

Full wwPDB NMR Structure Validation Report (i)

May 29, 2020 - 08:33 am BST

PDB ID	:	5TBG
Title	:	The Solution Structure of the Magnesium-bound Conantokin-R1B Mutant
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Deposited on	:	2016-09-12

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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

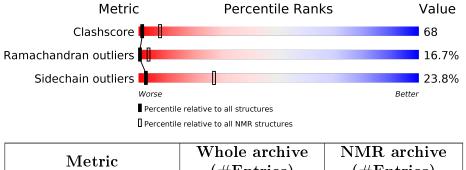
Cyrange	:	Kirchner and Güntert (2011)
NmrClust	:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI	:	$v_1n_11_5_13_A$ (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
${ m ShiftChecker}$:	2.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 84%.

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	(# Entries)	(#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 <=5%

Mol	Chain	Length	Quality of chain			
1	А	20	5%	30%	25%	40%



2 Ensemble composition and analysis (i)

This entry contains 20 models. Model 14 is the overall representative, medoid model (most similar to other models).

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:5-A:6, A:8-A:10, A:12-	0.18	14			
	A:14, A:16-A:19 (12)					

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 4 clusters. No single-model clusters were found.

Cluster number	Models		
1	2, 9, 10, 13, 14, 15, 16, 17, 18, 19		
2	3, 4, 6, 7, 12		
3	1, 5, 11		
4	8, 20		



3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 304 atoms, of which 136 are hydrogens and 0 are deuteriums.

• Molecule 1 is a protein called Conantokin-R1B.

Mol	Chain	Residues	Atoms				Trace	
1	Λ	20	Total	С	Η	Ν	Ο	1
	A	20	304	100	136	25	43	L

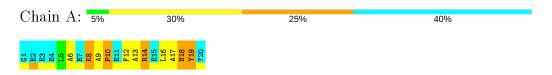


4 Residue-property plots (i)

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: Conantokin-R1B



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: Conantokin-R1B

Chain A: 5%	30%	25%	40%
61 62 63 63 64 64 64 75 712 712 712	A13 R14 E15 L16 A17 V19 Y19 ?20		
4.2.2 Score p	er residue for	model 2	
• Molecule 1: Co	onantokin-R1B		
Chain A:	40%	20%	40%
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	A13 R14 E15 A17 A17 Y19 ?20		

4.2.3 Score per residue for model 3



Chain A:	30%	30%		40%	
12 월 23 월	49 110 114 114 114 115 116 116 116 116 118 118 118 119 119				
4.2.4 Sco	ore per residue	for model 4			
• Molecule	1: Conantokin-RI	1B			
Chain A:					
Ullalli A:	10% 25%	20%	5%	40%	
G1 E3 E3 E4 E5 E4 E3 E3 E3 E3 E7	A9 F12 F12 F15 F15 F15 F15 F15 F15 F15 F15				
4.2.5 Sco	ore per residue	for model 5			
• Molecule	1: Conantokin-R	1B			
Chain A:	10% 25%	25%		40%	_
61 E3 E3 K8 K8 K8 K8 K8 K8 K8 K8 K8 K8 K8 K8 K8	P10 B11 F12 R14 B15 A16 A16 A16 719 Y19 Y19 Y19 Y19				
4.2.6 Sco	ore per residue	for model 6			
• Molecule	1: Conantokin-R	1B			
Chain A: 5				4007	
		25%		40%	
61 E 2 E 2 E 2 E 2 E 2 E 2 E 2 E 2 E 2 E 2	A9 F10 F12 F12 F12 F15 F15 F15 F15 F15 F15 F17 F15 F17 F17 F17 F17 F17 F17 F17 F17 F17 F17				
497 Sec	no non nociduo	for model 7			
4.2.7 Sco	ore per residue	ior model /			
• Molecule	1: Conantokin-R	1B			
Chain A: 5	% 30%	25%		40%	
8 년 <mark>8 년 12 년 13 년 1</mark>	A9 P10 F11 F12 A13 L16 L16 A17 N18 V19 V19 Y19				
100 0	• •	c 110			

4.2.8 Score per residue for model 8



Chain	A:	35%	25%	40%
<mark>2 명 명 목</mark> 권	A6 E7 A9 P10 F11 A13 B14	E15 116 117 118 118 119 119		
4.2.9	Score per	residue for 1	nodel 9	
• Mole	cule 1: Con	antokin-R1B		
Chain	A: 5%	30%	25%	40%
G1 E2 E5 L5	A6 E7 K8 A9 P10 E11 A13 A13 R14	E15 L16 A17 M18 Y19 ?20		
4.2.10	Score pe	er residue for	model 10	
• Mole	cule 1: Con	antokin-R1B		
Chain	A:	45%	15%	40%
61 E2 E4 L5	A6 E7 K8 K8 F12 A13 F12 A13	E15 L16 A17 A17 Y19 Y19 Y19		
4.2.11	Score pe	er residue for	model 11	
• Mole	cule 1: Con	antokin-R1B		
Chain	A: 5%	25%	30%	40%
61 E2 E3 L5	A6 E7 K8 A9 P10 F12 A13 R14 R14	E15 L16 A17 V19 ?20		
4.2.12	Score pe	er residue for	model 12	
• Mole	cule 1: Con	antokin-R1B		
Chain	A: 5%	40%	15%	40%
<u>ទ ន ន ន </u> ភ	A6 E7 A9 P10 F12 A13 A13 A13 B14	E15 L16 A17 Y19 ?20		

4.2.13 Score per residue for model 13



Chain A: 5%	35%	20%	40%	
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	112 116 116 117 117 117 117 117 117 117 117			
4.2.14 Score	per residue for	model 14 (medo	oid)	
• Molecule 1: C	onantokin-R1B			
Chain A:	50%	10%	40%	
61 82 83 84 84 84 84 84 81 811 811 811	A13 R14 E15 L16 M18 Y19 Y19 Y20			
4.2.15 Score	per residue for	model 15		
• Molecule 1: C	onantokin-R1B			
Chain A:	40%	20%	40%	
61 62 63 64 65 66 67 87 87 71 712 712	A12 R14 E15 A17 A17 A17 Y19 720			
4.2.16 Score	per residue for	model 16		
• Molecule 1: C	onantokin-R1B			
Chain A: 5%	40%	15%	40%	
61 82 84 84 87 810 810 811 811 811 811 811	R14 R14 B15 A17 A17 V19 Y19 720			
4.2.17 Score	per residue for	model 17		
• Molecule 1: C	onantokin-R1B			
Chain A: 10%	35%	15%	40%	
日 日 日 日 日 日 日 日 日 日 日 日 日 日	R14 R14 E15 L16 A17 N18 Y19 720			

4.2.18 Score per residue for model 18



Chain A:	5%	35%	20%	40%
15 [15] [15] [15] [15] [15] [15] [15] [1	K8 K8 P10 E11 F12	413 814 114 115 115 115 115 115 115 115 115 1		
4.2.19	Score	per residue for	model 19	
• Molecu	le 1: C	onantokin-R1B		
Chain A:	10%	40%	10%	40%
G1 E3 E4 E4 A6 F7	K8 A9 F10 F12	A13 R14 E15 L16 A17 V18 Y19 Y19 Y20		
4.2.20	Score	per residue for	model 20	
• Molecu	le 1: C	onantokin-R1B		
Chain A:	5%	30%	25%	40%
61 E3 E3 A6 A6 77	Ed K8 A9 E11 F12	A13 R14 E15 A17 N18 Y19 ?20		



5 Refinement protocol and experimental data overview (i)

The models were refined using the following method: simulated annealing.

Of the ? calculated structures, 20 were deposited, based on the following criterion: ?.

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

Software name	Classification	Version
X-PLOR NIH	structure calculation	
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)	$input_cs.cif$
Number of chemical shift lists	1
Total number of shifts	194
Number of shifts mapped to atoms	194
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	84%

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



6 Model quality (i)

6.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: CGU, NH2

There are no covalent bond-length or bond-angle outliers.

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	А	$0.0{\pm}0.0$	$1.0{\pm}0.0$
All	All	0	20

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

All unique planar outliers are listed below.

Mol	Chain	Res	Type	Group	Models (Total)
1	A	14	ARG	Sidechain	20

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	А	94	98	99	13 ± 2
All	All	1880	1960	1980	261

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 68.

All unique clashes are listed below, sorted by their clash magnitude.



Atom-1 1:A:16:LEU:HD22 1:A:16:LEU:HD22 1:A:16:LEU:HD22 1:A:16:LEU:HD22 1:A:12:PHE:CG 1:A:5:LEU:HD12 1:A:16:LEU:O 1:A:8:LYS:HG3 1:A:12:PHE:CD1	Atom-2 1:A:17:ALA:N 1:A:16:LEU:C 1:A:12:PHE:CZ 1:A:13:ALA:N 1:A:5:LEU:O 1:A:19:TYR:N 1:A:12:PHE:CE1 1:A:13:ALA:N	Clash(Å) 0.78 0.75 0.71 0.70 0.68 0.67	Distance(Å) 1.94 2.02 2.20 2.59 1.89	Worst 11 10 19 3	Total 1 20 20
1:A:16:LEU:HD22 1:A:8:LYS:HD3 1:A:12:PHE:CG 1:A:5:LEU:HD12 1:A:16:LEU:O 1:A:8:LYS:HG3 1:A:12:PHE:CD1	1:A:16:LEU:C 1:A:12:PHE:CZ 1:A:13:ALA:N 1:A:5:LEU:O 1:A:19:TYR:N 1:A:12:PHE:CE1	$\begin{array}{r} 0.75 \\ 0.71 \\ 0.70 \\ 0.68 \\ 0.67 \end{array}$	2.02 2.20 2.59	11 10 19	$\frac{1}{20}$
1:A:8:LYS:HD3 1:A:12:PHE:CG 1:A:5:LEU:HD12 1:A:16:LEU:O 1:A:8:LYS:HG3 1:A:12:PHE:CD1	1:A:12:PHE:CZ 1:A:13:ALA:N 1:A:5:LEU:O 1:A:19:TYR:N 1:A:12:PHE:CE1	$ \begin{array}{r} 0.71 \\ 0.70 \\ 0.68 \\ 0.67 \\ \end{array} $	2.20 2.59	10 19	20
1:A:12:PHE:CG 1:A:5:LEU:HD12 1:A:16:LEU:O 1:A:8:LYS:HG3 1:A:12:PHE:CD1	1:A:13:ALA:N 1:A:5:LEU:O 1:A:19:TYR:N 1:A:12:PHE:CE1	0.70 0.68 0.67	2.59	19	
1:A:5:LEU:HD12 1:A:16:LEU:O 1:A:8:LYS:HG3 1:A:12:PHE:CD1	1:A:5:LEU:O 1:A:19:TYR:N 1:A:12:PHE:CE1	0.68 0.67			20
1:A:16:LEU:O 1:A:8:LYS:HG3 1:A:12:PHE:CD1	1:A:19:TYR:N 1:A:12:PHE:CE1	0.67	1.89	2	1
1:A:8:LYS:HG3 1:A:12:PHE:CD1	1:A:12:PHE:CE1			O	1
1:A:12:PHE:CD1			2.27	10	20
	1:A:13:ALA:N	0.65	2.27	11	15
· · · · · · · · · · · · · · · · · · ·		0.65	2.65	17	15
1:A:5:LEU:HD12	1:A:5:LEU:C	0.64	2.12	3	1
1:A:10:PRO:O	1:A:14:ARG:NH2	0.64	2.27	3	7
1:A:10:PRO:O	1:A:14:ARG:NH1	0.64	2.31	4	3
1:A:8:LYS:HG3	1:A:12:PHE:CE2	0.62	2.29	15	5
1:A:18:ASN:HD22	1:A:18:ASN:N	0.60	1.93	17	6
1:A:12:PHE:CD2	1:A:13:ALA:N	0.60	2.69	8	5
1:A:18:ASN:N	1:A:18:ASN:HD22	0.60	1.95	20	14
1:A:8:LYS:CG	1:A:12:PHE:CE2	0.59	2.86	16	5
1:A:8:LYS:CG	1:A:12:PHE:CE1	0.57	2.86	13	15
1:A:16:LEU:C	1:A:16:LEU:CD2	0.57	2.72	11	1
1:A:18:ASN:ND2	1:A:18:ASN:N	0.57	2.53	3	8
1:A:16:LEU:H	1:A:16:LEU:HD13	0.56	1.60	11	1
1:A:18:ASN:N	1:A:18:ASN:ND2	0.56	2.53	17	12
1:A:18:ASN:H	1:A:18:ASN:ND2	0.52	2.03	11	7
1:A:18:ASN:ND2	1:A:18:ASN:H	0.51	2.04	6	13
1:A:5:LEU:O	1:A:9:ALA:N	0.48	2.45	8	5
1:A:8:LYS:HA	1:A:8:LYS:CE	0.47	2.39	14	2
1:A:16:LEU:HD12	1:A:16:LEU:C	0.47	2.30	5	3
1:A:8:LYS:CE	1:A:8:LYS:HA	0.46	2.40	10	2
1:A:18:ASN:ND2	1:A:19:TYR:CD1	0.46	2.83	17	6
1:A:12:PHE:O	1:A:16:LEU:CD1	0.46	2.64	11	1
1:A:13:ALA:O	1:A:17:ALA:HB2	0.45	2.11	11	1
1:A:16:LEU:O	1:A:17:ALA:C	0.44	2.56	12	14
1:A:8:LYS:HE3	1:A:8:LYS:HA	0.44	1.89	3	1
1:A:16:LEU:HD12	1:A:17:ALA:N	0.44	2.28	5	1
1:A:8:LYS:CD	1:A:12:PHE:CZ	0.44	3.00	8	3
1:A:14:ARG:HA	1:A:17:ALA:HB3	0.43	1.89	13	4
1:A:18:ASN:ND2	1:A:19:TYR:CD2	0.43	2.86	13	8
1:A:18:ASN:HD22	1:A:19:TYR:N	0.43	2.11	10	1
1:A:16:LEU:C	1:A:16:LEU:HD12	0.42	2.34	1	3
1:A:14:ARG:HA	1:A:17:ALA:CB	0.42	2.44	10	4
1:A:8:LYS:HE3	1:A:8:LYS:CA	0.42	2.45	3	1
1:A:8:LYS:NZ	1:A:12:PHE:CG	0.41	2.86	2	1
1:A:10:PRO:O	1:A:14:ARG:NE	0.41	2.37	18	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models		
Atom-1	Atom-2	Clash(A)	Distance(A)	Worst	Total	
1:A:8:LYS:HG3	1:A:12:PHE:CD1	0.41	2.51	10	1	
1:A:8:LYS:HD3	1:A:12:PHE:CE1	0.40	2.51	10	1	
1:A:8:LYS:HD3	1:A:12:PHE:CE2	0.40	2.52	16	1	

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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	12/20~(60%)	8±0 (67±3%)	2 ± 0 (16 $\pm3\%$)	2±0 (17±0%)	0 3
All	All	240/400~(60%)	161~(67%)	39 (16%)	40 (17%)	0 3

All 2 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	А	19	TYR	20
1	А	10	PRO	20

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	hain Analysed Rotameric		Outliers	Percentiles		
1	А	8/9~(89%)	$6\pm1~(76\pm8\%)$	$2\pm1~(24\pm8\%)$		2	27
All	All	160/180~(89%)	122~(76%)	38 (24%)		2	27

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	А	18	ASN	20
1	А	8	LYS	15
1	А	5	LEU	1
1	А	16	LEU	1
1	А	14	ARG	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)

5 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	Turne	Chain	Res	Link	Bond lengths		gths
	Type	Cham	nes		Counts	RMSZ	#Z>2
1	CGU	А	7	1	$3,\!11,\!12$	$0.51 {\pm} 0.02$	0±0 (0±0%)
1	CGU	А	3	1	3,11,12	$0.43 {\pm} 0.09$	0±0 (0±0%)
1	CGU	А	4	1	3,11,12	$0.40 {\pm} 0.05$	0±0 (0±0%)
1	CGU	А	11	1	3,11,12	$0.25 {\pm} 0.06$	0±0 (0±0%)
1	CGU	А	15	1	3,11,12	$0.46 {\pm} 0.04$	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	CGU	А	7	1	$1,\!14,\!16$	$0.41 {\pm} 0.16$	0±0 (0±0%)
1	CGU	А	3	1	$1,\!14,\!16$	$0.33 {\pm} 0.33$	0±0 (0±0%)
1	CGU	А	4	1	1,14,16	$0.30 {\pm} 0.24$	0±0 (0±0%)
1	CGU	А	11	1	$1,\!14,\!16$	0.45 ± 0.25	$0\pm0 (0\pm0\%)$



	Mol	Type	Chain	Res	Link	Bond angles		
						Counts	RMSZ	#Z>2
	1	CGU	А	15	1	$1,\!14,\!16$	$0.30{\pm}0.17$	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	\mathbf{Res}	Link	Chirals	Torsions	Rings
1	CGU	А	7	1	-	$0\pm0,5,14,16$	-
1	CGU	А	4	1	-	$0\pm0,5,14,16$	-
1	CGU	А	11	1	-	$0\pm 0,5,14,16$	-
1	CGU	А	3	1	-	$0\pm 0,5,14,16$	-
1	CGU	А	15	1	-	$0\pm 0,5,14,16$	-

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 (i)

The completeness of assignment taking into account all chemical shift lists is 84% for the well-defined parts and 82% for the entire structure.

7.1 Chemical shift list 1

File name: input_cs.cif

Chemical shift list name: ConRl10P_shifts_deposit_star.txt

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	194
Number of shifts mapped to atoms	194
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	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 84%, i.e. 130 atoms were assigned a chemical shift out of a possible 154. 0 out of 2 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^{1}\mathrm{H}$	$^{13}\mathrm{C}$	$^{15}\mathbf{N}$
Backbone	45/58~(78%)	23/23~(100%)	11/24~(46%)	11/11~(100%)
Sidechain	68/79~(86%)	42/47~(89%)	25/27~(93%)	1/5~(20%)
Aromatic	17/17~(100%)	9/9~(100%)	8/8~(100%)	$0/0 \ (-\%)$
Overall	130/154~(84%)	74/79~(94%)	44/59~(75%)	12/16~(75%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 82%, i.e. 141 atoms were assigned a chemical shift out of a possible 171. 0 out of 2 assigned methyl groups (LEU and VAL) were assigned stereospecifically.



	Total	$^{1}\mathbf{H}$	$^{13}\mathrm{C}$	$^{15}\mathbf{N}$
Backbone	50/68~(74%)	26/27~(96%)	13/28~(46%)	11/13~(85%)
Sidechain	74/86~(86%)	$46/51 \ (90\%)$	27/30~(90%)	1/5~(20%)
Aromatic	17/17~(100%)	9/9~(100%)	8/8~(100%)	$0/0 \ (\%)$
Overall	141/171~(82%)	81/87~(93%)	48/66~(73%)	12/18~(67%)

7.1.4 Statistically unusual chemical shifts (i)

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	А	2	GLU	CG	59.85	42.24 - 29.94	19.3

7.1.5 Random Coil Index (RCI) plots (1)

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:

