



# Full wwPDB NMR Structure Validation Report ⓘ

Feb 12, 2017 – 08:11 pm GMT

PDB ID : 1T5M  
Title : Structural transitions as determinants of the action of the calcium-dependent antibiotic daptomycin  
Authors : Jung, D.; Rozek, A.; Okon, M.; Hancock, R.E.  
Deposited on : 2004-05-04

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

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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
Mogul	:	1.7.2 (RC1), CSD as538be (2017)
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	:	trunk28760
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	recalc28949

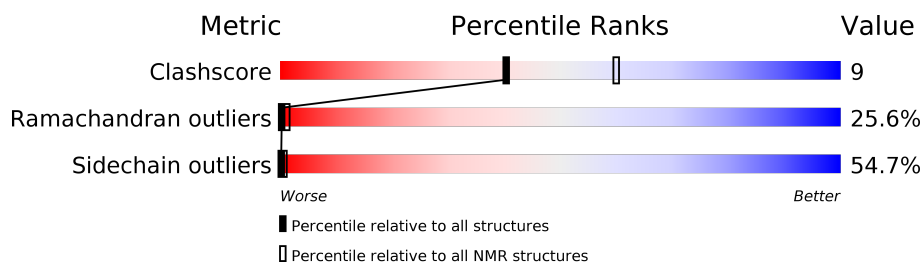
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*SOLUTION NMR*


The overall completeness of chemical shifts assignment was not calculated.

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



Metric	Whole archive (#Entries)	NMR archive (#Entries)
Clashscore	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	13	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA and RNA chains that are outliers for geometric criteria:

Mol	Chain	Compound	Res	Total models with violations	
				Chirality	Geometry
1	A	KYN	14	15	-
1	A	LME	13	15	-

## 2 Ensemble composition and analysis ⓘ

This entry contains 15 models.

Cyrange was unable to find well-defined residues.

Error message: The number of core atoms ( 7) was below the domain threshold value ( 8).

NmrClust was unable to cluster the ensemble.

Error message: Wrapper check: not enough residues in core to run NmrClust

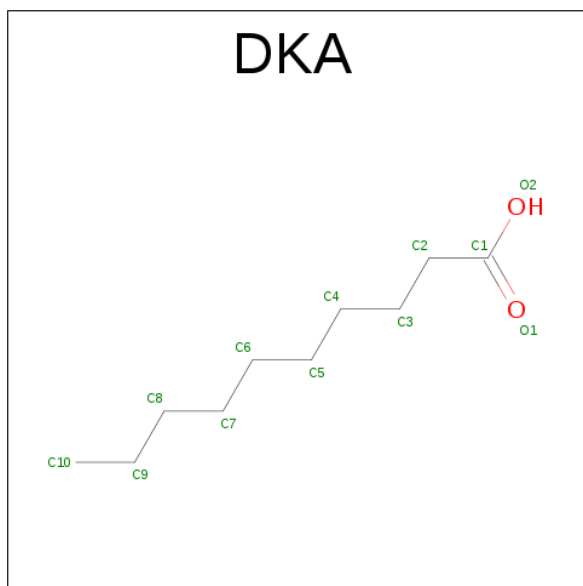
### 3 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 213 atoms, of which 98 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called DAPTOMYCIN.

Mol	Chain	Residues	Atoms					Trace
1	A	13	Total	C	H	N	O	0
			183	62	79	17	25	

- Molecule 2 is DECANOIC ACID (three-letter code: DKA) (formula:  $C_{10}H_{20}O_2$ ).



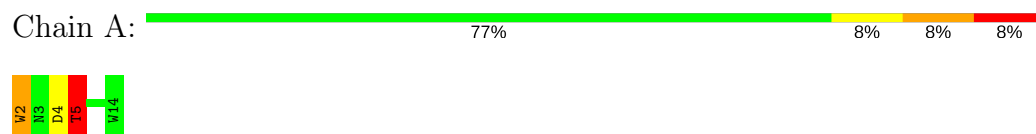
Mol	Chain	Residues	Atoms			
2	A	1	Total	C	H	O
			30	10	19	1

## 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: DAPTOMYCIN

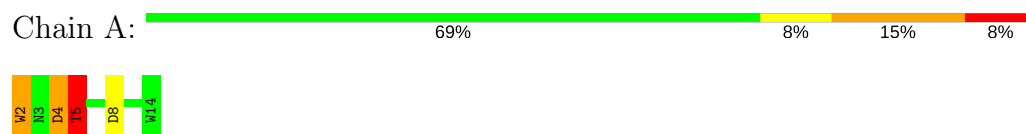


### 4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

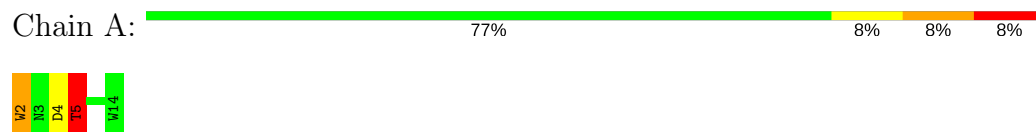
#### 4.2.1 Score per residue for model 1

- Molecule 1: DAPTOMYCIN



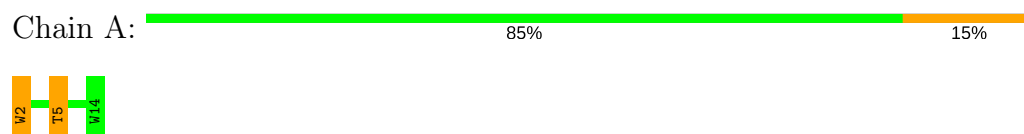
#### 4.2.2 Score per residue for model 2

- Molecule 1: DAPTOMYCIN



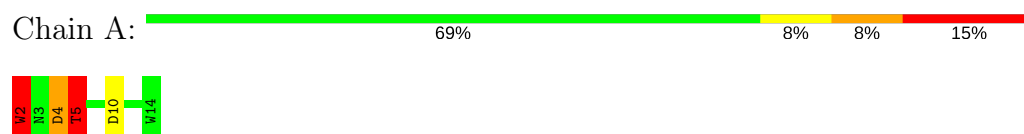
### 4.2.3 Score per residue for model 3

- Molecule 1: DAPTOMYCIN



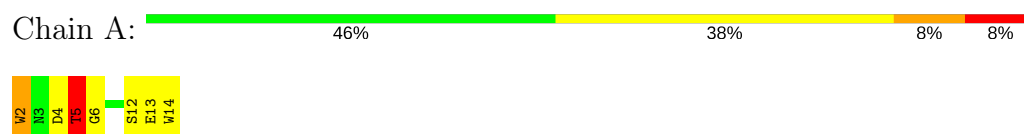
### 4.2.4 Score per residue for model 4

- Molecule 1: DAPTOMYCIN



### 4.2.5 Score per residue for model 5

- Molecule 1: DAPTOMYCIN



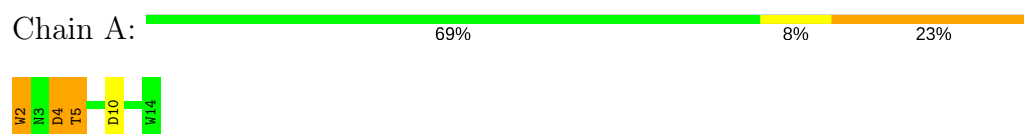
### 4.2.6 Score per residue for model 6

- Molecule 1: DAPTOMYCIN



### 4.2.7 Score per residue for model 7

- Molecule 1: DAPTOMYCIN



#### 4.2.8 Score per residue for model 8

- Molecule 1: DAPTOMYCIN



#### 4.2.9 Score per residue for model 9

- Molecule 1: DAPTOMYCIN



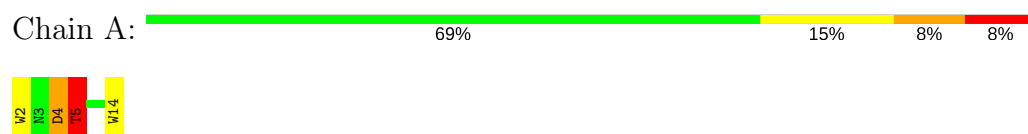
#### 4.2.10 Score per residue for model 10

- Molecule 1: DAPTOMYCIN



#### 4.2.11 Score per residue for model 11

- Molecule 1: DAPTOMYCIN



#### 4.2.12 Score per residue for model 12

- Molecule 1: DAPTOMYCIN



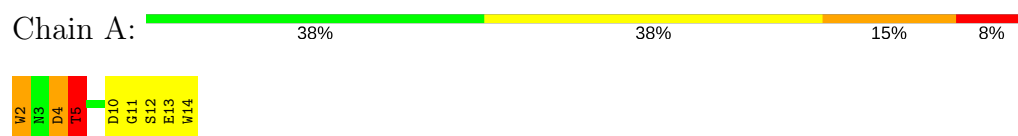
#### 4.2.13 Score per residue for model 13

- Molecule 1: DAPTOMYCIN



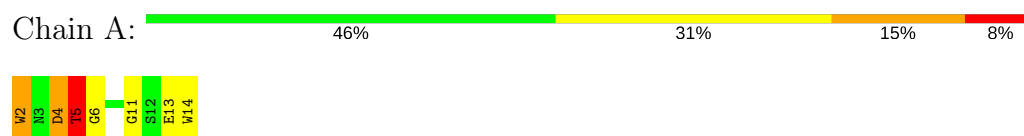
#### 4.2.14 Score per residue for model 14

- Molecule 1: DAPTOMYCIN



#### 4.2.15 Score per residue for model 15

- Molecule 1: DAPTOMYCIN





## 5 Refinement protocol and experimental data overview

Of the 50 calculated structures, 15 were deposited, based on the following criterion: *STRUCTURES WITH THE LEAST RESTRAINT VIOLATIONS*.

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

Software name	Classification	Version
DGII MODULE OF INSIGHT II VER 97.2	refinement	
DGII MODULE OF INSIGHT II VER 97.2	structure solution	
NMRPIPE 1	structure solution	
NMRVIEW 5.0.4	structure solution	

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 6246
Number of chemical shift lists	1
Total number of shifts	67
Number of shifts mapped to atoms	0
Number of unparsed shifts	0
Number of shifts with mapping errors	67
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	0%

No validations of the models with respect to experimental NMR restraints is performed at this time.

## 6 Model quality

### 6.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ORN, KYN, DAL, DSN, DKA, DSG, LME

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the (average) root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#Z>5	RMSZ	#Z>5
1	A	1.44±0.03	0±0/51 (0.0±0.0%)	1.76±0.03	1±0/64 (1.6±0.0%)
All	All	1.44	0/765 (0.0%)	1.76	15/960 (1.6%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	Chirality	Planarity
1	A	4.0±0.0	0.1±0.3
All	All	60	2

There are no bond-length outliers.

All unique angle outliers are listed below.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	2	TRP	CD1-NE1-CE2	-5.56	104.00	109.00	3	15

All unique chiral outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Models (Total)
1	A	5	THR	CB,CA	15
1	A	13	LME	CB	15
1	A	14	KYN	CA	15

All unique planar outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Group	Models (Total)
1	A	6	GLY	Peptide	1
1	A	4	ASP	Peptide	1

## 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	104	79	71	2±1
All	All	1725	1470	1365	27

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:12:DSN:HB2	1:A:13:LME:OE1	0.65	1.91	5	1
1:A:4:ASP:O	1:A:5:THR:HG23	0.59	1.97	1	2
1:A:2:TRP:CE3	1:A:2:TRP:N	0.58	2.71	4	1
1:A:5:THR:HG22	1:A:14:KYN:O	0.58	1.97	12	4
1:A:13:LME:H2	1:A:13:LME:CD	0.57	2.13	9	1
1:A:13:LME:N	1:A:13:LME:CD	0.57	2.68	9	2
1:A:11:GLY:HA2	1:A:12:DSN:HB2	0.52	1.79	14	1
1:A:7:ORN:O	1:A:7:ORN:HD2	0.51	2.05	6	1
1:A:13:LME:H13	1:A:14:KYN:C1	0.51	2.36	5	1
1:A:13:LME:CD	1:A:13:LME:N	0.50	2.73	5	1
1:A:3:DSG:N	1:A:3:DSG:ND2	0.49	2.59	12	1
1:A:10:ASP:OD1	1:A:12:DSN:HB2	0.47	2.08	8	1
1:A:2:TRP:CD1	1:A:3:DSG:N	0.47	2.82	8	1
1:A:2:TRP:CG	1:A:3:DSG:N	0.47	2.82	8	1
1:A:5:THR:CG2	1:A:14:KYN:O	0.47	2.63	12	1
1:A:13:LME:OE2	1:A:13:LME:H11	0.46	2.10	15	1
1:A:7:ORN:N	1:A:7:ORN:CD	0.45	2.80	6	1
1:A:2:TRP:CD1	1:A:3:DSG:HA	0.43	2.49	8	1
1:A:13:LME:H13	1:A:14:KYN:H2	0.42	1.74	14	1
1:A:13:LME:O	1:A:14:KYN:C	0.42	2.68	9	1
1:A:2:TRP:CD2	1:A:2:TRP:N	0.41	2.87	4	1
1:A:11:GLY:HA2	1:A:12:DSN:CB	0.41	2.46	14	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	6/13 (46%)	3±1 (49±17%)	2±1 (26±16%)	2±1 (26±15%)	0	1
All	All	90/195 (46%)	44 (49%)	23 (26%)	23 (26%)	0	1

All 5 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	5	THR	12
1	A	4	ASP	7
1	A	6	GLY	2
1	A	11	GLY	1
1	A	8	ASP	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	5/5 (100%)	2±1 (45±15%)	3±1 (55±15%)	0	1
All	All	75/75 (100%)	34 (45%)	41 (55%)	0	1

All 5 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	2	TRP	14
1	A	5	THR	11
1	A	4	ASP	10
1	A	10	ASP	5
1	A	8	ASP	1

### 6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 6.4 Non-standard residues in protein, DNA, RNA chains ⓘ

6 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds for which Mogul statistics could be retrieved, the number of bonds that are observed in the model and the number of bonds that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length is the number of standard deviations the observed value is removed from the expected value. A bond length with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond lengths.

Mol	Type	Chain	Res	Link	Counts	Bond lengths	
						RMSZ	#Z>2
1	DSN	A	12	1	5,5,6	2.23±0.03	0±0 (0±0%)
1	LME	A	13	1	6,9,10	2.65±0.13	1±0 (15±4%)
1	KYN	A	14	1	14,14,15	1.77±0.16	0±0 (0±1%)
1	DSG	A	3	1	7,7,8	2.04±0.09	0±0 (3±6%)
1	ORN	A	7	1	7,7,8	2.00±0.02	0±0 (0±0%)
1	DAL	A	9	1	4,4,5	2.44±0.03	0±0 (0±0%)

In the following table, the Counts columns list the number of angles for which Mogul statistics could be retrieved, the number of angles that are observed in the model and the number of angles that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond angle is the number of standard deviations the observed value is removed from the expected value. A bond angle with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond angles.

Mol	Type	Chain	Res	Link	Counts	Bond angles	
						RMSZ	#Z>2
1	DSN	A	12	1	1,5,7	2.42±0.04	0±0 (0±0%)
1	LME	A	13	1	6,11,13	2.83±0.15	0±0 (1±4%)
1	KYN	A	14	1	16,18,20	2.13±0.18	1±0 (6±0%)
1	DSG	A	3	1	7,8,10	1.35±0.08	0±0 (0±0%)
1	ORN	A	7	1	4,7,9	1.12±0.06	0±0 (0±0%)
1	DAL	A	9	1	1,4,6	3.12±0.02	0±0 (0±0%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical

component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	DSN	A	12	1	-	0±0,2,4,6	0±0,0,0,0
1	LME	A	13	1	1±0,1,3,4	0±0,7,10,12	0±0,0,0,0
1	KYN	A	14	1	1±0,1,2,3	0±0,8,10,12	0±0,1,1,1
1	DSG	A	3	1	-	0±0,4,6,8	0±0,0,0,0
1	ORN	A	7	1	-	0±0,4,6,8	0±0,0,0,0
1	DAL	A	9	1	-	0±0,0,2,4	0±0,0,0,0

All unique bond outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
1	A	14	KYN	CB-C1	6.95	1.60	1.51	5	1
1	A	13	LME	CA-C	6.39	1.58	1.50	8	14
1	A	3	DSG	CA-C	5.48	1.57	1.50	15	4

All unique angle outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	14	KYN	O2-C1-CB	8.72	110.92	120.76	5	15
1	A	13	LME	CB-CA-C	5.01	120.61	112.84	10	1

All unique chiral outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Models (Total)
1	A	13	LME	CB	15
1	A	14	KYN	CA	15

There are no torsion outliers.

There are no ring outliers.

## 6.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 6.6 Ligand geometry

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds for which Mogul statistics could be retrieved, the number of bonds that are observed in the model and the number of bonds that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length is the number of standard deviations the observed value is removed from the expected value. A bond length with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond lengths.

Mol	Type	Chain	Res	Link	Bond lengths		
					Counts	RMSZ	#Z>2
2	DKA	A	1	1	10,10,11	0.89±0.01	0±0 (0±0%)

In the following table, the Counts columns list the number of angles for which Mogul statistics could be retrieved, the number of angles that are observed in the model and the number of angles that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond angle is the number of standard deviations the observed value is removed from the expected value. A bond angle with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond angles.

Mol	Type	Chain	Res	Link	Bond angles		
					Counts	RMSZ	#Z>2
2	DKA	A	1	1	9,9,11	0.67±0.01	0±0 (0±0%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	DKA	A	1	1	-	0±0,7,8,9	0±0,0,0,0

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 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 0% for the well-defined parts and 0% for the entire structure.

### 7.1 Chemical shift list 1

File name: BMRB entry 6246

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	67
Number of shifts mapped to atoms	0
Number of unparsed shifts	0
Number of shifts with mapping errors	67
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

The following assigned chemical shifts were not mapped to the molecules present in the coordinate file.

- Chain not found in structure. All 67 occurrences are reported below.

Chain	Res	Type	Atom	Shift Data		
				Value	Uncertainty	Ambiguity
UNMAPPED	10	GLY	HA2	4.01	-1.0	1
UNMAPPED	9	ASP	HB3	2.67	-1.0	1
UNMAPPED	9	ASP	HB2	2.74	-1.0	1
UNMAPPED	12	MEG	HA	4.51	-1.0	1
UNMAPPED	2	ASN	HA	4.53	-1.0	1
UNMAPPED	5	GLY	HA3	4.02	-1.0	1
UNMAPPED	1	TRP	HB3	3.17	-1.0	1
UNMAPPED	13	KYN	H	8.45	-1.0	1
UNMAPPED	2	ASN	HB2	2.54	-1.0	1
UNMAPPED	13	KYN	HA	4.75	-1.0	1
UNMAPPED	1	TRP	H	8.1	-1.0	1
UNMAPPED	1	TRP	HZ3	7.07	-1.0	3
UNMAPPED	11	DSN	HA	4.58	-1.0	1
UNMAPPED	11	DSN	HB2	3.89	-1.0	1

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Chain	Res	Type	Atom	Shift Data		
				Value	Uncertainty	Ambiguity
UNMAPPED	1	TRP	HH2	7.17	-1.0	3
UNMAPPED	5	GLY	HA2	4.02	-1.0	1
UNMAPPED	1	TRP	HE1	10.18	-1.0	3
UNMAPPED	12	MEG	HG13	2.05	-1.0	1
UNMAPPED	13	KYN	HB3	3.13	-1.0	1
UNMAPPED	12	MEG	HB3	2.43	-1.0	2
UNMAPPED	7	ASP	HB3	2.43	-1.0	1
UNMAPPED	6	ORN	HG3	1.7	-1.0	2
UNMAPPED	6	ORN	HB2	1.9	-1.0	1
UNMAPPED	12	MEG	H	8.33	-1.0	1
UNMAPPED	6	ORN	H	8.38	-1.0	1
UNMAPPED	6	ORN	HA	4.39	-1.0	1
UNMAPPED	4	THR	HA	4.69	-1.0	1
UNMAPPED	1	TRP	HB2	3.27	-1.0	1
UNMAPPED	2	ASN	HB3	2.44	-1.0	1
UNMAPPED	12	MEG	HB2	2.43	-1.0	2
UNMAPPED	2	ASN	HD22	6.77	-1.0	1
UNMAPPED	4	THR	HG21	1.17	-1.0	1
UNMAPPED	11	DSN	HB3	3.89	-1.0	1
UNMAPPED	4	THR	HG22	1.17	-1.0	1
UNMAPPED	3	DAS	HA	4.66	-1.0	1
UNMAPPED	3	DAS	H	8.28	-1.0	1
UNMAPPED	13	KYN	HB2	3.45	-1.0	1
UNMAPPED	1	TRP	HE3	7.63	-1.0	3
UNMAPPED	4	THR	H	8.18	-1.0	1
UNMAPPED	7	ASP	HB2	2.58	-1.0	1
UNMAPPED	7	ASP	HA	4.49	-1.0	1
UNMAPPED	3	DAS	HB3	2.61	-1.0	1
UNMAPPED	8	DAL	HA	4.34	-1.0	1
UNMAPPED	1	TRP	HZ2	7.45	-1.0	3
UNMAPPED	10	GLY	HA3	4.01	-1.0	1
UNMAPPED	11	DSN	H	8.21	-1.0	1
UNMAPPED	4	THR	HB	5.51	-1.0	1
UNMAPPED	12	MEG	HG23	0.93	-1.0	2
UNMAPPED	6	ORN	HD	3.0	-1.0	1
UNMAPPED	9	ASP	H	8.49	-1.0	1
UNMAPPED	1	TRP	HD1	7.28	-1.0	3
UNMAPPED	12	MEG	HG22	0.93	-1.0	2
UNMAPPED	2	ASN	HD21	7.41	-1.0	1
UNMAPPED	5	GLY	H	8.34	-1.0	1
UNMAPPED	2	ASN	H	8.36	-1.0	1

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Chain	Res	Type	Atom	Shift Data		
				Value	Uncertainty	Ambiguity
UNMAPPED	4	THR	HG23	1.17	-1.0	1
UNMAPPED	9	ASP	HA	4.63	-1.0	1
UNMAPPED	1	TRP	HA	4.63	-1.0	1
UNMAPPED	13	KYN	HE1	7.38	-1.0	1
UNMAPPED	7	ASP	H	8.39	-1.0	1
UNMAPPED	12	MEG	HG12	2.33	-1.0	1
UNMAPPED	8	DAL	HB	1.36	-1.0	1
UNMAPPED	8	DAL	H	8.28	-1.0	1
UNMAPPED	10	GLY	H	8.38	-1.0	1
UNMAPPED	6	ORN	HG2	1.7	-1.0	2
UNMAPPED	3	DAS	HB2	2.74	-1.0	1
UNMAPPED	6	ORN	HB3	1.79	-1.0	1

### 7.1.2 Chemical shift referencing [i](#)

No chemical shift referencing corrections were calculated (not enough data).

### 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 0%, i.e. 0 atoms were assigned a chemical shift out of a possible 66. 0 out of 0 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Backbone	0/35 (0%)	0/14 (0%)	0/14 (0%)	0/7 (0%)
Sidechain	0/19 (0%)	0/10 (0%)	0/9 (0%)	0/0 (—%)
Aromatic	0/12 (0%)	0/6 (0%)	0/5 (0%)	0/1 (0%)
Overall	0/66 (0%)	0/30 (0%)	0/28 (0%)	0/8 (0%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 0%, i.e. 0 atoms were assigned a chemical shift out of a possible 66. 0 out of 0 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Backbone	0/35 (0%)	0/14 (0%)	0/14 (0%)	0/7 (0%)
Sidechain	0/19 (0%)	0/10 (0%)	0/9 (0%)	0/0 (—%)
Aromatic	0/12 (0%)	0/6 (0%)	0/5 (0%)	0/1 (0%)
Overall	0/66 (0%)	0/30 (0%)	0/28 (0%)	0/8 (0%)

#### 7.1.4 Statistically unusual chemical shifts

There are no statistically unusual chemical shifts.

#### 7.1.5 Random Coil Index (RCI) plots

No *random coil index* (RCI) plot could be generated from the current chemical shift list (assigned\_chem\_shift\_list\_1). RCI is only applicable to proteins.