



# Full wwPDB NMR Structure Validation Report ⓘ

Nov 6, 2017 – 03:30 PM EST

PDB ID : 5KQJ  
Title : Solution Structure of Antibiotic-Resistance Factor ANT(2'')-Ia Reveals Substrate-Regulated Conformation Dynamics  
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Deposited on : unknown

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

Cyrange	:	Kirchner and Güntert (2011)
NmrClust	:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	rb-20030345
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20030345

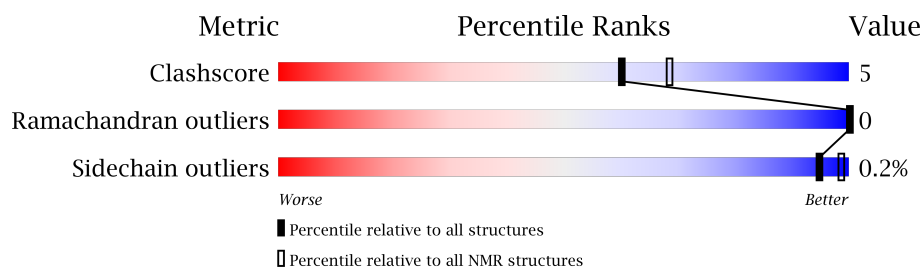
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*SOLUTION NMR*

The overall completeness of chemical shifts assignment is 79%.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	NMR archive (#Entries)
Clashscore	125131	11601
Ramachandran outliers	121729	10391
Sidechain outliers	121581	10367

The table below summarises the geometric issues observed across the polymeric chains and their fit to the experimental data. The red, orange, yellow and green segments indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A cyan segment indicates the fraction of residues that are not part of the well-defined cores, and a grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	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)	0.59	6
2	A:145-A:180 (36)	0.20	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
1	A	185	Total	C	H	N	O	S	0
			2857	937	1379	257	277	7	

There are 8 discrepancies between the modelled and reference sequences:

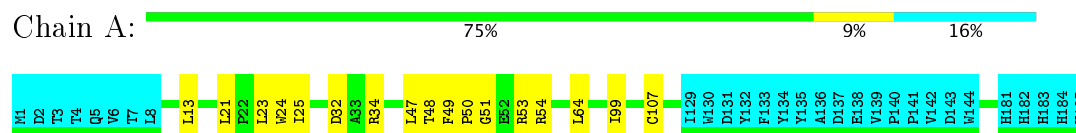
Chain	Residue	Modelled	Actual	Comment	Reference
A	178	LEU	-	expression tag	UNP P0AE05
A	179	GLU	-	expression tag	UNP P0AE05
A	180	HIS	-	expression tag	UNP P0AE05
A	181	HIS	-	expression tag	UNP P0AE05
A	182	HIS	-	expression tag	UNP P0AE05
A	183	HIS	-	expression tag	UNP P0AE05
A	184	HIS	-	expression tag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

## 4 Residue-property plots

### 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: 2'-aminoglycoside nucleotidyltransferase

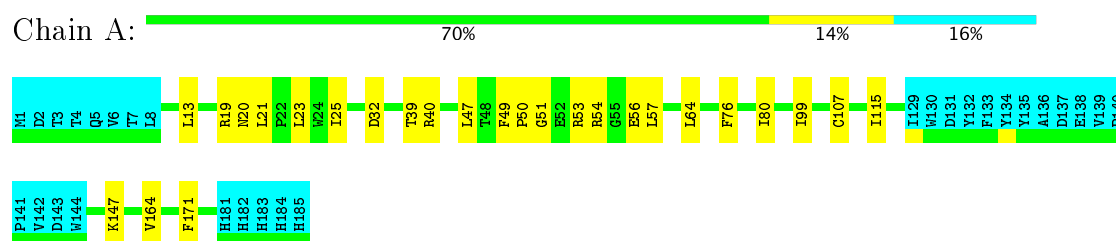


### 4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

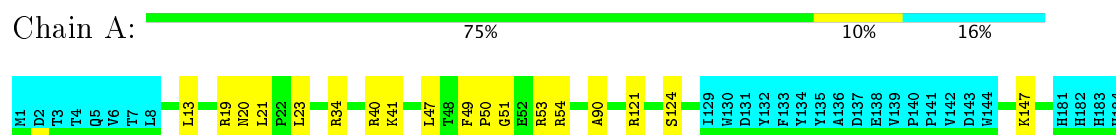
#### 4.2.1 Score per residue for model 1

- Molecule 1: 2'-aminoglycoside nucleotidyltransferase



#### 4.2.2 Score per residue for model 2

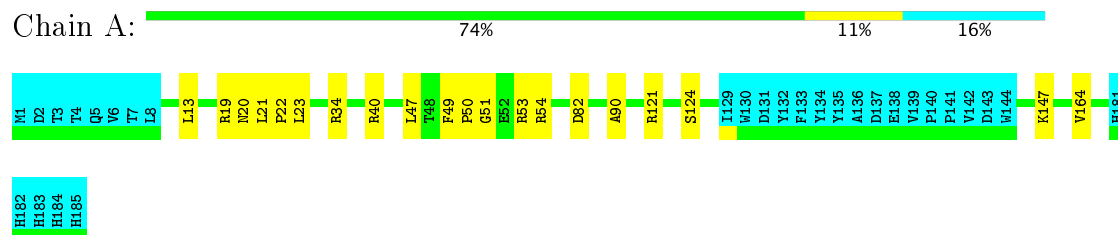
- Molecule 1: 2'-aminoglycoside nucleotidyltransferase



H185

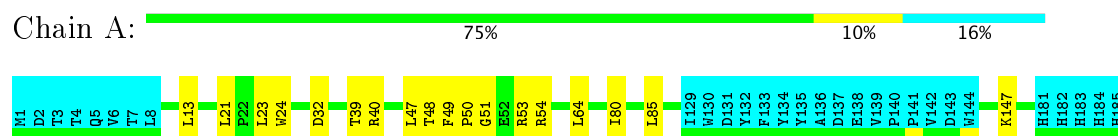
### 4.2.3 Score per residue for model 3

- Molecule 1: 2'-aminoglycoside nucleotidyltransferase

H182  
H183  
H184  
H185

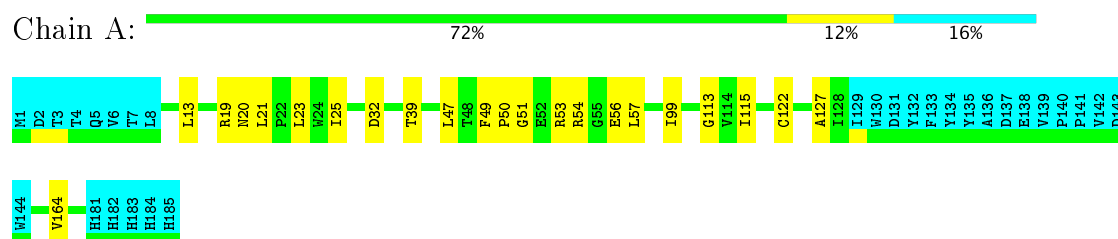
### 4.2.4 Score per residue for model 4

- Molecule 1: 2'-aminoglycoside nucleotidyltransferase



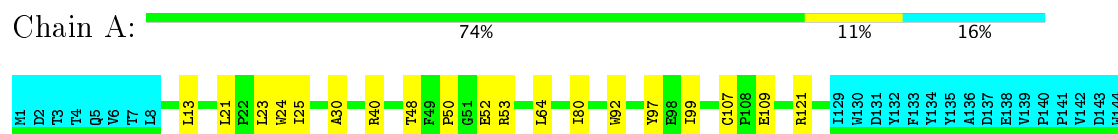
### 4.2.5 Score per residue for model 5

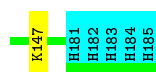
- Molecule 1: 2'-aminoglycoside nucleotidyltransferase

H144  
V164  
H181  
H182  
H183  
H184  
H185

### 4.2.6 Score per residue for model 6 (medoid)

- Molecule 1: 2'-aminoglycoside nucleotidyltransferase

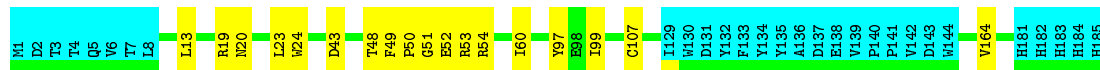




#### 4.2.7 Score per residue for model 7

- Molecule 1: 2'-aminoglycoside nucleotidyltransferase

Chain A: 75% 10% 16%



#### 4.2.8 Score per residue for model 8

- Molecule 1: 2'-aminoglycoside nucleotidyltransferase

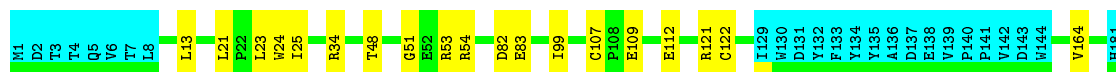
Chain A: 74% 10% 16%



#### 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

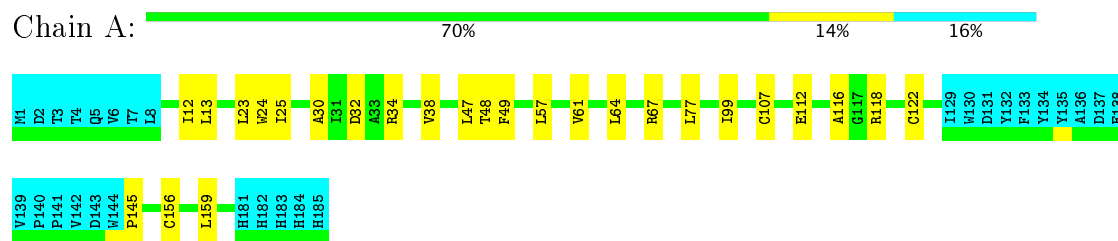
- Molecule 1: 2'-aminoglycoside nucleotidyltransferase

Chain A: 75% 9% 16%



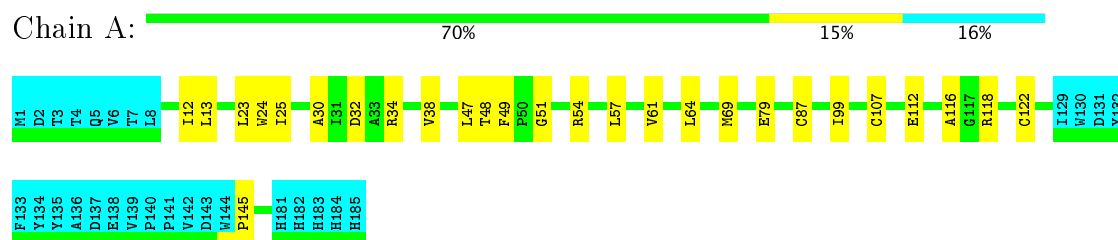
### 4.2.11 Score per residue for model 11

- Molecule 1: 2'-aminoglycoside nucleotidyltransferase



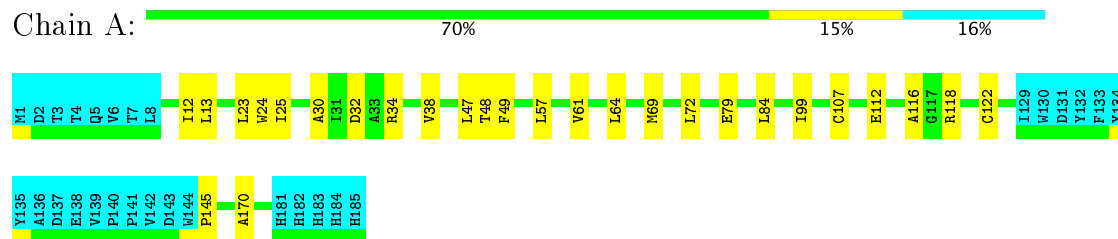
### 4.2.12 Score per residue for model 12

- Molecule 1: 2'-aminoglycoside nucleotidyltransferase



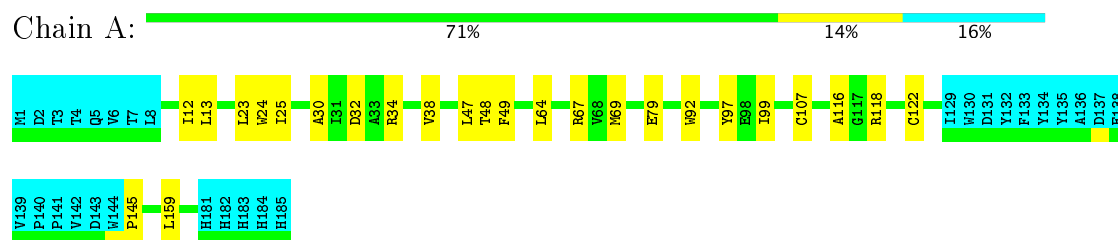
### 4.2.13 Score per residue for model 13

- Molecule 1: 2'-aminoglycoside nucleotidyltransferase



### 4.2.14 Score per residue for model 14

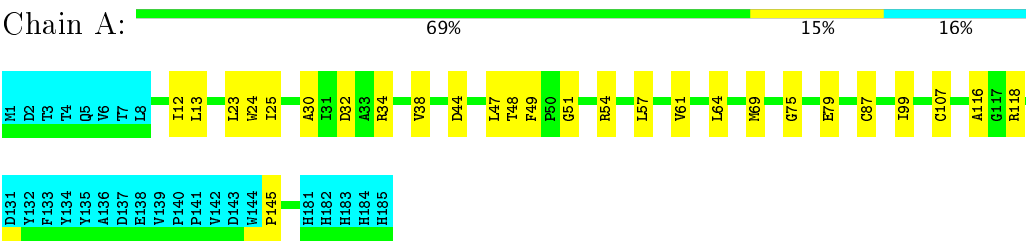
- Molecule 1: 2'-aminoglycoside nucleotidyltransferase





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)	5kqj_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)	79%

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	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

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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:HG22	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:109:GLU:O	1:A:121:ARG:HD3	0.42	2.14	8	2
1:A:34:ARG:HD3	1:A:112:GLU:HG2	0.42	1.90	8	3
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

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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%)	95	99
All	All	1800/2220 (81%)	1796 (100%)	4 (0%)	95	99

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	44	ASP	1
1	A	43	ASP	1
1	A	82	ASP	1
1	A	163	LYS	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 79% for the well-defined parts and 78% for the entire structure.

### 7.1 Chemical shift list 1

File name: 5kqj\_cs.cif

Chemical shift list name: *ANT2\_June2016\_BMRB31\_final.str*

#### 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	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)	51

#### 7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	176	$-0.37 \pm 0.33$	None needed ( $< 0.5$ ppm)
$^{13}\text{C}_\beta$	162	$-0.19 \pm 0.19$	None needed ( $< 0.5$ ppm)
$^{13}\text{C}'$	164	$-0.16 \pm 0.16$	None needed ( $< 0.5$ ppm)
$^{15}\text{N}$	165	$0.03 \pm 0.30$	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 79%, i.e. 1491 atoms were assigned a chemical shift out of a possible 1886. 21 out of 22 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^1\text{H}$	$^{13}\text{C}$	$^{15}\text{N}$
Backbone	717/766 (94%)	286/305 (94%)	290/312 (93%)	141/149 (95%)
Sidechain	733/976 (75%)	449/570 (79%)	283/360 (79%)	1/46 (2%)

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	<b>Total</b>	<b><sup>1</sup>H</b>	<b><sup>13</sup>C</b>	<b><sup>15</sup>N</b>
Aromatic	41/144 (28%)	0/77 (0%)	41/61 (67%)	0/6 (0%)
Overall	1491/1886 (79%)	735/952 (77%)	614/733 (84%)	142/201 (71%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 78%, i.e. 1751 atoms were assigned a chemical shift out of a possible 2257. 24 out of 26 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	<b>Total</b>	<b><sup>1</sup>H</b>	<b><sup>13</sup>C</b>	<b><sup>15</sup>N</b>
Backbone	840/907 (93%)	335/361 (93%)	340/370 (92%)	165/176 (94%)
Sidechain	842/1118 (75%)	514/653 (79%)	326/418 (78%)	2/47 (4%)
Aromatic	69/232 (30%)	0/126 (0%)	69/97 (71%)	0/9 (0%)
Overall	1751/2257 (78%)	849/1140 (74%)	735/885 (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.

Mol	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	11	LYS	HB3	5.68	3.10 – 0.40	14.5
1	A	119	PRO	CD	36.27	55.31 – 45.41	-14.2
1	A	82	ASP	H	14.79	11.17 – 5.47	11.3
1	A	38	VAL	H	0.71	11.69 – 4.89	-11.1
1	A	34	ARG	CD	34.02	47.57 – 38.77	-10.4
1	A	1	MET	H1	2.24	11.26 – 5.26	-10.0
1	A	159	LEU	H	1.71	11.47 – 4.97	-10.0
1	A	40	ARG	H	2.34	11.29 – 5.19	-9.7
1	A	146	THR	H	2.71	11.34 – 5.14	-8.9
1	A	123	ASN	H	3.12	11.45 – 5.25	-8.4
1	A	167	LEU	CG	36.28	32.55 – 21.05	8.2
1	A	84	LEU	CD1	12.15	32.77 – 16.57	-7.7
1	A	141	PRO	CG	19.24	32.66 – 21.76	-7.3
1	A	84	LEU	CD2	11.77	32.60 – 15.60	-7.3
1	A	41	LYS	CE	36.23	46.00 – 37.80	-6.9
1	A	178	LEU	HD11	2.65	2.16 – -0.64	6.8
1	A	178	LEU	HD12	2.65	2.16 – -0.64	6.8
1	A	178	LEU	HD13	2.65	2.16 – -0.64	6.8
1	A	19	ARG	CD	49.09	47.57 – 38.77	6.7
1	A	41	LYS	CG	17.22	30.67 – 19.17	-6.7
1	A	178	LEU	HD23	2.60	2.14 – -0.66	6.6
1	A	178	LEU	HD22	2.60	2.14 – -0.66	6.6

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Mol	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	178	LEU	HD21	2.60	2.14 – -0.66	6.6
1	A	12	ILE	CD1	24.60	21.91 – 5.01	6.6
1	A	150	GLU	CG	28.01	42.24 – 29.94	-6.6
1	A	172	ARG	HD2	1.64	4.27 – 1.97	-6.4
1	A	172	ARG	HD3	1.50	4.36 – 1.86	-6.4
1	A	128	ILE	HG23	2.48	2.13 – -0.57	6.3
1	A	128	ILE	HG22	2.48	2.13 – -0.57	6.3
1	A	128	ILE	HG21	2.48	2.13 – -0.57	6.3
1	A	100	ALA	CB	7.72	28.03 – 9.93	-6.2
1	A	178	LEU	CD1	14.95	32.77 – 16.57	-6.0
1	A	23	LEU	CG	20.36	32.55 – 21.05	-5.6
1	A	178	LEU	CD2	14.63	32.60 – 15.60	-5.6
1	A	129	ILE	HG22	2.25	2.13 – -0.57	5.4
1	A	129	ILE	HG23	2.25	2.13 – -0.57	5.4
1	A	129	ILE	HG21	2.25	2.13 – -0.57	5.4
1	A	129	ILE	HD13	2.20	2.13 – -0.77	5.2
1	A	129	ILE	HD11	2.20	2.13 – -0.77	5.2
1	A	129	ILE	HD12	2.20	2.13 – -0.77	5.2
1	A	12	ILE	CG2	24.96	24.63 – 10.43	5.2
1	A	22	PRO	CA	55.22	71.13 – 55.53	-5.2
1	A	29	TRP	CB	40.32	40.02 – 19.92	5.1
1	A	33	ALA	HB1	2.64	2.61 – 0.11	5.1
1	A	33	ALA	HB2	2.64	2.61 – 0.11	5.1
1	A	33	ALA	HB3	2.64	2.61 – 0.11	5.1
1	A	80	ILE	CD1	22.11	21.91 – 5.01	5.1
1	A	153	ARG	CD	38.67	47.57 – 38.77	-5.1
1	A	41	LYS	CD	23.00	34.86 – 23.06	-5.0
1	A	61	VAL	CG1	28.46	28.40 – 14.60	5.0
1	A	40	ARG	HG2	0.21	2.92 – 0.22	-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.

Random coil index (RCI) for chain A:

