



Full wwPDB NMR Structure Validation Report ⓘ

Feb 13, 2017 – 12:05 am GMT

PDB ID : 2LIU
Title : NMR structure of holo-ACPI domain from CurA module from *Lyngbya majuscula*
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Deposited on : 2011-09-01

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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.

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

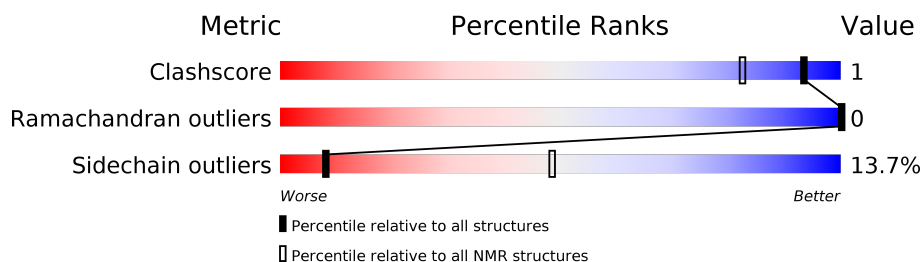
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 93%.

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	99	

2 Ensemble composition and analysis

This entry contains 20 models. Model 12 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *closest to the average*.

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:1955-A:2031 (77)	0.12	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 5 clusters. No single-model clusters were found.

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

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 1548 atoms, of which 774 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called CurA.

Mol	Chain	Residues	Atoms						Trace
1	A	99	Total	C	H	N	O	S	0
			1548	490	774	124	159	1	

There are 10 discrepancies between the modelled and reference sequences:

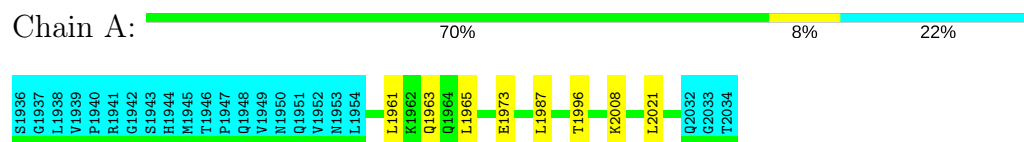
Chain	Residue	Modelled	Actual	Comment	Reference
A	1936	SER	-	EXPRESSION TAG	UNP Q6DNF2
A	1937	GLY	-	EXPRESSION TAG	UNP Q6DNF2
A	1938	LEU	-	EXPRESSION TAG	UNP Q6DNF2
A	1939	VAL	-	EXPRESSION TAG	UNP Q6DNF2
A	1940	PRO	-	EXPRESSION TAG	UNP Q6DNF2
A	1941	ARG	-	EXPRESSION TAG	UNP Q6DNF2
A	1942	GLY	-	EXPRESSION TAG	UNP Q6DNF2
A	1943	SER	-	EXPRESSION TAG	UNP Q6DNF2
A	1944	HIS	-	EXPRESSION TAG	UNP Q6DNF2
A	1945	MET	-	EXPRESSION TAG	UNP Q6DNF2

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: CurA

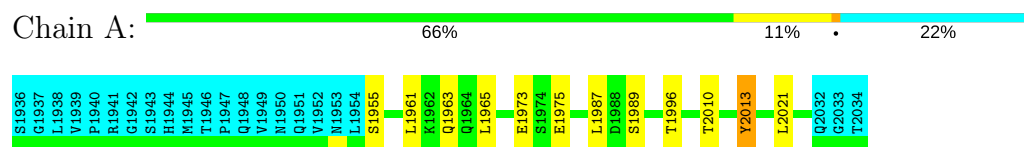


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

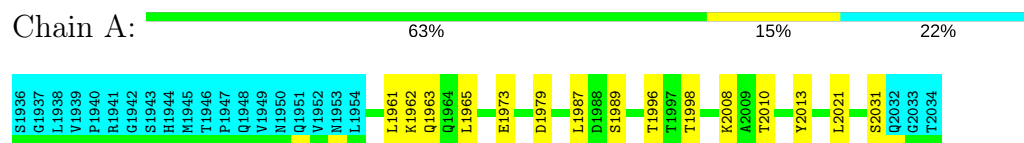
4.2.1 Score per residue for model 1

- Molecule 1: CurA



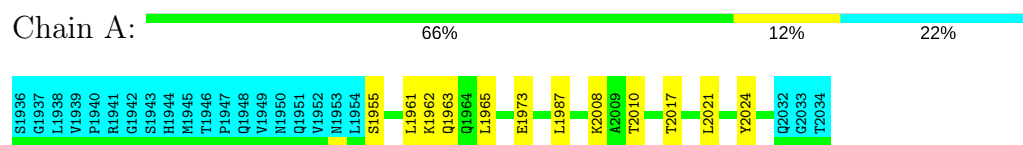
4.2.2 Score per residue for model 2

- Molecule 1: CurA



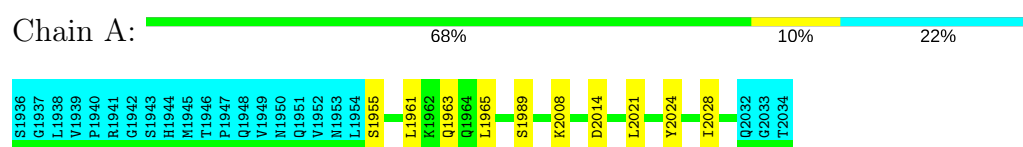
4.2.3 Score per residue for model 3

- Molecule 1: CurA



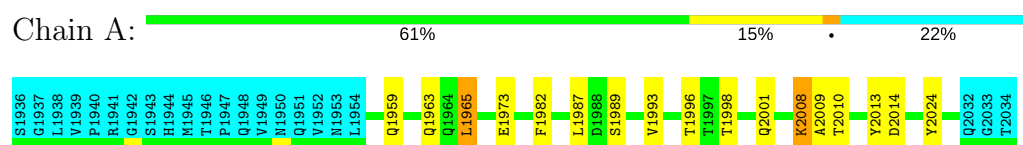
4.2.4 Score per residue for model 4

- Molecule 1: CurA



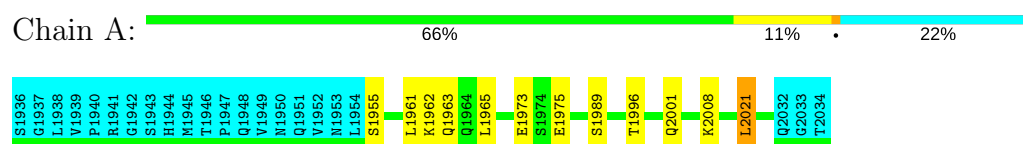
4.2.5 Score per residue for model 5

- Molecule 1: CurA



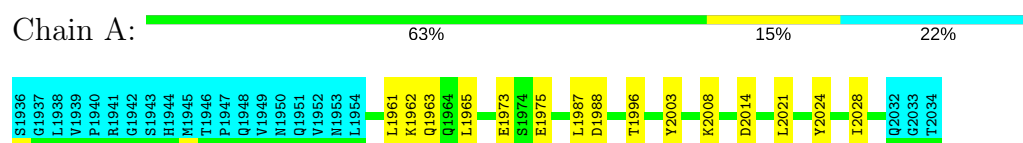
4.2.6 Score per residue for model 6

- Molecule 1: CurA



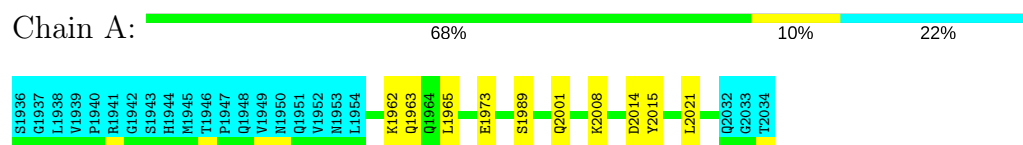
4.2.7 Score per residue for model 7

- Molecule 1: CurA



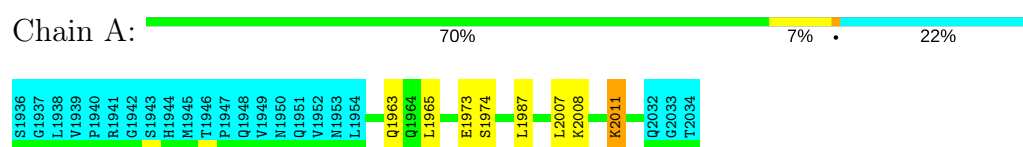
4.2.8 Score per residue for model 8

- Molecule 1: CurA



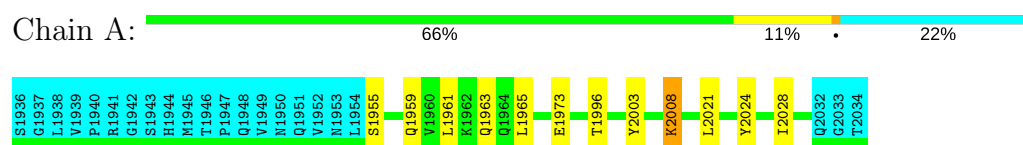
4.2.9 Score per residue for model 9

- Molecule 1: CurA



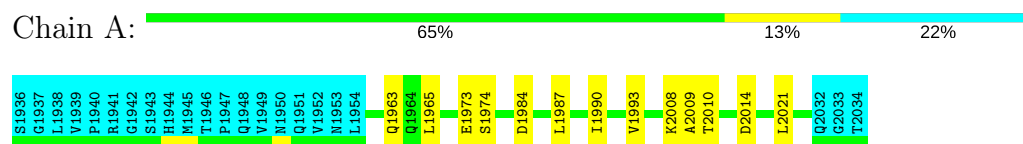
4.2.10 Score per residue for model 10

- Molecule 1: CurA



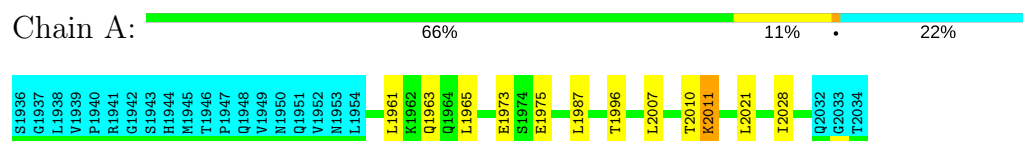
4.2.11 Score per residue for model 11

- Molecule 1: CurA



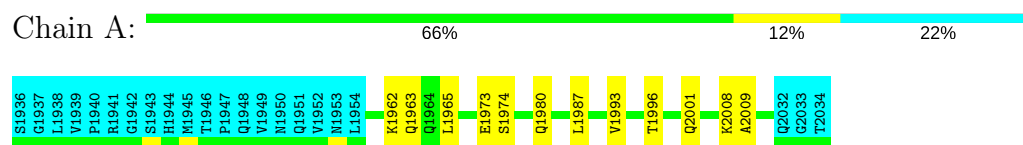
4.2.12 Score per residue for model 12 (medoid)

- Molecule 1: CurA



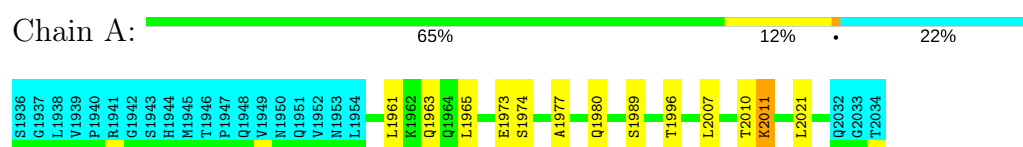
4.2.13 Score per residue for model 13

- Molecule 1: CurA



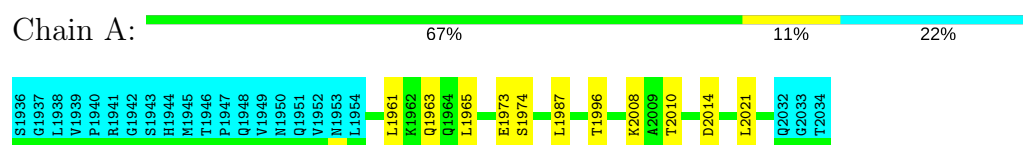
4.2.14 Score per residue for model 14

- Molecule 1: CurA



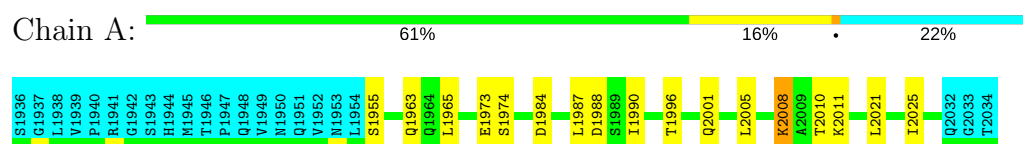
4.2.15 Score per residue for model 15

- Molecule 1: CurA



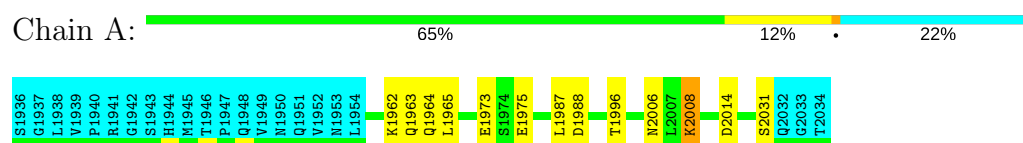
4.2.16 Score per residue for model 16

- Molecule 1: CurA



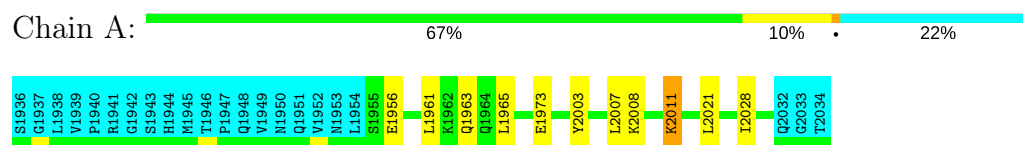
4.2.17 Score per residue for model 17

- Molecule 1: CurA



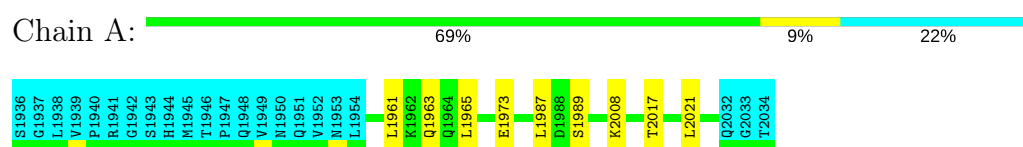
4.2.18 Score per residue for model 18

• Molecule 1: CurA



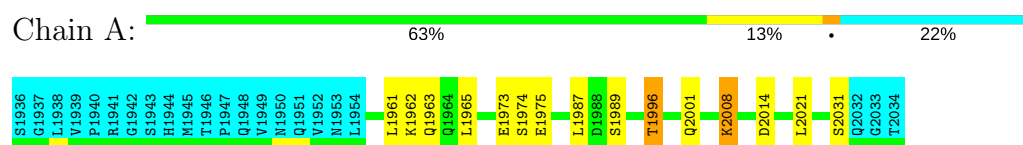
4.2.19 Score per residue for model 19

• Molecule 1: CurA



4.2.20 Score per residue for model 20

• Molecule 1: CurA



5 Refinement protocol and experimental data overview

The models were refined using the following method: *torsion angle dynamics*.

Of the 100 calculated structures, 20 were deposited, based on the following criterion: *target function*.

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

Software name	Classification	Version
CYANA	structure solution	2.1 and 3.0
CYANA	refinement	2.1 and 3.0

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)	2liu_cs.str
Number of chemical shift lists	1
Total number of shifts	1214
Number of shifts mapped to atoms	1214
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	93%

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.

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	0.0±0.0	0.3±0.5
All	All	0	7

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

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	2003	TYR	Sidechain	3
1	A	2024	TYR	Sidechain	2
1	A	2015	TYR	Sidechain	1
1	A	2013	TYR	Sidechain	1

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	613	613	613	2±1
All	All	12260	12260	12260	36

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 1.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:1961:LEU:HD13	1:A:2021:LEU:HD23	0.72	1.61	10	13
1:A:2005:LEU:HD11	1:A:2025:ILE:HG23	0.54	1.78	16	1
1:A:2007:LEU:HD22	1:A:2011:LYS:HD2	0.47	1.86	9	4
1:A:1993:VAL:HG22	1:A:2009:ALA:HB2	0.45	1.88	11	3
1:A:2007:LEU:HD21	1:A:2028:ILE:CD1	0.45	2.42	18	2
1:A:1996:THR:HG21	1:A:2008:LYS:HA	0.44	1.90	5	4
1:A:2024:TYR:CE2	1:A:2028:ILE:HD11	0.42	2.49	7	3
1:A:1990:ILE:H	1:A:1990:ILE:HD12	0.42	1.74	11	1
1:A:1965:LEU:HD22	1:A:1982:PHE:CE1	0.42	2.50	5	1
1:A:1977:ALA:HB3	1:A:1980:GLN:CB	0.42	2.44	14	1
1:A:1961:LEU:CD1	1:A:2021:LEU:HD23	0.41	2.45	14	1
1:A:1990:ILE:HD12	1:A:1990:ILE:H	0.41	1.75	16	1
1:A:2008:LYS:HG3	1:A:2010:THR:HG22	0.41	1.92	16	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	77/99 (78%)	74±1 (96±1%)	3±1 (4±1%)	0±0 (0±0%)	100	100
All	All	1540/1980 (78%)	1484 (96%)	56 (4%)	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	69/88 (78%)	60±2 (86±3%)	9±2 (14±3%)	8	48
All	All	1380/1760 (78%)	1191 (86%)	189 (14%)	8	48

All 28 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	1963	GLN	20
1	A	1965	LEU	20
1	A	1973	GLU	19
1	A	2008	LYS	17
1	A	1987	LEU	14
1	A	1996	THR	10
1	A	1989	SER	9
1	A	2010	THR	8
1	A	2014	ASP	8
1	A	1962	LYS	8
1	A	1974	SER	7
1	A	1975	GLU	6
1	A	1955	SER	6
1	A	2001	GLN	6
1	A	2011	LYS	5
1	A	2021	LEU	4
1	A	2013	TYR	3
1	A	1988	ASP	3
1	A	2031	SER	3
1	A	1959	GLN	2
1	A	1984	ASP	2
1	A	1998	THR	2
1	A	2017	THR	2
1	A	2006	ASN	1
1	A	1964	GLN	1
1	A	1979	ASP	1
1	A	1956	GLU	1
1	A	1980	GLN	1

6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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 93% for the well-defined parts and 90% for the entire structure.

7.1 Chemical shift list 1

File name: 2liu_cs.str

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	1214
Number of shifts mapped to atoms	1214
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	2

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	98	-0.30 ± 0.20	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	90	0.23 ± 0.06	None needed (< 0.5 ppm)
$^{13}\text{C}'$	92	-0.55 ± 0.27	Should be applied
^{15}N	94	-0.11 ± 0.25	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 93%, i.e. 871 atoms were assigned a chemical shift out of a possible 934. 9 out of 16 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	382/383 (100%)	153/153 (100%)	153/154 (99%)	76/76 (100%)
Sidechain	433/490 (88%)	266/281 (95%)	158/195 (81%)	9/14 (64%)

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	Total	¹H	¹³C	¹⁵N
Aromatic	56/61 (92%)	30/31 (97%)	26/29 (90%)	0/1 (0%)
Overall	871/934 (93%)	449/465 (97%)	337/378 (89%)	85/91 (93%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 90%, i.e. 1067 atoms were assigned a chemical shift out of a possible 1188. 11 out of 21 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Backbone	474/489 (97%)	190/195 (97%)	190/198 (96%)	94/96 (98%)
Sidechain	537/631 (85%)	329/364 (90%)	194/245 (79%)	14/22 (64%)
Aromatic	56/68 (82%)	30/35 (86%)	26/31 (84%)	0/2 (0%)
Overall	1067/1188 (90%)	549/594 (92%)	410/474 (86%)	108/120 (90%)

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	2029	LEU	CD1	12.68	32.77 – 16.57	-7.4
1	A	1986	GLY	HA3	1.45	5.80 – 2.00	-6.4

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:

