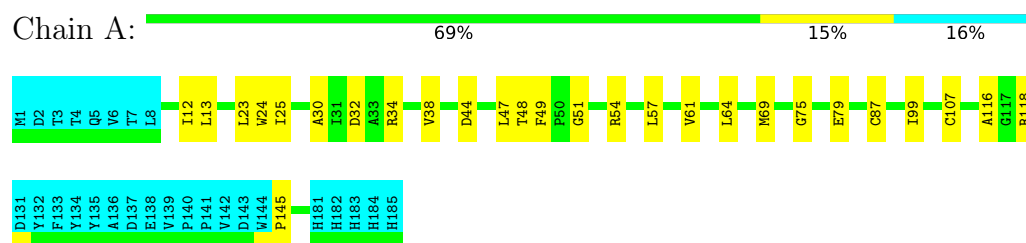
4.2.14 Score per residue for model 14

- Molecule 1: 2''-aminoglycoside nucleotidyltransferase



4.2.15 Score per residue for model 15

- Molecule 1: 2'-aminoglycoside nucleotidyltransferase



5 Refinement protocol and experimental data overview

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

Of the 15 calculated structures, 15 were deposited, based on the following criterion: *back calculated data agree with experimental NOESY spectrum*.

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

Software name	Classification	Version
X-PLOR NIH	refinement	

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	2015
Number of shifts mapped to atoms	2015
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	81%

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	1217	1170	1179	13±3
All	All	18255	17550	17685	193

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:99:ILE:HG13	1:A:107:CYS:SG	0.92	2.04	14	9
1:A:23:LEU:H	1:A:121:ARG:HH21	0.79	1.20	2	2
1:A:99:ILE:CG1	1:A:107:CYS:SG	0.71	2.78	15	5
1:A:21:LEU:HD13	1:A:53:ARG:HD3	0.71	1.62	5	1
1:A:13:LEU:HD23	1:A:23:LEU:HD13	0.70	1.64	7	5
1:A:32:ASP:HB3	1:A:38:VAL:HA	0.69	1.64	13	5
1:A:67:ARG:HG2	1:A:159:LEU:HD23	0.68	1.64	11	2
1:A:24:TRP:HB2	1:A:48:THR:HB	0.67	1.66	12	11
1:A:21:LEU:HD13	1:A:53:ARG:HG3	0.66	1.66	4	8
1:A:53:ARG:HE	1:A:56:GLU:HG3	0.66	1.49	1	1
1:A:12:ILE:HD13	1:A:64:LEU:HD23	0.66	1.67	12	5
1:A:23:LEU:HD13	1:A:49:PHE:CZ	0.63	2.28	12	10
1:A:40:ARG:HE	1:A:147:LYS:HG2	0.62	1.55	2	3
1:A:13:LEU:HD23	1:A:23:LEU:HD23	0.62	1.71	5	5

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:34:ARG:HD2	1:A:122:CYS:SG	0.60	2.35	12	3
1:A:23:LEU:HD11	1:A:47:LEU:HD22	0.59	1.73	12	5
1:A:57:LEU:HD21	1:A:87:CYS:SG	0.59	2.38	15	2
1:A:51:GLY:O	1:A:54:ARG:HG3	0.58	1.99	4	11
1:A:19:ARG:O	1:A:20:ASN:HB2	0.57	2.00	7	5
1:A:21:LEU:HD11	1:A:50:PRO:HD2	0.57	1.75	6	6
1:A:25:ILE:HG2	1:A:30:ALA:HB2	0.57	1.76	11	5
1:A:13:LEU:HD12	1:A:116:ALA:HB3	0.56	1.76	15	5
1:A:61:VAL:HA	1:A:64:LEU:HD12	0.54	1.78	15	4
1:A:23:LEU:HB3	1:A:118:ARG:HH12	0.53	1.64	14	2
1:A:112:GLU:OE1	1:A:122:CYS:HB2	0.52	2.04	12	2
1:A:23:LEU:HD11	1:A:47:LEU:HB3	0.50	1.83	1	5
1:A:109:GLU:HA	1:A:121:ARG:NH2	0.50	2.21	6	2
1:A:57:LEU:HD13	1:A:76:PHE:HE2	0.50	1.66	1	1
1:A:69:MET:SD	1:A:79:GLU:HB2	0.50	2.47	15	4
1:A:50:PRO:HA	1:A:90:ALA:O	0.50	2.07	2	2
1:A:25:ILE:HD13	1:A:115:ILE:HD12	0.49	1.83	5	2
1:A:19:ARG:O	1:A:20:ASN:CB	0.48	2.61	7	2
1:A:64:LEU:HD13	1:A:80:ILE:HD13	0.48	1.85	1	3
1:A:34:ARG:HD3	1:A:122:CYS:SG	0.48	2.48	14	2
1:A:113:GLY:HA3	1:A:122:CYS:SG	0.48	2.49	5	1
1:A:82:ASP:OD1	1:A:83:GLU:HG3	0.47	2.08	9	1
1:A:23:LEU:HD13	1:A:49:PHE:CE2	0.46	2.45	2	1
1:A:40:ARG:HD3	1:A:147:LYS:HG2	0.46	1.88	4	1
1:A:32:ASP:OD1	1:A:39:THR:N	0.45	2.49	5	3
1:A:52:GLU:HG3	1:A:53:ARG:HG2	0.45	1.88	7	4
1:A:13:LEU:HB3	1:A:118:ARG:HD2	0.45	1.88	12	4
1:A:50:PRO:HB3	1:A:97:TYR:CE2	0.45	2.47	6	3
1:A:156:CYS:HA	1:A:159:LEU:HD12	0.44	1.90	11	1
1:A:40:ARG:HD2	1:A:147:LYS:HG2	0.43	1.88	6	1
1:A:47:LEU:HB3	1:A:49:PHE:CE1	0.43	2.48	12	3
1:A:25:ILE:O	1:A:30:ALA:HB2	0.42	2.14	6	2
1:A:53:ARG:CZ	1:A:56:GLU:HG3	0.42	2.45	5	1
1:A:49:PHE:CG	1:A:57:LEU:HD21	0.42	2.50	5	1
1:A:34:ARG:HD3	1:A:112:GLU:HG2	0.42	1.90	8	3
1:A:109:GLU:O	1:A:121:ARG:HD3	0.42	2.14	8	2
1:A:112:GLU:HB2	1:A:122:CYS:SG	0.42	2.54	13	1
1:A:54:ARG:HH12	1:A:75:GLY:HA2	0.42	1.74	15	1
1:A:92:TRP:HB2	1:A:97:TYR:CE2	0.42	2.50	6	1
1:A:47:LEU:HD12	1:A:85:LEU:HD11	0.41	1.92	4	1
1:A:34:ARG:NH2	1:A:124:SER:HA	0.41	2.30	2	2

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:99:ILE:HD12	1:A:127:ALA:HB1	0.41	1.92	5	1
1:A:49:PHE:CE1	1:A:57:LEU:HD13	0.41	2.51	13	2
1:A:19:ARG:HG3	1:A:60:ILE:HD11	0.40	1.91	7	1
1:A:23:LEU:HG	1:A:49:PHE:CE2	0.40	2.51	7	1
1:A:163:LYS:HA	1:A:163:LYS:HE3	0.40	1.93	10	1
1:A:25:ILE:HB	1:A:122:CYS:SG	0.40	2.57	9	1
1:A:29:TRP:CZ2	1:A:42:HIS:HB2	0.40	2.51	10	1
1:A:92:TRP:CE3	1:A:97:TYR:HB2	0.40	2.50	14	1
1:A:21:LEU:HD12	1:A:22:PRO:HD2	0.40	1.92	3	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	156/185 (84%)	154±1 (99±1%)	2±1 (1±1%)	0±0 (0±0%)	100	100
All	All	2340/2775 (84%)	2310 (99%)	30 (1%)	0 (0%)	100	100

There are no Ramachandran outliers.

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	120/148 (81%)	120±0 (100±0%)	0±0 (0±0%)	93	98
All	All	1800/2220 (81%)	1796 (100%)	4 (0%)	93	98

All 4 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	82	ASP	1
1	A	43	ASP	1
1	A	163	LYS	1
1	A	44	ASP	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 81% for the well-defined parts and 79% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *ANT2_June2016_BMRB31_final.str*

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	2015
Number of shifts mapped to atoms	2015
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	54

7.1.2 Chemical shift referencing [i](#)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	176	-0.35 ± 0.29	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	162	-0.19 ± 0.12	None needed (< 0.5 ppm)
$^{13}\text{C}'$	164	-0.16 ± 0.21	None needed (< 0.5 ppm)
^{15}N	165	0.02 ± 0.31	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 81%, i.e. 1687 atoms were assigned a chemical shift out of a possible 2095. 0 out of 22 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	731/780 (94%)	300/319 (94%)	290/312 (93%)	141/149 (95%)
Sidechain	912/1164 (78%)	626/758 (83%)	285/360 (79%)	1/46 (2%)

Continued on next page...

Continued from previous page...

	Total	¹ H	¹³ C	¹⁵ N
Aromatic	44/151 (29%)	0/77 (0%)	44/68 (65%)	0/6 (0%)
Overall	1687/2095 (81%)	926/1154 (80%)	619/740 (84%)	142/201 (71%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 79%, i.e. 1980 atoms were assigned a chemical shift out of a possible 2500. 0 out of 26 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	854/921 (93%)	349/375 (93%)	340/370 (92%)	165/176 (94%)
Sidechain	1053/1336 (79%)	720/871 (83%)	331/418 (79%)	2/47 (4%)
Aromatic	73/243 (30%)	0/126 (0%)	73/108 (68%)	0/9 (0%)
Overall	1980/2500 (79%)	1069/1372 (78%)	744/896 (83%)	167/232 (72%)

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.

List Id	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	11	LYS	HB3	5.68	0.46 – 3.04	15.2
1	A	119	PRO	CD	36.27	45.11 – 55.58	-13.4
1	A	82	ASP	H	14.79	5.52 – 11.08	11.7
1	A	38	VAL	H	0.71	4.98 – 11.56	-11.5
1	A	159	LEU	H	1.71	5.09 – 11.34	-10.4
1	A	34	ARG	CD	34.02	38.57 – 47.75	-9.9
1	A	40	ARG	H	2.34	5.25 – 11.22	-9.9
1	A	146	THR	H	2.71	5.19 – 11.27	-9.1
1	A	167	LEU	CG	36.28	21.37 – 32.19	8.8
1	A	123	ASN	H	3.12	5.28 – 11.36	-8.6
1	A	84	LEU	CD1	12.15	16.71 – 32.55	-7.9
1	A	84	LEU	CD2	11.77	15.73 – 32.47	-7.4
1	A	141	PRO	CG	19.24	21.69 – 32.72	-7.2
1	A	178	LEU	HD11	2.65	-0.61 – 2.12	6.9
1	A	178	LEU	HD12	2.65	-0.61 – 2.12	6.9
1	A	178	LEU	HD13	2.65	-0.61 – 2.12	6.9
1	A	41	LYS	CG	17.22	19.35 – 30.45	-6.9
1	A	150	GLU	CG	28.01	30.20 – 42.01	-6.9
1	A	12	ILE	CD1	24.60	5.18 – 21.60	6.8
1	A	178	LEU	HD21	2.60	-0.65 – 2.13	6.7
1	A	178	LEU	HD22	2.60	-0.65 – 2.13	6.7
1	A	178	LEU	HD23	2.60	-0.65 – 2.13	6.7

Continued on next page...

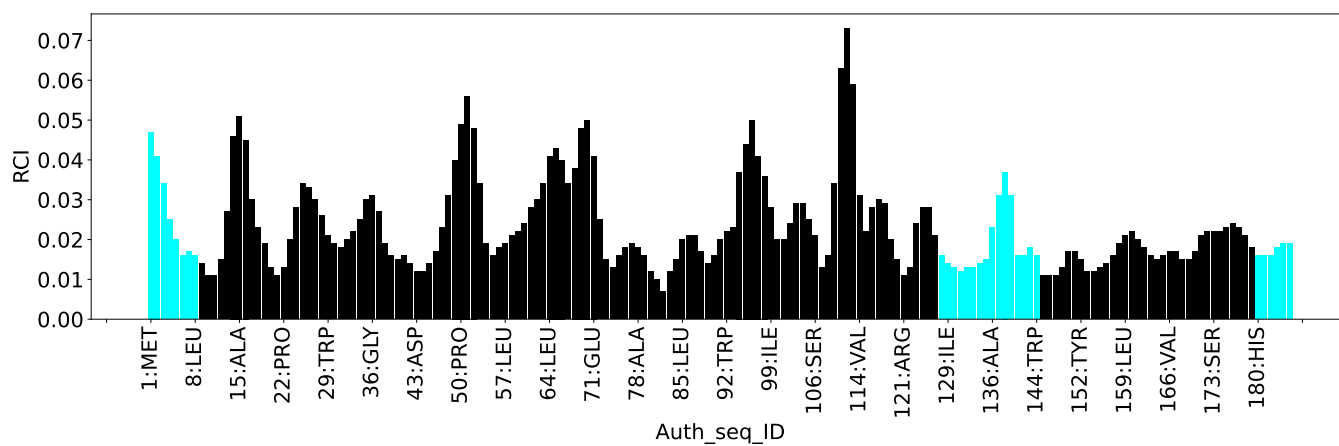
Continued from previous page...

List Id	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	41	LYS	CE	36.23	37.57 – 46.21	-6.5
1	A	19	ARG	CD	49.09	38.57 – 47.75	6.5
1	A	172	ARG	HD2	1.64	1.97 – 4.26	-6.5
1	A	100	ALA	CB	7.72	10.19 – 27.75	-6.4
1	A	128	ILE	HG21	2.48	-0.56 – 2.11	6.4
1	A	128	ILE	HG22	2.48	-0.56 – 2.11	6.4
1	A	128	ILE	HG23	2.48	-0.56 – 2.11	6.4
1	A	172	ARG	HD3	1.50	1.81 – 4.39	-6.2
1	A	178	LEU	CD1	14.95	16.71 – 32.55	-6.1
1	A	23	LEU	CG	20.36	21.37 – 32.19	-5.9
1	A	178	LEU	CD2	14.63	15.73 – 32.47	-5.7
1	A	12	ILE	CG2	24.96	10.93 – 24.12	5.6
1	A	129	ILE	HG21	2.25	-0.56 – 2.11	5.5
1	A	129	ILE	HG22	2.25	-0.56 – 2.11	5.5
1	A	129	ILE	HG23	2.25	-0.56 – 2.11	5.5
1	A	41	LYS	CD	23.00	23.50 – 34.42	-5.5
1	A	22	PRO	CA	55.22	55.85 – 70.84	-5.4
1	A	129	ILE	HD11	2.20	-0.72 – 2.09	5.4
1	A	129	ILE	HD12	2.20	-0.72 – 2.09	5.4
1	A	129	ILE	HD13	2.20	-0.72 – 2.09	5.4
1	A	80	ILE	CD1	22.11	5.18 – 21.60	5.3
1	A	80	ILE	CG2	24.52	10.93 – 24.12	5.3
1	A	29	TRP	CB	40.32	20.06 – 39.75	5.3
1	A	33	ALA	HB1	2.64	0.14 – 2.58	5.3
1	A	33	ALA	HB2	2.64	0.14 – 2.58	5.3
1	A	33	ALA	HB3	2.64	0.14 – 2.58	5.3
1	A	76	PHE	CZ	121.47	121.82 – 136.66	-5.2
1	A	40	ARG	HG2	0.21	0.26 – 2.87	-5.2
1	A	133	PHE	CZ	121.58	121.82 – 136.66	-5.2
1	A	61	VAL	CG1	28.46	14.71 – 28.29	5.1
1	A	115	ILE	CD1	21.73	5.18 – 21.60	5.1
1	A	35	LEU	CG	32.21	21.37 – 32.19	5.0

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. 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:



Restraints validation did not run