



wwPDB NMR Structure Validation Summary Report ⓘ

Dec 18, 2019 – 08:47 PM EST

PDB ID : 2A9H
Title : NMR structural studies of a potassium channel / charybdotoxin complex
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Deposited on : 2005-07-11

This is a wwPDB NMR Structure Validation Summary 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 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	:	1.8.0 (224370), CSD as540be (2019)
Percentile statistics	:	20171227.v01 (using entries in the PDB archive December 27th 2017)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	2.4
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.4

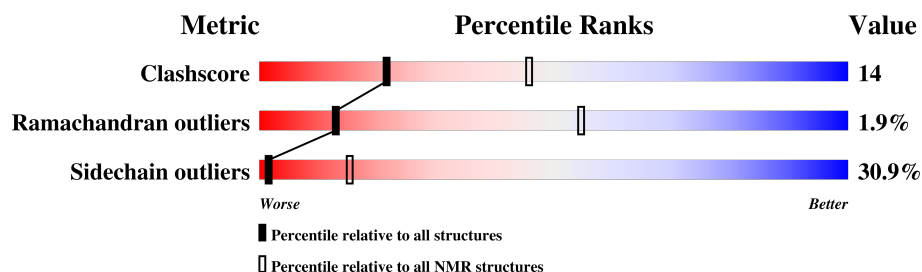
1 Overall quality at a glance

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	136327	12091
Ramachandran outliers	132723	10835
Sidechain outliers	132532	10811

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	155	<div> <div>34%</div> <div>24%</div> <div>5%</div> <div>37%</div> </div>
1	B	155	<div> <div>34%</div> <div>25%</div> <div>.</div> <div>37%</div> </div>
1	C	155	<div> <div>30%</div> <div>28%</div> <div>5%</div> <div>37%</div> </div>
1	D	155	<div> <div>30%</div> <div>27%</div> <div>5%</div> <div>37%</div> </div>
2	E	37	<div> <div>46%</div> <div>54%</div> </div>

2 Ensemble composition and analysis ⓘ

This entry contains 1 models. Identification of well-defined residues and clustering analysis are not possible.

3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6381 atoms, of which 3202 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Voltage-gated potassium channel.

Mol	Chain	Residues	Atoms						Trace
1	A	97	Total	C	H	N	O	S	0
			1451	478	730	117	124	2	
1	B	97	Total	C	H	N	O	S	0
			1451	478	730	117	124	2	
1	C	97	Total	C	H	N	O	S	0
			1451	478	730	117	124	2	
1	D	97	Total	C	H	N	O	S	0
			1451	478	730	117	124	2	

There are 120 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-22	MET	-	cloning artifact	UNP P0A334
A	-21	SER	-	cloning artifact	UNP P0A334
A	-20	GLY	-	cloning artifact	UNP P0A334
A	-19	SER	-	cloning artifact	UNP P0A334
A	-18	HIS	-	expression tag	UNP P0A334
A	-17	HIS	-	expression tag	UNP P0A334
A	-16	HIS	-	expression tag	UNP P0A334
A	-15	HIS	-	expression tag	UNP P0A334
A	-14	HIS	-	expression tag	UNP P0A334
A	-13	HIS	-	expression tag	UNP P0A334
A	-12	SER	-	cloning artifact	UNP P0A334
A	-11	SER	-	cloning artifact	UNP P0A334
A	-10	GLY	-	cloning artifact	UNP P0A334
A	-9	ILE	-	cloning artifact	UNP P0A334
A	-8	GLU	-	cloning artifact	UNP P0A334
A	-7	GLY	-	cloning artifact	UNP P0A334
A	-6	ARG	-	cloning artifact	UNP P0A334
A	-5	GLY	-	cloning artifact	UNP P0A334
A	-4	ARG	-	cloning artifact	UNP P0A334
A	-3	LEU	-	cloning artifact	UNP P0A334
A	-2	ILE	-	cloning artifact	UNP P0A334
A	-1	LYS	-	cloning artifact	UNP P0A334
A	0	HIS	-	cloning artifact	UNP P0A334
A	58	ALA	GLN	ENGINEERED	UNP P0A334
A	61	SER	THR	ENGINEERED	UNP P0A334

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Chain	Residue	Modelled	Actual	Comment	Reference
A	64	ASP	ARG	ENGINEERED	UNP P0A334
A	90	CYS	LEU	ENGINEERED	UNP P0A334
A	103	TYR	PHE	ENGINEERED	UNP P0A334
A	107	PHE	THR	ENGINEERED	UNP P0A334
A	110	VAL	LEU	ENGINEERED	UNP P0A334
B	-22	MET	-	cloning artifact	UNP P0A334
B	-21	SER	-	cloning artifact	UNP P0A334
B	-20	GLY	-	cloning artifact	UNP P0A334
B	-19	SER	-	cloning artifact	UNP P0A334
B	-18	HIS	-	expression tag	UNP P0A334
B	-17	HIS	-	expression tag	UNP P0A334
B	-16	HIS	-	expression tag	UNP P0A334
B	-15	HIS	-	expression tag	UNP P0A334
B	-14	HIS	-	expression tag	UNP P0A334
B	-13	HIS	-	expression tag	UNP P0A334
B	-12	SER	-	cloning artifact	UNP P0A334
B	-11	SER	-	cloning artifact	UNP P0A334
B	-10	GLY	-	cloning artifact	UNP P0A334
B	-9	ILE	-	cloning artifact	UNP P0A334
B	-8	GLU	-	cloning artifact	UNP P0A334
B	-7	GLY	-	cloning artifact	UNP P0A334
B	-6	ARG	-	cloning artifact	UNP P0A334
B	-5	GLY	-	cloning artifact	UNP P0A334
B	-4	ARG	-	cloning artifact	UNP P0A334
B	-3	LEU	-	cloning artifact	UNP P0A334
B	-2	ILE	-	cloning artifact	UNP P0A334
B	-1	LYS	-	cloning artifact	UNP P0A334
B	0	HIS	-	cloning artifact	UNP P0A334
B	58	ALA	GLN	ENGINEERED	UNP P0A334
B	61	SER	THR	ENGINEERED	UNP P0A334
B	64	ASP	ARG	ENGINEERED	UNP P0A334
B	90	CYS	LEU	ENGINEERED	UNP P0A334
B	103	TYR	PHE	ENGINEERED	UNP P0A334
B	107	PHE	THR	ENGINEERED	UNP P0A334
B	110	VAL	LEU	ENGINEERED	UNP P0A334
C	-22	MET	-	cloning artifact	UNP P0A334
C	-21	SER	-	cloning artifact	UNP P0A334
C	-20	GLY	-	cloning artifact	UNP P0A334
C	-19	SER	-	cloning artifact	UNP P0A334
C	-18	HIS	-	expression tag	UNP P0A334
C	-17	HIS	-	expression tag	UNP P0A334
C	-16	HIS	-	expression tag	UNP P0A334

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-15	HIS	-	expression tag	UNP P0A334
C	-14	HIS	-	expression tag	UNP P0A334
C	-13	HIS	-	expression tag	UNP P0A334
C	-12	SER	-	cloning artifact	UNP P0A334
C	-11	SER	-	cloning artifact	UNP P0A334
C	-10	GLY	-	cloning artifact	UNP P0A334
C	-9	ILE	-	cloning artifact	UNP P0A334
C	-8	GLU	-	cloning artifact	UNP P0A334
C	-7	GLY	-	cloning artifact	UNP P0A334
C	-6	ARG	-	cloning artifact	UNP P0A334
C	-5	GLY	-	cloning artifact	UNP P0A334
C	-4	ARG	-	cloning artifact	UNP P0A334
C	-3	LEU	-	cloning artifact	UNP P0A334
C	-2	ILE	-	cloning artifact	UNP P0A334
C	-1	LYS	-	cloning artifact	UNP P0A334
C	0	HIS	-	cloning artifact	UNP P0A334
C	58	ALA	GLN	ENGINEERED	UNP P0A334
C	61	SER	THR	ENGINEERED	UNP P0A334
C	64	ASP	ARG	ENGINEERED	UNP P0A334
C	90	CYS	LEU	ENGINEERED	UNP P0A334
C	103	TYR	PHE	ENGINEERED	UNP P0A334
C	107	PHE	THR	ENGINEERED	UNP P0A334
C	110	VAL	LEU	ENGINEERED	UNP P0A334
D	-22	MET	-	cloning artifact	UNP P0A334
D	-21	SER	-	cloning artifact	UNP P0A334
D	-20	GLY	-	cloning artifact	UNP P0A334
D	-19	SER	-	cloning artifact	UNP P0A334
D	-18	HIS	-	expression tag	UNP P0A334
D	-17	HIS	-	expression tag	UNP P0A334
D	-16	HIS	-	expression tag	UNP P0A334
D	-15	HIS	-	expression tag	UNP P0A334
D	-14	HIS	-	expression tag	UNP P0A334
D	-13	HIS	-	expression tag	UNP P0A334
D	-12	SER	-	cloning artifact	UNP P0A334
D	-11	SER	-	cloning artifact	UNP P0A334
D	-10	GLY	-	cloning artifact	UNP P0A334
D	-9	ILE	-	cloning artifact	UNP P0A334
D	-8	GLU	-	cloning artifact	UNP P0A334
D	-7	GLY	-	cloning artifact	UNP P0A334
D	-6	ARG	-	cloning artifact	UNP P0A334
D	-5	GLY	-	cloning artifact	UNP P0A334
D	-4	ARG	-	cloning artifact	UNP P0A334

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-3	LEU	-	cloning artifact	UNP P0A334
D	-2	ILE	-	cloning artifact	UNP P0A334
D	-1	LYS	-	cloning artifact	UNP P0A334
D	0	HIS	-	cloning artifact	UNP P0A334
D	58	ALA	GLN	ENGINEERED	UNP P0A334
D	61	SER	THR	ENGINEERED	UNP P0A334
D	64	ASP	ARG	ENGINEERED	UNP P0A334
D	90	CYS	LEU	ENGINEERED	UNP P0A334
D	103	TYR	PHE	ENGINEERED	UNP P0A334
D	107	PHE	THR	ENGINEERED	UNP P0A334
D	110	VAL	LEU	ENGINEERED	UNP P0A334

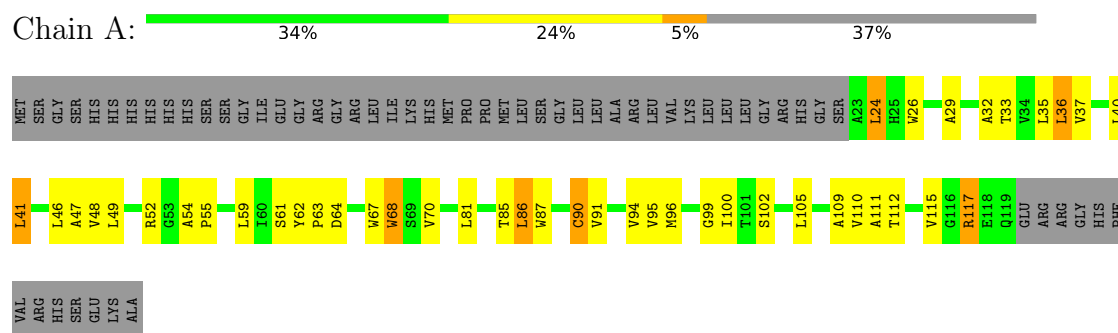
- Molecule 2 is a protein called charybdotoxin.

Mol	Chain	Residues	Atoms						Trace
2	E	37	Total	C	H	N	O	S	0
			577	176	282	57	55	7	

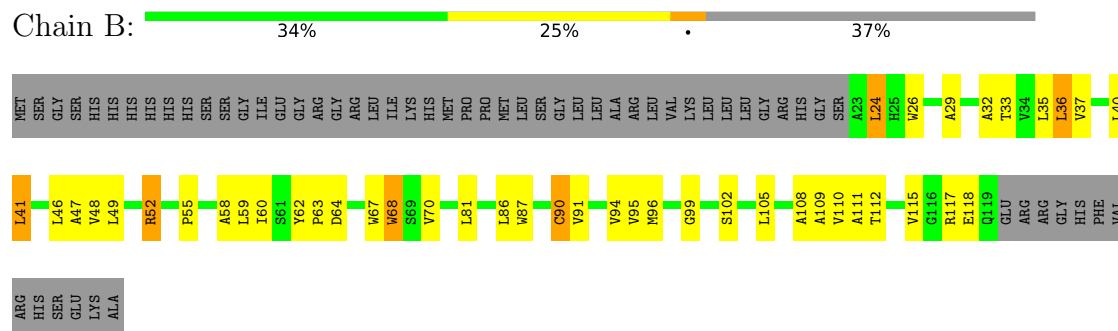
4 Residue-property plots [i](#)

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.

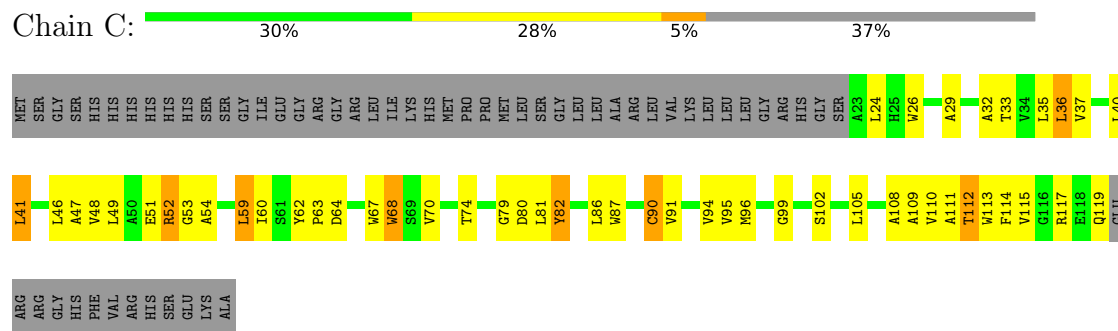
• Molecule 1: Voltage-gated potassium channel



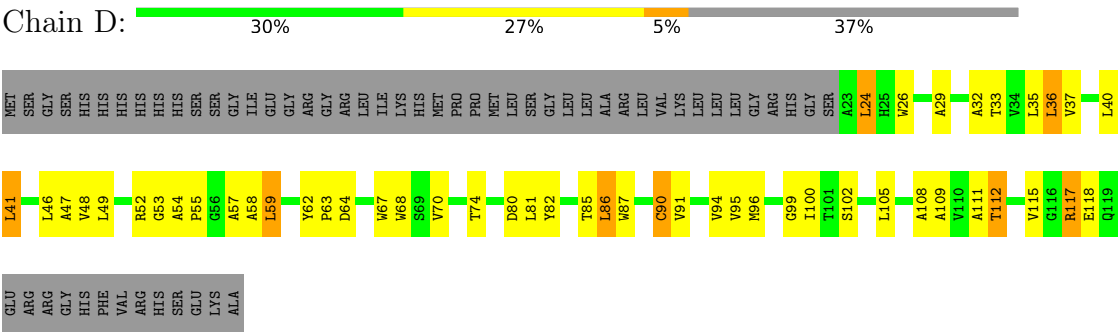
• Molecule 1: Voltage-gated potassium channel



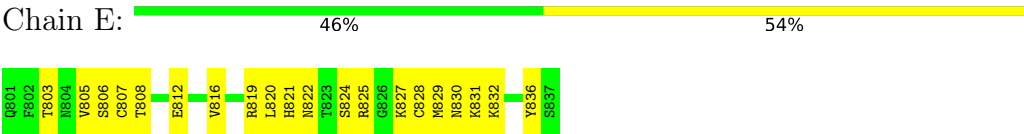
• Molecule 1: Voltage-gated potassium channel



• Molecule 1: Voltage-gated potassium channel



● Molecule 2: charybdotoxin



5 Refinement protocol and experimental data overview ⓘ

The models were refined using the following method: *molecular SIMULATED ANNEALING / dynamics / docking*.

Of the ? calculated structures, 1 were deposited, based on the following criterion: ?.

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

Software name	Classification	Version
CNS	structure solution	2002
CNS	refinement	2002

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: PCA

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	721	730	729	21
1	B	721	730	729	25
1	C	721	730	729	28
1	D	721	730	729	28
2	E	295	282	281	2
All	All	3179	3202	3197	90

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 14.

5 of 90 clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)
1:D:57:ALA:HB2	1:D:82:TYR:O	0.77	1.79
1:A:24:LEU:HD22	1:D:117:ARG:HD2	0.69	1.63
1:D:80:ASP:O	1:D:81:LEU:HD23	0.68	1.89
1:A:24:LEU:HD22	1:D:117:ARG:CD	0.67	2.19
1:B:32:ALA:HB1	1:B:102:SER:HA	0.66	1.66

6.3 Torsion angles ⓘ

6.3.1 Protein backbone ⓘ

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	95/155 (61%)	78 (82%)	16 (17%)	1 (1%)	20	67
1	B	95/155 (61%)	78 (82%)	15 (16%)	2 (2%)	12	52
1	C	95/155 (61%)	77 (81%)	17 (18%)	1 (1%)	20	67
1	D	95/155 (61%)	76 (80%)	17 (18%)	2 (2%)	12	52
2	E	35/37 (95%)	27 (77%)	6 (17%)	2 (6%)	4	22
All	All	415/657 (63%)	336 (81%)	71 (17%)	8 (2%)	13	54

5 of 8 Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type
2	E	825	ARG
1	D	55	PRO
1	B	55	PRO
2	E	822	ASN
1	A	24	LEU

6.3.2 Protein sidechains ⓘ

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	69/117 (59%)	49 (71%)	20 (29%)	2	18
1	B	69/117 (59%)	50 (72%)	19 (28%)	2	21
1	C	69/117 (59%)	48 (70%)	21 (30%)	1	16
1	D	69/117 (59%)	49 (71%)	20 (29%)	2	18
2	E	35/35 (100%)	19 (54%)	16 (46%)	0	2

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	311/503 (62%)	215 (69%)	96 (31%)	1 15

5 of 96 residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type
1	A	95	VAL
1	A	49	LEU
1	D	46	LEU
1	A	33	THR
2	E	820	LEU

6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue 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	PCA	E	801	2	8,8,9	1.34	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	PCA	E	801	2	9,10,12	1.21	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	PCA	E	801	2	-	0,0,11,13	0,1,1,1

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](#)

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

No chemical shift data were provided