



Full wwPDB NMR Structure Validation Report ⓘ

Oct 29, 2017 – 07:27 AM EDT

PDB ID : 2DA8
Title : SOLUTION STRUCTURE OF A COMPLEX BETWEEN (N-MECYS3,N-M
ECYS7)TANDEM AND (D(GATATC))2
Authors : Address, K.J.; Sinsheimer, J.S.; Feigon, J.
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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

Cyrange : Kirchner and Güntert (2011)
NmrClust : Kelley et al. (1996)
MolProbity : 4.02b-467
Mogul : 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 : rb-20030345
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20030345

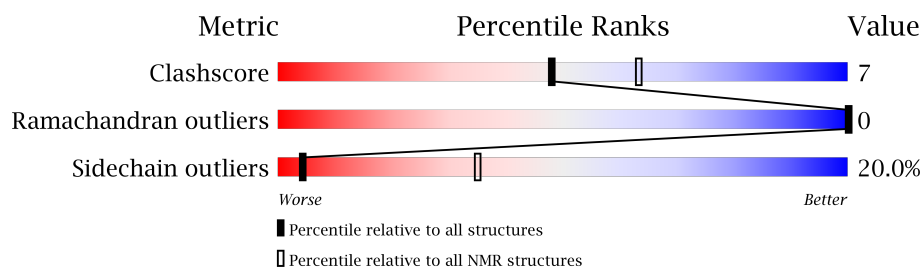
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment 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 ≥ 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	8	
2	C	6	
2	D	6	

2 Ensemble composition and analysis ⓘ

This entry contains 8 models. The atoms present in the NMR models are not consistent. Some calculations may have failed as a result. All residues are included in the validation scores.

Cyrange was unable to find well-defined residues.

Error message: The number of core atoms (2) 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 3 unique types of molecules in this entry. The entry contains 512 atoms, of which 198 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called TRIOSTIN A.

Mol	Chain	Residues	Atoms						Trace
1	A	8	Total	C	H	N	O	S	0
			98	30	48	8	10	2	

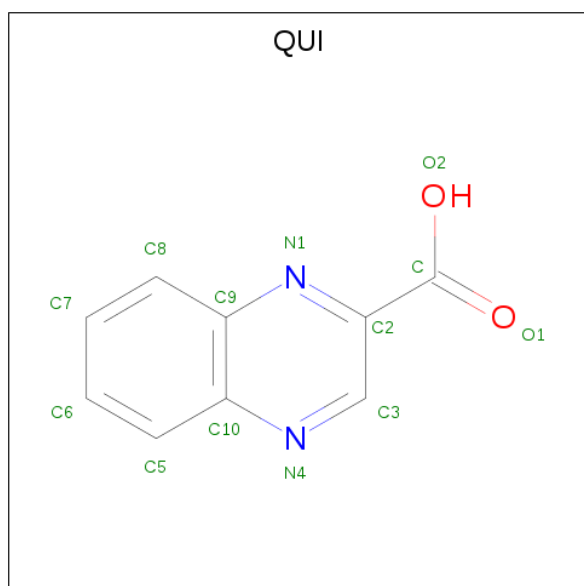
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	4	VAL	MVA	ENGINEERED MUTATION	NOR NOR01129
A	8	VAL	MVA	ENGINEERED MUTATION	NOR NOR01129

- Molecule 2 is a DNA chain called DNA (5'-D(*GP*AP*TP*AP*TP*C)-3').

Mol	Chain	Residues	Atoms						Trace
2	C	6	Total	C	H	N	O	P	0
			190	59	70	22	34	5	
2	D	6	Total	C	H	N	O	P	0
			190	59	70	22	34	5	

- Molecule 3 is 2-CARBOXYQUINOXALINE (three-letter code: QUI) (formula: C₉H₆N₂O₂).



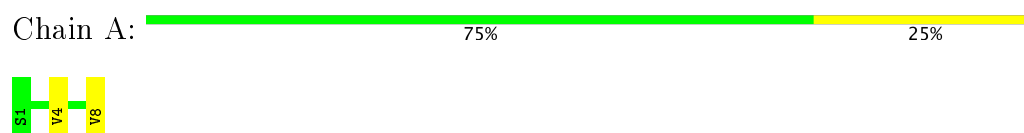
Mol	Chain	Residues	Atoms				
3	A	1	Total	C	H	N	O
			17	9	5	2	1
3	A	1	Total	C	H	N	O
			17	9	5	2	1

4 Residue-property plots

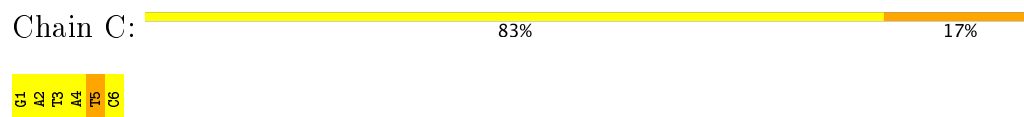
4.1 Average score per residue in the NMR ensemble

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.

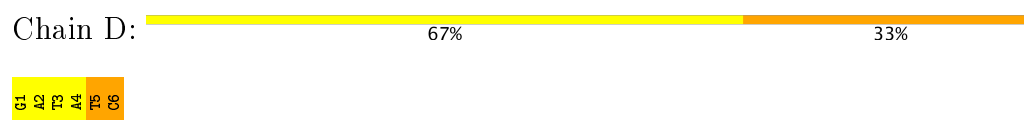
- Molecule 1: TRIOSTIN A



- Molecule 2: DNA (5'-D(*GP*AP*TP*AP*TP*C)-3')



- Molecule 2: DNA (5'-D(*GP*AP*TP*AP*TP*C)-3')

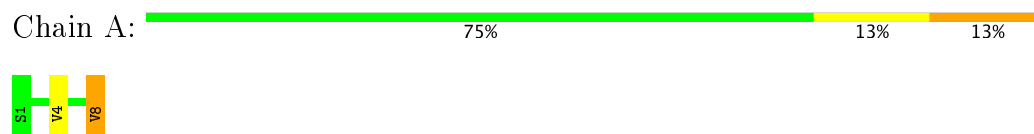


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

- Molecule 1: TRIOSTIN A



- Molecule 2: DNA (5'-D(*GP*AP*TP*AP*TP*C)-3')

Chain C:  100%

G1
A2
T3
A4
T5
C6

- Molecule 2: DNA (5'-D(*GP*AP*TP*AP*TP*C)-3')

Chain D:  67% 33%

G1
A2
T3
A4
T5
C6


4.2.2 Score per residue for model 2

- Molecule 1: TRIOSTIN A

Chain A:  75% 13% 13%


S1
V4
V8

- Molecule 2: DNA (5'-D(*GP*AP*TP*AP*TP*C)-3')

Chain C:  83% 17%

G1
A2
T3
A4
T5
C6


- Molecule 2: DNA (5'-D(*GP*AP*TP*AP*TP*C)-3')

Chain D:  17% 50% 33%

G1
A2
T3
A4
T5
C6

4.2.3 Score per residue for model 3

- Molecule 1: TRIOSTIN A

Chain A:  75% 25%

S1
V4
V8

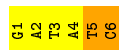
- Molecule 2: DNA (5'-D(*GP*AP*TP*AP*TP*C)-3')

Chain C:  67% 33%

G1
A2
T3
A4
T5
C6

- Molecule 2: DNA (5'-D(*GP*AP*TP*AP*TP*C)-3')

Chain D:  67% 33%



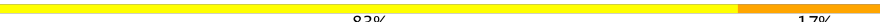
4.2.4 Score per residue for model 4

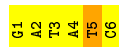
- Molecule 1: TRIOSTIN A

Chain A:  75% 25%




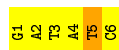
- Molecule 2: DNA (5'-D(*GP*AP*TP*AP*TP*C)-3')

Chain C:  83% 17%



- Molecule 2: DNA (5'-D(*GP*AP*TP*AP*TP*C)-3')

Chain D:  83% 17%



4.2.5 Score per residue for model 5

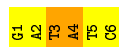
- Molecule 1: TRIOSTIN A

Chain A:  50% 50%



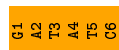
- Molecule 2: DNA (5'-D(*GP*AP*TP*AP*TP*C)-3')

Chain C:  67% 33%



- Molecule 2: DNA (5'-D(*GP*AP*TP*AP*TP*C)-3')

Chain D:  100%



4.2.6 Score per residue for model 6

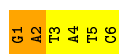
- Molecule 1: TRIOSTIN A

Chain A: 75% 25%



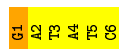
- Molecule 2: DNA (5'-D(*GP*AP*TP*AP*TP*C)-3')

Chain C: 67% 33%



- Molecule 2: DNA (5'-D(*GP*AP*TP*AP*TP*C)-3')

Chain D: 83% 17%



4.2.7 Score per residue for model 7

- Molecule 1: TRIOSTIN A

Chain A: 50% 50%



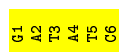
- Molecule 2: DNA (5'-D(*GP*AP*TP*AP*TP*C)-3')

Chain C: 50% 50%



- Molecule 2: DNA (5'-D(*GP*AP*TP*AP*TP*C)-3')

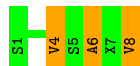
Chain D: 100%



4.2.8 Score per residue for model 8

- Molecule 1: TRIOSTIN A

Chain A:  63% 38%



- Molecule 2: DNA (5'-D(*GP*AP*TP*AP*TP*C)-3')

Chain C:  50% 50%



- Molecule 2: DNA (5'-D(*GP*AP*TP*AP*TP*C)-3')

Chain D:  17% 67% 17%



5 Refinement protocol and experimental data overview

The models were refined using the following method: *ENERGY MINIMIZATION, RESTRAINED MOLECULAR DYNAMICS, NOE BASED RELAXATION REFINEMENT*.

Of the 8 calculated structures, 8 were deposited, based on the following criterion: *all calculated structures submitted*.

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

Software name	Classification	Version
X-PLOR	refinement	
DSPACE	structure solution	

No chemical shift data was provided. 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: DSN, NCY, QUI

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	3.94±0.83	4±2/20 (18.1±10.9%)	3.66±0.89	4±1/22 (18.2±4.5%)
2	C	1.74±0.09	2±0/134 (1.6±0.2%)	2.38±0.10	13±2/205 (6.5±1.1%)
2	D	1.77±0.08	2±0/134 (1.6±0.2%)	2.42±0.10	12±2/205 (6.0±0.8%)
All	All	1.98	63/2294 (2.7%)	2.49	238/3445 (6.9%)

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	6	ALA	CA-CB	18.18	1.90	1.52	8	1
2	D	5	DT	C5-C7	11.46	1.56	1.50	6	8
2	C	5	DT	C5-C7	11.19	1.56	1.50	3	8
2	D	3	DT	C5-C7	9.58	1.55	1.50	8	8
2	C	3	DT	C5-C7	9.50	1.55	1.50	8	8
1	A	8	VAL	CB-CG2	8.50	1.70	1.52	3	5
1	A	4	VAL	CB-CG2	8.24	1.70	1.52	6	6
1	A	8	VAL	CB-CG1	7.57	1.68	1.52	2	5
1	A	4	VAL	CB-CG1	7.53	1.68	1.52	8	6
1	A	8	VAL	CA-CB	6.87	1.69	1.54	2	2
1	A	4	VAL	CA-CB	6.63	1.68	1.54	8	3
2	C	5	DT	C5-C6	5.68	1.38	1.34	8	1
2	D	3	DT	C5-C6	5.38	1.38	1.34	6	1
1	A	2	ALA	CA-CB	5.21	1.63	1.52	6	1

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	6	ALA	CB-CA-C	17.64	136.56	110.10	8	1

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
2	C	3	DT	O4'-C1'-N1	16.55	119.58	108.00	6	6
1	A	6	ALA	N-CA-CB	-14.12	90.33	110.10	8	1
2	D	6	DC	O4'-C1'-N1	13.56	117.49	108.00	4	8
2	D	3	DT	O4'-C1'-N1	11.37	115.96	108.00	6	4
2	C	1	DG	P-O3'-C3'	10.18	131.92	119.70	7	6
2	D	2	DA	O4'-C1'-N9	9.40	114.58	108.00	8	3
1	A	4	VAL	CG1-CB-CG2	-9.03	96.45	110.90	3	8
2	D	1	DG	P-O3'-C3'	8.51	129.91	119.70	4	4
2	C	6	DC	O4'-C1'-N1	8.27	113.79	108.00	5	8
1	A	8	VAL	CG1-CB-CG2	-8.24	97.72	110.90	2	7
2	C	3	DT	P-O3'-C3'	7.84	129.10	119.70	5	4
2	D	3	DT	O4'-C4'-C3'	-7.75	101.35	106.00	6	2
2	D	4	DA	C8-N9-C4	-7.62	102.75	105.80	3	4
2	C	1	DG	O4'-C1'-N9	7.56	113.29	108.00	4	3
1	A	8	VAL	CA-CB-CG1	7.53	122.20	110.90	1	4
1	A	4	VAL	CA-CB-CG1	7.45	122.07	110.90	2	6
2	C	4	DA	O4'-C1'-C2'	-7.33	100.03	105.90	8	4
2	D	4	DA	P-O3'-C3'	6.94	128.03	119.70	6	1
2	C	6	DC	C4'-C3'-C2'	-6.90	96.89	103.10	2	8
2	D	6	DC	C4'-C3'-C2'	-6.84	96.95	103.10	4	8
2	D	1	DG	N7-C8-N9	6.78	116.49	113.10	7	8
2	C	4	DA	C8-N9-C4	-6.77	103.09	105.80	3	6
2	C	1	DG	N7-C8-N9	6.72	116.46	113.10	8	8
2	C	5	DT	O4'-C1'-N1	6.70	112.69	108.00	8	2
2	D	2	DA	C8-N9-C4	-6.66	103.14	105.80	6	7
1	A	8	VAL	CA-CB-CG2	6.64	120.86	110.90	5	3
2	C	2	DA	C8-N9-C4	-6.64	103.15	105.80	6	7
2	C	4	DA	O4'-C1'-N9	6.56	112.59	108.00	3	2
2	D	1	DG	C4'-C3'-C2'	-6.47	97.28	103.10	6	8
2	C	2	DA	O4'-C1'-N9	6.47	112.53	108.00	5	2
2	C	1	DG	C8-N9-C4	-6.44	103.82	106.40	7	8
2	C	5	DT	O4'-C1'-C2'	-6.43	100.75	105.90	8	2
2	C	1	DG	C4'-C3'-C2'	-6.42	97.33	103.10	6	8
2	D	5	DT	O4'-C1'-N1	6.35	112.44	108.00	1	2
2	D	3	DT	P-O3'-C3'	6.24	127.19	119.70	5	2
2	D	2	DA	N7-C8-N9	6.22	116.91	113.80	6	8
2	D	1	DG	C8-N9-C4	-6.19	103.92	106.40	4	8
2	D	2	DA	O4'-C1'-C2'	-6.09	101.02	105.90	3	7
1	A	4	VAL	CA-CB-CG2	6.01	119.92	110.90	7	2
2	D	4	DA	N7-C8-N9	5.86	116.73	113.80	3	3
2	C	6	DC	N1-C2-O2	5.84	122.40	118.90	3	8

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
2	D	2	DA	P-O3'-C3'	5.74	126.58	119.70	6	3
2	D	4	DA	O4'-C1'-C2'	-5.62	101.41	105.90	5	1
2	C	2	DA	N7-C8-N9	5.56	116.58	113.80	7	7
2	C	2	DA	P-O3'-C3'	5.47	126.27	119.70	1	3
2	C	4	DA	N7-C8-N9	5.31	116.46	113.80	3	3
2	D	6	DC	N1-C2-O2	5.25	122.05	118.90	6	4
2	D	4	DA	O4'-C1'-N9	5.21	111.65	108.00	3	1
2	D	3	DT	N1-C1'-C2'	5.19	122.46	112.60	8	1
2	C	3	DT	C5-C6-N1	-5.09	120.64	123.70	8	1
2	C	2	DA	O4'-C1'-C2'	-5.07	101.84	105.90	8	1
2	D	3	DT	C5-C6-N1	-5.05	120.67	123.70	8	2

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	50	48	46	1±1
2	D	120	70	70	1±1
2	C	120	70	70	2±1
3	A	24	10	10	0±0
All	All	2475	1553	1542	29

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 7.

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:ALA:CA	1:A:6:ALA:CB	1.45	1.90	8	1
1:A:6:ALA:N	1:A:6:ALA:CB	0.81	2.43	8	1
2:D:5:DT:H2''	2:D:6:DC:O4'	0.66	1.91	3	4
2:C:2:DA:H3'	2:C:2:DA:OP2	0.56	2.01	8	1
2:C:5:DT:H6	2:C:5:DT:OP2	0.54	1.84	3	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:C:3:DT:H5'	2:C:4:DA:OP1	0.54	2.02	7	1
2:C:5:DT:OP2	2:C:5:DT:H6	0.50	1.90	7	2
1:A:3:NCY:HA	1:A:7:NCY:HA	0.49	1.84	5	2
2:D:1:DG:H1'	2:D:2:DA:O5'	0.49	2.07	5	1
2:D:5:DT:H6	2:D:5:DT:OP2	0.49	1.91	5	4
2:C:1:DG:H1'	2:C:2:DA:O5'	0.43	2.13	6	1
2:C:5:DT:C6	2:C:5:DT:OP2	0.42	2.71	3	2
2:C:3:DT:H4'	2:C:4:DA:OP1	0.42	2.14	5	1
2:D:1:DG:H2'	2:D:1:DG:O5'	0.42	2.14	6	1
1:A:8:VAL:HG21	3:A:0:QUI:H8	0.42	1.92	8	1
3:A:9:QUI:C7	2:C:3:DT:C2	0.41	3.03	3	1
2:D:3:DT:H4'	2:D:4:DA:OP1	0.41	2.16	5	1
2:C:1:DG:O5'	2:C:1:DG:H2'	0.40	2.16	8	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	2/8 (25%)	2±0 (94±17%)	0±0 (0±0%)	0±0 (0±0%)	100	100
All	All	15/64 (23%)	15 (100%)	0 (0%)	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	2/2 (100%)	2±1 (75±25%)	0±0 (19±24%)	5	37
All	All	15/16 (94%)	12 (80%)	3 (20%)	4	35

All 2 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	8	VAL	2
1	A	4	VAL	1

6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

4 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	Bond lengths		
					Counts	RMSZ	#Z>2
1	DSN	A	1	1,3	5,5,6	1.61±0.18	0±0 (0±0%)
1	NCY	A	3	1	6,6,7	1.44±0.16	0±0 (0±0%)
1	DSN	A	5	1,3	5,5,6	1.36±0.54	0±0 (0±0%)
1	NCY	A	7	1	6,6,7	1.24±0.52	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
1	DSN	A	1	1,3	1,5,7	2.33±0.18	0±0 (0±0%)
1	NCY	A	3	1	6,6,8	1.47±0.41	0±0 (0±0%)
1	DSN	A	5	1,3	1,5,7	2.13±0.84	0±0 (0±0%)
1	NCY	A	7	1	6,6,8	1.25±0.63	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	1	1,3	-	0±0,2,4,6	0±0,0,0,0
1	NCY	A	3	1	-	0±0,2,6,8	0±0,0,0,0
1	DSN	A	5	1,3	-	0±0,2,4,6	0±0,0,0,0
1	NCY	A	7	1	-	0±0,2,6,8	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.

6.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.6 Ligand geometry [i](#)

2 ligands 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	Bond lengths		
					Counts	RMSZ	#Z>2
3	QUI	A	0	1	13,13,14	1.32±0.02	0±0 (0±0%)
3	QUI	A	9	1	13,13,14	1.15±0.43	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
3	QUI	A	0	1	15,17,19	1.64±0.25	1±0 (4±3%)
3	QUI	A	9	1	15,17,19	1.46±0.56	1±0 (4±3%)

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
3	QUI	A	0	1	-	0±0,2,2,4	0±0,2,2,2
3	QUI	A	9	1	-	0±0,2,2,4	0±0,2,2,2

There are no bond-length outliers.

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
3	A	0	QUI	O1-C-C2	6.81	118.43	124.32	6	5
3	A	9	QUI	O1-C-C2	6.22	118.94	124.32	8	5

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

No chemical shift data were provided