



Full wwPDB NMR Structure Validation Report ⓘ

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PDB ID : 2M6N / pdb_00002m6n
BMRB ID : 19147
Title : 3D solution structure of EMI1 (Early Mitotic Inhibitor 1)
Authors : Frye, J.J.; Brown, N.G.; Petzold, G.; Watson, E.R.; Royappa, G.R.; Nourse, A.; Jarvis, M.; Kriwacki, R.W.; Peters, J.; Stark, H.; Schulman, B.A.
Deposited on : 2013-04-06

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 ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
wwPDB-RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
wwPDB-ShiftChecker : v1.2
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

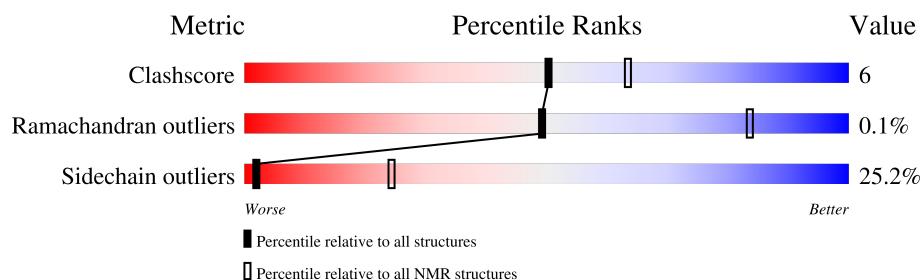
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 90%.

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	229148	14424
Ramachandran outliers	224038	12848
Sidechain outliers	223484	12823

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	86	31% 13% 9% 47%

2 Ensemble composition and analysis

This entry contains 20 models. Model 3 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *lowest energy*.

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:15-A:52 (38)	0.31	3

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 and 2 single-model clusters were found.

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

3 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 712 atoms, of which 349 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called F-box only protein 5.

Mol	Chain	Residues	Atoms						Trace
1	A	46	Total	C	H	N	O	S	0
			710	220	349	65	67	9	

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	expression tag	UNP Q9UKT4
A	2	SER	-	expression tag	UNP Q9UKT4

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

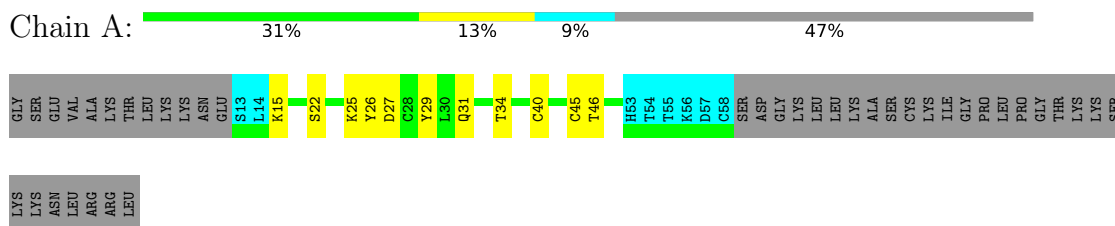
Mol	Chain	Residues	Atoms	
2	A	2	Total	Zn
			2	2

4 Residue-property plots

4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA, DNA and oligosaccharide 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: F-box only protein 5

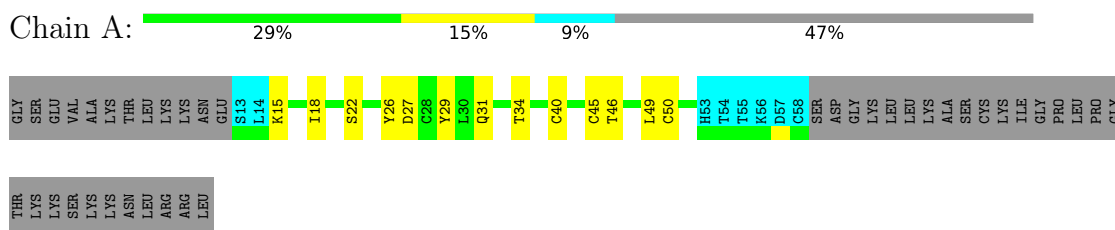


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

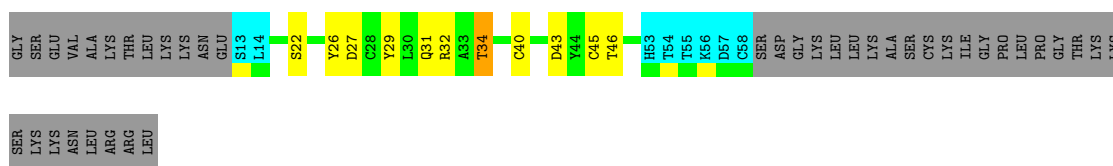
- Molecule 1: F-box only protein 5



4.2.2 Score per residue for model 2

- Molecule 1: F-box only protein 5

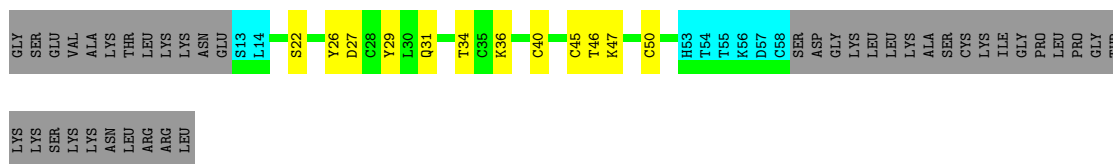




4.2.3 Score per residue for model 3 (medoid)

- Molecule 1: F-box only protein 5

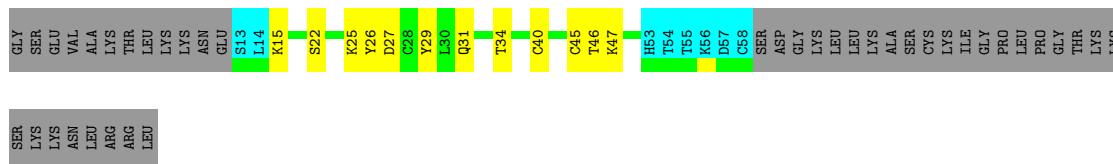
Chain A: 30% 14% 9% 47%



4.2.4 Score per residue for model 4

- Molecule 1: F-box only protein 5

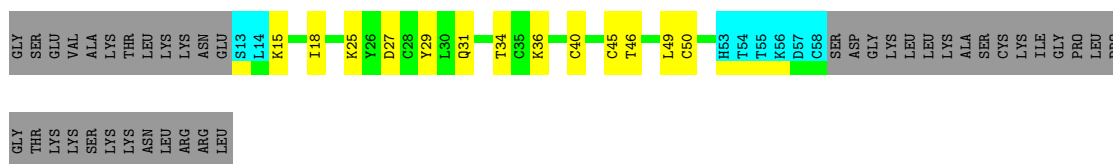
Chain A: 30% 14% 9% 47%



4.2.5 Score per residue for model 5

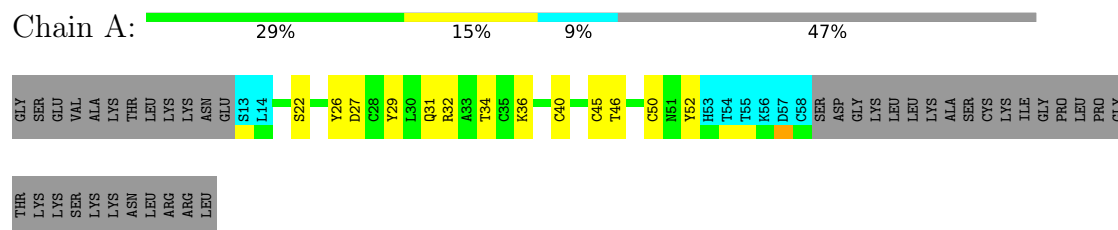
- Molecule 1: F-box only protein 5

Chain A: 29% 15% 9% 47%



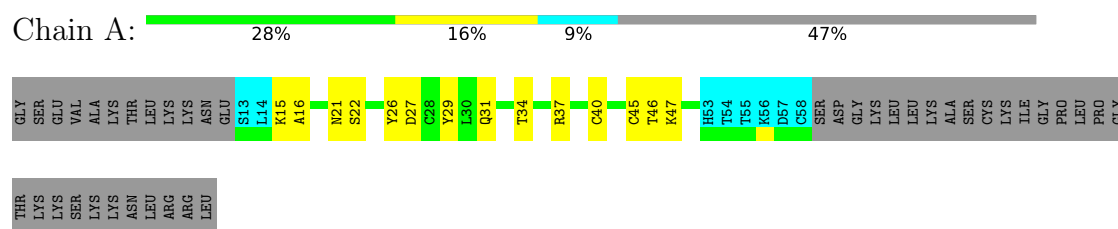
4.2.6 Score per residue for model 6

- Molecule 1: F-box only protein 5



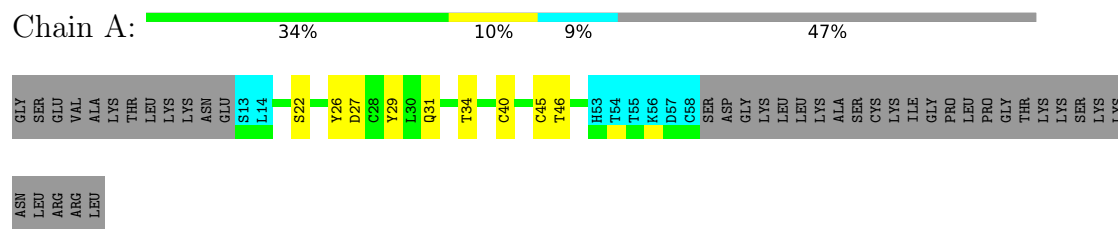
4.2.7 Score per residue for model 7

- Molecule 1: F-box only protein 5



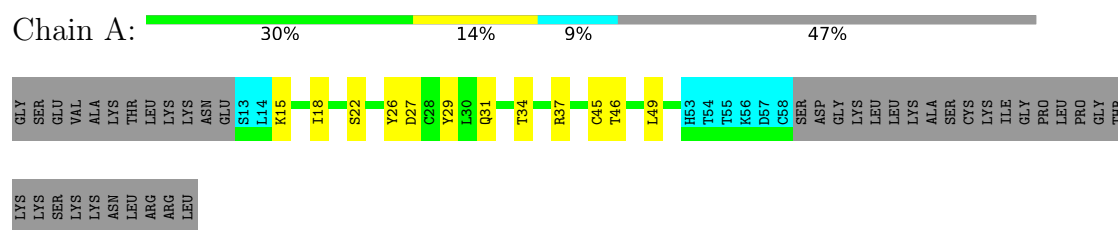
4.2.8 Score per residue for model 8

- Molecule 1: F-box only protein 5



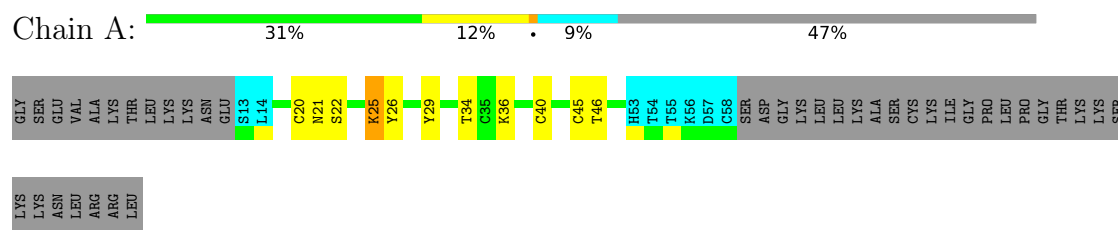
4.2.9 Score per residue for model 9

- Molecule 1: F-box only protein 5



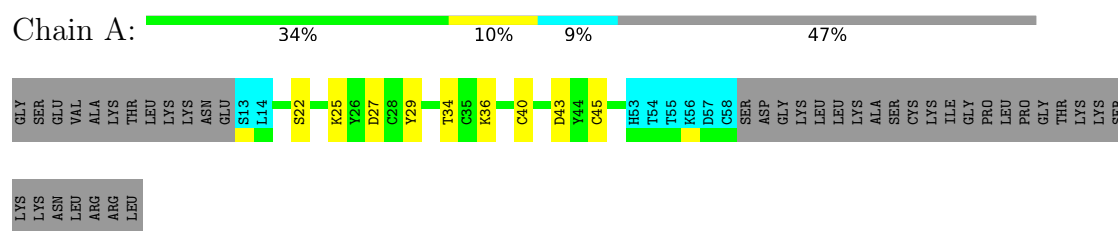
4.2.14 Score per residue for model 14

- Molecule 1: F-box only protein 5



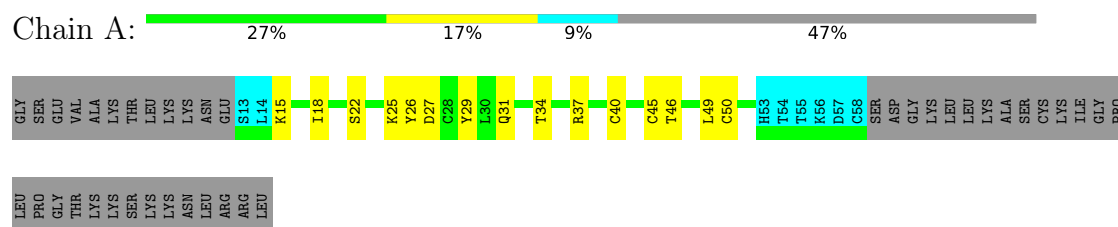
4.2.15 Score per residue for model 15

- Molecule 1: F-box only protein 5



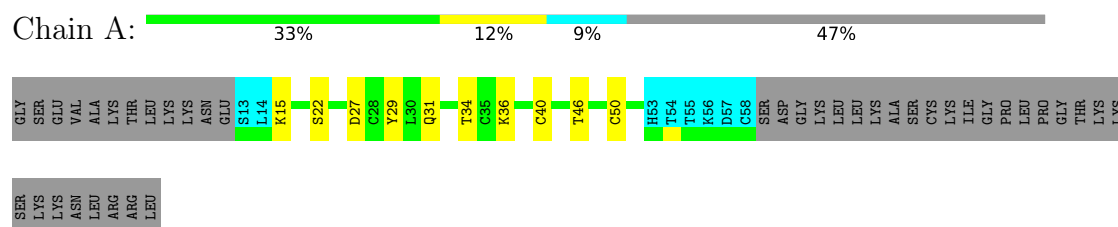
4.2.16 Score per residue for model 16

- Molecule 1: F-box only protein 5



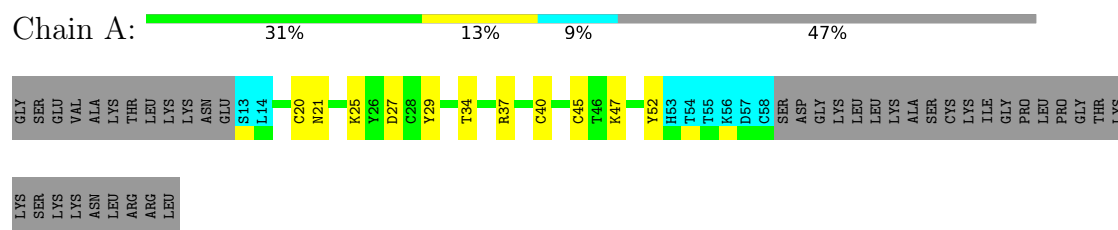
4.2.17 Score per residue for model 17

- Molecule 1: F-box only protein 5



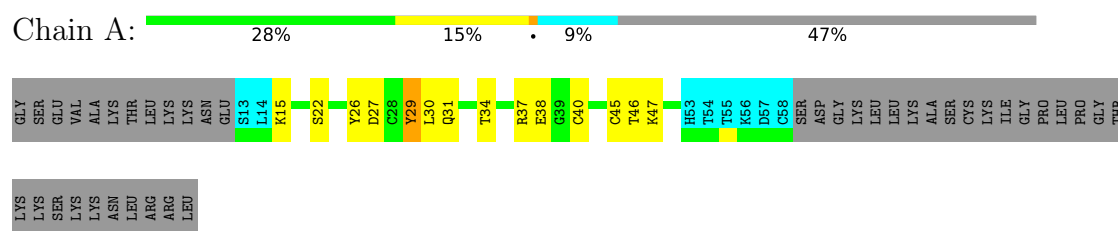
4.2.18 Score per residue for model 18

- Molecule 1: F-box only protein 5



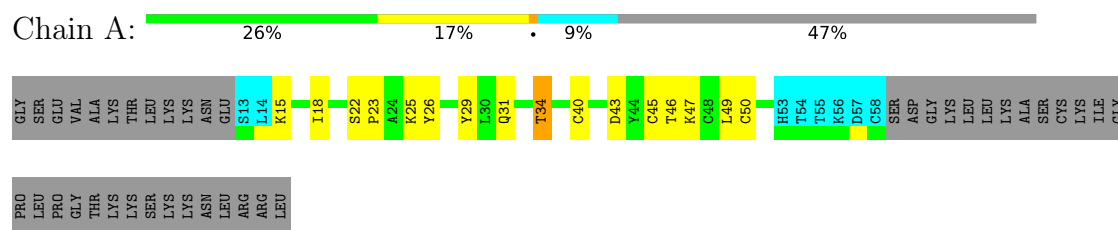
4.2.19 Score per residue for model 19

- Molecule 1: F-box only protein 5



4.2.20 Score per residue for model 20

- Molecule 1: F-box only protein 5



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
CYANA	refinement	2.1

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)	working_cs.cif
Number of chemical shift lists	1
Total number of shifts	1043
Number of shifts mapped to atoms	542
Number of unparsed shifts	0
Number of shifts with mapping errors	501
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	90%

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:
ZN

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 [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	300	290	290	3±1
All	All	6040	5800	5800	66

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 6.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:26:TYR:CE1	1:A:46:THR:HG21	0.65	2.26	12	15
1:A:31:GLN:C	1:A:46:THR:HG22	0.62	2.20	1	16
1:A:31:GLN:O	1:A:46:THR:HG22	0.61	1.95	11	16
1:A:18:ILE:HG22	1:A:49:LEU:HD13	0.58	1.75	1	4
1:A:18:ILE:CG2	1:A:49:LEU:HD22	0.54	2.32	5	2
1:A:34:THR:HG23	1:A:43:ASP:HA	0.52	1.81	12	2
1:A:15:LYS:HG3	1:A:33:ALA:HB2	0.50	1.82	13	1
1:A:26:TYR:CD1	1:A:46:THR:HG21	0.49	2.41	14	1
1:A:18:ILE:HG21	1:A:49:LEU:HB3	0.47	1.85	20	2
1:A:16:ALA:HB1	1:A:21:ASN:CG	0.46	2.35	7	1
1:A:34:THR:HG23	1:A:43:ASP:CG	0.45	2.36	20	1
1:A:18:ILE:HG23	1:A:49:LEU:HD22	0.42	1.90	20	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:20:CYS:O	1:A:21:ASN:C	0.41	2.63	14	2
1:A:18:ILE:HD13	1:A:49:LEU:O	0.40	2.16	5	1
1:A:29:TYR:O	1:A:30:LEU:HD23	0.40	2.16	19	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	38/86 (44%)	32±2 (84±5%)	6±2 (16±4%)	0±0 (0±1%)	49	83
All	All	760/1720 (44%)	641 (84%)	118 (16%)	1 (0%)	49	83

All 1 unique Ramachandran outliers are listed below.

Mol	Chain	Res	Type	Models (Total)
1	A	25	LYS	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	33/75 (44%)	25±1 (75±3%)	8±1 (25±3%)	2	24
All	All	660/1500 (44%)	494 (75%)	166 (25%)	2	24

All 15 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	29	TYR	20
1	A	34	THR	20

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Mol	Chain	Res	Type	Models (Total)
1	A	40	CYS	19
1	A	27	ASP	18
1	A	45	CYS	18
1	A	22	SER	17
1	A	15	LYS	12
1	A	50	CYS	9
1	A	36	LYS	9
1	A	47	LYS	7
1	A	25	LYS	7
1	A	37	ARG	5
1	A	32	ARG	2
1	A	43	ASP	2
1	A	38	GLU	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](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

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

7.1 Chemical shift list 1

File name: working_cs.cif

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	1043
Number of shifts mapped to atoms	542
Number of unparsed shifts	0
Number of shifts with mapping errors	501
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	2

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

- No matching atom found in the structure. All 501 occurrences are reported below.

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	2	SER	HA	4.341	0.020	1
1	A	2	SER	HB2	3.788	0.020	.
1	A	2	SER	HB3	3.788	0.020	.
1	A	2	SER	CA	58.096	0.300	1
1	A	2	SER	CB	63.354	0.300	1
1	A	3	GLU	H	8.675	0.020	1
1	A	3	GLU	HA	4.246	0.020	1
1	A	3	GLU	HB2	1.958	0.020	.
1	A	3	GLU	HB3	1.854	0.020	.
1	A	3	GLU	HG2	2.11	0.020	.
1	A	3	GLU	HG3	2.11	0.020	.
1	A	3	GLU	C	176.655	0.300	1
1	A	3	GLU	CA	56.16	0.300	1
1	A	3	GLU	CB	29.45	0.300	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	3	GLU	CG	36.237	0.300	1
1	A	3	GLU	N	123.284	0.300	1
1	A	4	VAL	H	8.1	0.020	1
1	A	4	VAL	HA	3.963	0.020	1
1	A	4	VAL	HB	1.971	0.020	1
1	A	4	VAL	HG11	0.862	0.020	.
1	A	4	VAL	HG12	0.862	0.020	.
1	A	4	VAL	HG13	0.862	0.020	.
1	A	4	VAL	HG21	0.855	0.020	.
1	A	4	VAL	HG22	0.855	0.020	.
1	A	4	VAL	HG23	0.855	0.020	.
1	A	4	VAL	C	176.11	0.300	1
1	A	4	VAL	CA	62.034	0.300	1
1	A	4	VAL	CB	32.213	0.300	1
1	A	4	VAL	CG1	20.212	0.300	.
1	A	4	VAL	CG2	20.678	0.300	.
1	A	4	VAL	N	121.453	0.300	1
1	A	5	ALA	H	8.274	0.020	1
1	A	5	ALA	HA	4.202	0.020	1
1	A	5	ALA	HB1	1.299	0.020	1
1	A	5	ALA	HB2	1.299	0.020	1
1	A	5	ALA	HB3	1.299	0.020	1
1	A	5	ALA	C	177.887	0.300	1
1	A	5	ALA	CA	52.245	0.300	1
1	A	5	ALA	CB	18.705	0.300	1
1	A	5	ALA	N	127.448	0.300	1
1	A	6	LYS	H	8.212	0.020	1
1	A	6	LYS	HA	4.23	0.020	1
1	A	6	LYS	HB2	1.746	0.020	.
1	A	6	LYS	HB3	1.673	0.020	.
1	A	6	LYS	HD2	1.714	0.020	.
1	A	6	LYS	HD3	1.714	0.020	.
1	A	6	LYS	HE2	2.903	0.020	.
1	A	6	LYS	HE3	2.903	0.020	.
1	A	6	LYS	HG2	1.358	0.020	.
1	A	6	LYS	HG3	1.358	0.020	.
1	A	6	LYS	C	175.28	0.300	1
1	A	6	LYS	CA	56.123	0.300	1
1	A	6	LYS	CB	32.499	0.300	1
1	A	6	LYS	CD	29.064	0.300	1
1	A	6	LYS	CE	41.747	0.300	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	6	LYS	CG	24.37	0.300	1
1	A	6	LYS	N	120.601	0.300	1
1	A	7	THR	H	8.0	0.020	1
1	A	7	THR	HA	4.232	0.020	1
1	A	7	THR	HB	4.129	0.020	1
1	A	7	THR	HG21	1.111	0.020	1
1	A	7	THR	HG22	1.111	0.020	1
1	A	7	THR	HG23	1.111	0.020	1
1	A	7	THR	C	174.332	0.300	1
1	A	7	THR	CA	61.555	0.300	1
1	A	7	THR	CB	69.505	0.300	1
1	A	7	THR	CG2	21.212	0.300	1
1	A	7	THR	N	115.127	0.300	1
1	A	8	LEU	H	8.153	0.020	1
1	A	8	LEU	HA	4.271	0.020	1
1	A	8	LEU	HB2	1.553	0.020	.
1	A	8	LEU	HB3	1.499	0.020	.
1	A	8	LEU	HD11	0.83	0.020	.
1	A	8	LEU	HD12	0.83	0.020	.
1	A	8	LEU	HD13	0.83	0.020	.
1	A	8	LEU	HD21	0.78	0.020	.
1	A	8	LEU	HD22	0.78	0.020	.
1	A	8	LEU	HD23	0.78	0.020	.
1	A	8	LEU	HG	1.504	0.020	1
1	A	8	LEU	C	174.474	0.300	1
1	A	8	LEU	CA	54.689	0.300	1
1	A	8	LEU	CB	41.856	0.300	1
1	A	8	LEU	CD1	24.484	0.300	.
1	A	8	LEU	CD2	23.098	0.300	.
1	A	8	LEU	CG	26.469	0.300	1
1	A	8	LEU	N	124.868	0.300	1
1	A	9	LYS	H	8.099	0.020	1
1	A	9	LYS	HA	4.213	0.020	1
1	A	9	LYS	HB2	1.627	0.020	.
1	A	9	LYS	HB3	1.627	0.020	.
1	A	9	LYS	HD2	1.727	0.020	.
1	A	9	LYS	HD3	1.727	0.020	.
1	A	9	LYS	HE2	2.921	0.020	.
1	A	9	LYS	HE3	2.921	0.020	.
1	A	9	LYS	HG2	1.318	0.020	.
1	A	9	LYS	HG3	1.318	0.020	.

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	9	LYS	C	176.252	0.300	1
1	A	9	LYS	CA	55.405	0.300	1
1	A	9	LYS	CB	32.467	0.300	1
1	A	9	LYS	CD	28.642	0.300	1
1	A	9	LYS	CE	41.652	0.300	1
1	A	9	LYS	CG	24.277	0.300	1
1	A	9	LYS	N	121.871	0.300	1
1	A	10	LYS	H	8.079	0.020	1
1	A	10	LYS	HA	4.216	0.020	1
1	A	10	LYS	HB2	1.602	0.020	.
1	A	10	LYS	HB3	1.602	0.020	.
1	A	10	LYS	HD2	1.713	0.020	.
1	A	10	LYS	HD3	1.713	0.020	.
1	A	10	LYS	HE2	2.915	0.020	.
1	A	10	LYS	HE3	2.915	0.020	.
1	A	10	LYS	HG2	1.323	0.020	.
1	A	10	LYS	HG3	1.323	0.020	.
1	A	10	LYS	C	176.394	0.300	1
1	A	10	LYS	CA	56.518	0.300	1
1	A	10	LYS	CB	32.825	0.300	1
1	A	10	LYS	CD	28.595	0.300	1
1	A	10	LYS	CE	41.666	0.300	1
1	A	10	LYS	CG	24.229	0.300	1
1	A	10	LYS	N	122.056	0.300	1
1	A	11	ASN	H	8.455	0.020	1
1	A	11	ASN	HA	4.597	0.020	1
1	A	11	ASN	HB2	2.75	0.020	.
1	A	11	ASN	HB3	2.66	0.020	.
1	A	11	ASN	HD21	7.553	0.020	.
1	A	11	ASN	HD22	6.86	0.020	.
1	A	11	ASN	C	175.209	0.300	1
1	A	11	ASN	CA	52.699	0.300	1
1	A	11	ASN	CB	38.192	0.300	1
1	A	11	ASN	N	119.458	0.300	1
1	A	11	ASN	ND2	112.766	0.300	1
1	A	12	GLU	H	8.298	0.020	1
1	A	12	GLU	HA	4.373	0.020	1
1	A	12	GLU	HB2	1.98	0.020	.
1	A	12	GLU	HB3	1.898	0.020	.
1	A	12	GLU	HG2	2.181	0.020	.
1	A	12	GLU	HG3	2.181	0.020	.

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	12	GLU	C	176.252	0.300	1
1	A	12	GLU	CA	56.171	0.300	1
1	A	12	GLU	CB	30.369	0.300	1
1	A	12	GLU	CG	36.011	0.300	1
1	A	12	GLU	N	121.687	0.300	1
1	A	59	SER	H	8.293	0.020	1
1	A	59	SER	HA	4.25	0.020	1
1	A	59	SER	HB2	3.759	0.020	.
1	A	59	SER	HB3	3.759	0.020	.
1	A	59	SER	C	174.356	0.300	1
1	A	59	SER	CA	58.168	0.300	1
1	A	59	SER	CB	63.177	0.300	1
1	A	59	SER	N	115.879	0.300	1
1	A	60	ASP	H	8.086	0.020	1
1	A	60	ASP	HA	4.433	0.020	1
1	A	60	ASP	HB2	2.6	0.020	.
1	A	60	ASP	HB3	2.6	0.020	.
1	A	60	ASP	C	177.176	0.300	1
1	A	60	ASP	CA	54.262	0.300	1
1	A	60	ASP	CB	40.84	0.300	1
1	A	60	ASP	N	122.154	0.300	1
1	A	61	GLY	H	8.323	0.020	1
1	A	61	GLY	HA2	3.805	0.020	.
1	A	61	GLY	HA3	3.805	0.020	.
1	A	61	GLY	C	174.83	0.300	1
1	A	61	GLY	CA	45.597	0.300	1
1	A	61	GLY	N	109.614	0.300	1
1	A	62	LYS	H	8.014	0.020	1
1	A	62	LYS	HA	4.156	0.020	1
1	A	62	LYS	HB2	1.744	0.020	.
1	A	62	LYS	HB3	1.744	0.020	.
1	A	62	LYS	HD2	1.59	0.020	.
1	A	62	LYS	HD3	1.59	0.020	.
1	A	62	LYS	HE2	2.9	0.020	.
1	A	62	LYS	HE3	2.9	0.020	.
1	A	62	LYS	HG2	1.346	0.020	.
1	A	62	LYS	HG3	1.346	0.020	.
1	A	62	LYS	C	177.01	0.300	1
1	A	62	LYS	CA	56.56	0.300	1
1	A	62	LYS	CB	32.351	0.300	1
1	A	62	LYS	CD	28.42	0.300	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	62	LYS	CE	41.487	0.300	1
1	A	62	LYS	CG	24.157	0.300	1
1	A	62	LYS	N	120.306	0.300	1
1	A	63	LEU	H	8.012	0.020	1
1	A	63	LEU	HA	4.212	0.020	1
1	A	63	LEU	HB2	1.496	0.020	.
1	A	63	LEU	HB3	1.496	0.020	.
1	A	63	LEU	HD11	0.826	0.020	.
1	A	63	LEU	HD12	0.826	0.020	.
1	A	63	LEU	HD13	0.826	0.020	.
1	A	63	LEU	HD21	0.826	0.020	.
1	A	63	LEU	HD22	0.826	0.020	.
1	A	63	LEU	HD23	0.826	0.020	.
1	A	63	LEU	HG	1.527	0.020	1
1	A	63	LEU	C	177.461	0.300	1
1	A	63	LEU	CA	55.168	0.300	1
1	A	63	LEU	CB	41.675	0.300	1
1	A	63	LEU	CD1	24.2	0.300	.
1	A	63	LEU	CG	26.473	0.300	1
1	A	63	LEU	N	121.439	0.300	1
1	A	64	LEU	H	7.988	0.020	1
1	A	64	LEU	HA	4.243	0.020	1
1	A	64	LEU	HB2	1.572	0.020	.
1	A	64	LEU	HB3	1.572	0.020	.
1	A	64	LEU	HD11	0.815	0.020	.
1	A	64	LEU	HD12	0.815	0.020	.
1	A	64	LEU	HD13	0.815	0.020	.
1	A	64	LEU	HD21	0.815	0.020	.
1	A	64	LEU	HD22	0.815	0.020	.
1	A	64	LEU	HD23	0.815	0.020	.
1	A	64	LEU	HG	1.5	0.020	1
1	A	64	LEU	C	177.176	0.300	1
1	A	64	LEU	CA	54.84	0.300	1
1	A	64	LEU	CB	41.681	0.300	1
1	A	64	LEU	CD1	24.753	0.300	.
1	A	64	LEU	CG	26.411	0.300	1
1	A	64	LEU	N	122.593	0.300	1
1	A	65	LYS	H	8.27	0.020	1
1	A	65	LYS	HA	4.226	0.020	1
1	A	65	LYS	HB2	1.635	0.020	.
1	A	65	LYS	HB3	1.635	0.020	.

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	65	LYS	HD2	1.721	0.020	.
1	A	65	LYS	HD3	1.721	0.020	.
1	A	65	LYS	HE2	2.913	0.020	.
1	A	65	LYS	HE3	2.913	0.020	.
1	A	65	LYS	HG2	1.376	0.020	.
1	A	65	LYS	HG3	1.376	0.020	.
1	A	65	LYS	C	176.489	0.300	1
1	A	65	LYS	CA	55.965	0.300	1
1	A	65	LYS	CB	32.443	0.300	1
1	A	65	LYS	CD	28.583	0.300	1
1	A	65	LYS	CE	41.606	0.300	1
1	A	65	LYS	CG	24.302	0.300	1
1	A	65	LYS	N	122.764	0.300	1
1	A	66	ALA	H	8.184	0.020	1
1	A	66	ALA	HA	4.222	0.020	1
1	A	66	ALA	HB1	1.328	0.020	1
1	A	66	ALA	HB2	1.328	0.020	1
1	A	66	ALA	HB3	1.328	0.020	1
1	A	66	ALA	C	177.959	0.300	1
1	A	66	ALA	CA	52.199	0.300	1
1	A	66	ALA	CB	18.837	0.300	1
1	A	66	ALA	N	124.736	0.300	1
1	A	67	SER	H	8.201	0.020	1
1	A	67	SER	HA	4.377	0.020	1
1	A	67	SER	HB2	3.754	0.020	.
1	A	67	SER	HB3	3.754	0.020	.
1	A	67	SER	C	177.129	0.300	1
1	A	67	SER	CA	58.266	0.300	1
1	A	67	SER	CB	63.615	0.300	1
1	A	67	SER	N	114.679	0.300	1
1	A	68	CYS	H	8.195	0.020	1
1	A	68	CYS	HA	4.432	0.020	1
1	A	68	CYS	HB2	2.856	0.020	.
1	A	68	CYS	HB3	2.856	0.020	.
1	A	68	CYS	C	174.427	0.300	1
1	A	68	CYS	CA	58.153	0.300	1
1	A	68	CYS	CB	27.648	0.300	1
1	A	68	CYS	N	121.407	0.300	1
1	A	69	LYS	H	8.302	0.020	1
1	A	69	LYS	HA	4.268	0.020	1
1	A	69	LYS	HB2	1.621	0.020	.

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	69	LYS	HB3	1.621	0.020	.
1	A	69	LYS	HD2	1.726	0.020	.
1	A	69	LYS	HD3	1.726	0.020	.
1	A	69	LYS	HE2	2.921	0.020	.
1	A	69	LYS	HE3	2.921	0.020	.
1	A	69	LYS	HG2	1.325	0.020	.
1	A	69	LYS	HG3	1.325	0.020	.
1	A	69	LYS	C	176.821	0.300	1
1	A	69	LYS	CA	56.059	0.300	1
1	A	69	LYS	CB	32.494	0.300	1
1	A	69	LYS	CD	28.583	0.300	1
1	A	69	LYS	CE	41.666	0.300	1
1	A	69	LYS	CG	24.242	0.300	1
1	A	69	LYS	N	123.832	0.300	1
1	A	70	ILE	H	8.08	0.020	1
1	A	70	ILE	HA	4.122	0.020	1
1	A	70	ILE	HB	1.778	0.020	1
1	A	70	ILE	HD11	0.766	0.020	1
1	A	70	ILE	HD12	0.766	0.020	1
1	A	70	ILE	HD13	0.766	0.020	1
1	A	70	ILE	HG12	1.397	0.020	.
1	A	70	ILE	HG13	1.094	0.020	.
1	A	70	ILE	HG21	0.839	0.020	1
1	A	70	ILE	HG22	0.839	0.020	1
1	A	70	ILE	HG23	0.839	0.020	1
1	A	70	ILE	C	176.299	0.300	1
1	A	70	ILE	CA	60.619	0.300	1
1	A	70	ILE	CB	38.407	0.300	1
1	A	70	ILE	CD1	12.431	0.300	1
1	A	70	ILE	CG1	26.513	0.300	1
1	A	70	ILE	CG2	17.046	0.300	1
1	A	70	ILE	N	122.258	0.300	1
1	A	71	GLY	H	8.214	0.020	1
1	A	71	GLY	HA2	4.077	0.020	.
1	A	71	GLY	HA3	3.926	0.020	.
1	A	71	GLY	CA	43.952	0.300	1
1	A	71	GLY	N	113.226	0.300	1
1	A	72	PRO	HA	4.334	0.020	1
1	A	72	PRO	HB2	2.154	0.020	.
1	A	72	PRO	HB3	1.794	0.020	.
1	A	72	PRO	HD2	3.527	0.020	.

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	72	PRO	HD3	3.527	0.020	.
1	A	72	PRO	HG2	1.896	0.020	.
1	A	72	PRO	HG3	1.896	0.020	.
1	A	72	PRO	CA	62.334	0.300	1
1	A	72	PRO	CB	31.687	0.300	1
1	A	72	PRO	CD	49.324	0.300	1
1	A	72	PRO	CG	26.597	0.300	1
1	A	73	LEU	H	8.324	0.020	1
1	A	73	LEU	HA	4.495	0.020	1
1	A	73	LEU	HB2	1.524	0.020	.
1	A	73	LEU	HB3	1.476	0.020	.
1	A	73	LEU	HD11	0.872	0.020	.
1	A	73	LEU	HD12	0.872	0.020	.
1	A	73	LEU	HD13	0.872	0.020	.
1	A	73	LEU	HD21	0.834	0.020	.
1	A	73	LEU	HD22	0.834	0.020	.
1	A	73	LEU	HD23	0.834	0.020	.
1	A	73	LEU	HG	1.567	0.020	1
1	A	73	LEU	CA	52.74	0.300	1
1	A	73	LEU	CB	41.166	0.300	1
1	A	73	LEU	CD1	24.801	0.300	.
1	A	73	LEU	CD2	22.586	0.300	.
1	A	73	LEU	CG	26.406	0.300	1
1	A	73	LEU	N	123.76	0.300	1
1	A	74	PRO	HA	4.329	0.020	1
1	A	74	PRO	HB2	2.231	0.020	.
1	A	74	PRO	HB3	1.845	0.020	.
1	A	74	PRO	HD2	3.772	0.020	.
1	A	74	PRO	HD3	3.576	0.020	.
1	A	74	PRO	HG2	1.961	0.020	.
1	A	74	PRO	HG3	1.961	0.020	.
1	A	74	PRO	CA	63.078	0.300	1
1	A	74	PRO	CB	31.672	0.300	1
1	A	74	PRO	CD	50.145	0.300	1
1	A	74	PRO	CG	26.979	0.300	1
1	A	75	GLY	H	8.431	0.020	1
1	A	75	GLY	HA2	3.908	0.020	.
1	A	75	GLY	HA3	3.908	0.020	.
1	A	75	GLY	C	174.545	0.300	1
1	A	75	GLY	CA	44.951	0.300	1
1	A	75	GLY	N	109.007	0.300	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	76	THR	H	7.908	0.020	1
1	A	76	THR	HA	4.197	0.020	1
1	A	76	THR	HB	4.089	0.020	1
1	A	76	THR	HG21	1.118	0.020	1
1	A	76	THR	HG22	1.118	0.020	1
1	A	76	THR	HG23	1.118	0.020	1
1	A	76	THR	C	174.759	0.300	1
1	A	76	THR	CA	61.478	0.300	1
1	A	76	THR	CB	69.369	0.300	1
1	A	76	THR	CG2	21.295	0.300	1
1	A	76	THR	N	113.511	0.300	1
1	A	77	LYS	H	8.347	0.020	1
1	A	77	LYS	HA	4.209	0.020	1
1	A	77	LYS	HB2	1.643	0.020	.
1	A	77	LYS	HB3	1.643	0.020	.
1	A	77	LYS	HD2	1.709	0.020	.
1	A	77	LYS	HD3	1.709	0.020	.
1	A	77	LYS	HE2	2.92	0.020	.
1	A	77	LYS	HE3	2.92	0.020	.
1	A	77	LYS	HG2	1.36	0.020	.
1	A	77	LYS	HG3	1.36	0.020	.
1	A	77	LYS	C	176.679	0.300	1
1	A	77	LYS	CA	56.052	0.300	1
1	A	77	LYS	CB	32.529	0.300	1
1	A	77	LYS	CD	28.643	0.300	1
1	A	77	LYS	CE	41.666	0.300	1
1	A	77	LYS	CG	24.242	0.300	1
1	A	77	LYS	N	123.805	0.300	1
1	A	78	LYS	H	8.309	0.020	1
1	A	78	LYS	HA	4.241	0.020	1
1	A	78	LYS	HB2	1.638	0.020	.
1	A	78	LYS	HB3	1.638	0.020	.
1	A	78	LYS	HD2	1.714	0.020	.
1	A	78	LYS	HD3	1.714	0.020	.
1	A	78	LYS	HE2	2.88	0.020	.
1	A	78	LYS	HE3	2.88	0.020	.
1	A	78	LYS	HG2	1.401	0.020	.
1	A	78	LYS	HG3	1.401	0.020	.
1	A	78	LYS	C	176.536	0.300	1
1	A	78	LYS	CA	56.195	0.300	1
1	A	78	LYS	CB	32.826	0.300	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	78	LYS	CD	28.342	0.300	1
1	A	78	LYS	CE	41.666	0.300	1
1	A	78	LYS	CG	24.193	0.300	1
1	A	78	LYS	N	122.668	0.300	1
1	A	79	SER	H	8.268	0.020	1
1	A	79	SER	HA	4.347	0.020	1
1	A	79	SER	HB2	3.731	0.020	.
1	A	79	SER	HB3	3.731	0.020	.
1	A	79	SER	C	177.034	0.300	1
1	A	79	SER	CA	57.852	0.300	1
1	A	79	SER	CB	63.473	0.300	1
1	A	79	SER	N	117.303	0.300	1
1	A	80	LYS	H	8.324	0.020	1
1	A	80	LYS	HA	4.23	0.020	1
1	A	80	LYS	HB2	1.641	0.020	.
1	A	80	LYS	HB3	1.641	0.020	.
1	A	80	LYS	HD2	1.777	0.020	.
1	A	80	LYS	HD3	1.777	0.020	.
1	A	80	LYS	HE2	2.914	0.020	.
1	A	80	LYS	HE3	2.914	0.020	.
1	A	80	LYS	HG2	1.367	0.020	.
1	A	80	LYS	HG3	1.367	0.020	.
1	A	80	LYS	C	176.607	0.300	1
1	A	80	LYS	CA	56.564	0.300	1
1	A	80	LYS	CB	32.496	0.300	1
1	A	80	LYS	CD	30.175	0.300	1
1	A	80	LYS	CE	41.606	0.300	1
1	A	80	LYS	CG	24.302	0.300	1
1	A	80	LYS	N	123.959	0.300	1
1	A	81	LYS	H	8.217	0.020	1
1	A	81	LYS	HA	4.148	0.020	1
1	A	81	LYS	HB2	1.638	0.020	.
1	A	81	LYS	HB3	1.638	0.020	.
1	A	81	LYS	HD2	1.715	0.020	.
1	A	81	LYS	HD3	1.715	0.020	.
1	A	81	LYS	HE2	2.915	0.020	.
1	A	81	LYS	HE3	2.915	0.020	.
1	A	81	LYS	HG2	1.304	0.020	.
1	A	81	LYS	HG3	1.304	0.020	.
1	A	81	LYS	C	176.276	0.300	1
1	A	81	LYS	CA	56.036	0.300	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	81	LYS	CB	32.643	0.300	1
1	A	81	LYS	CD	28.707	0.300	1
1	A	81	LYS	CE	41.854	0.300	1
1	A	81	LYS	CG	24.182	0.300	1
1	A	81	LYS	N	121.975	0.300	1
1	A	82	ASN	H	8.372	0.020	1
1	A	82	ASN	HA	4.609	0.020	1
1	A	82	ASN	HB2	2.69	0.020	.
1	A	82	ASN	HB3	2.69	0.020	.
1	A	82	ASN	HD21	7.579	0.020	.
1	A	82	ASN	HD22	6.879	0.020	.
1	A	82	ASN	C	174.996	0.300	1
1	A	82	ASN	CA	53.008	0.300	1
1	A	82	ASN	CB	38.42	0.300	1
1	A	82	ASN	N	119.696	0.300	1
1	A	82	ASN	ND2	113.098	0.300	1
1	A	83	LEU	H	8.115	0.020	1
1	A	83	LEU	HA	4.224	0.020	1
1	A	83	LEU	HB2	1.49	0.020	.
1	A	83	LEU	HB3	1.49	0.020	.
1	A	83	LEU	HD11	0.839	0.020	.
1	A	83	LEU	HD12	0.839	0.020	.
1	A	83	LEU	HD13	0.839	0.020	.
1	A	83	LEU	HD21	0.839	0.020	.
1	A	83	LEU	HD22	0.839	0.020	.
1	A	83	LEU	HD23	0.839	0.020	.
1	A	83	LEU	HG	1.492	0.020	1
1	A	83	LEU	C	177.153	0.300	1
1	A	83	LEU	CA	54.888	0.300	1
1	A	83	LEU	CB	42.242	0.300	1
1	A	83	LEU	CD1	22.756	0.300	.
1	A	83	LEU	CG	26.917	0.300	1
1	A	83	LEU	N	122.869	0.300	1
1	A	84	ARG	H	8.18	0.020	1
1	A	84	ARG	HA	4.23	0.020	1
1	A	84	ARG	HB2	1.652	0.020	.
1	A	84	ARG	HB3	1.463	0.020	.
1	A	84	ARG	HD2	3.146	0.020	.
1	A	84	ARG	HD3	3.146	0.020	.
1	A	84	ARG	HG2	1.597	0.020	.
1	A	84	ARG	HG3	1.597	0.020	.

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	84	ARG	C	175.802	0.300	1
1	A	84	ARG	CA	55.545	0.300	1
1	A	84	ARG	CB	30.218	0.300	1
1	A	84	ARG	CD	41.134	0.300	1
1	A	84	ARG	CG	24.604	0.300	1
1	A	84	ARG	N	121.586	0.300	1
1	A	85	ARG	H	8.25	0.020	1
1	A	85	ARG	HA	4.217	0.020	1
1	A	85	ARG	HB2	1.741	0.020	.
1	A	85	ARG	HB3	1.678	0.020	.
1	A	85	ARG	HD2	3.108	0.020	.
1	A	85	ARG	HD3	3.108	0.020	.
1	A	85	ARG	HG2	1.533	0.020	.
1	A	85	ARG	HG3	1.533	0.020	.
1	A	85	ARG	C	175.091	0.300	1
1	A	85	ARG	CA	55.611	0.300	1
1	A	85	ARG	CB	30.364	0.300	1
1	A	85	ARG	CD	42.872	0.300	1
1	A	85	ARG	CG	26.962	0.300	1
1	A	85	ARG	N	123.315	0.300	1
1	A	86	LEU	H	7.862	0.020	1
1	A	86	LEU	HA	4.094	0.020	1
1	A	86	LEU	HB2	1.485	0.020	.
1	A	86	LEU	HB3	1.485	0.020	.
1	A	86	LEU	HD11	0.861	0.020	.
1	A	86	LEU	HD12	0.861	0.020	.
1	A	86	LEU	HD13	0.861	0.020	.
1	A	86	LEU	HD21	0.861	0.020	.
1	A	86	LEU	HD22	0.861	0.020	.
1	A	86	LEU	HD23	0.861	0.020	.
1	A	86	LEU	HG	1.378	0.020	1
1	A	86	LEU	CA	56.494	0.300	1
1	A	86	LEU	CB	42.902	0.300	1
1	A	86	LEU	CD1	24.735	0.300	.
1	A	86	LEU	CG	26.78	0.300	1
1	A	86	LEU	N	129.646	0.300	1

7.1.2 Chemical shift referencing ⓘ

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	85	0.42 ± 0.43	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	80	0.62 ± 0.29	Should be applied
$^{13}\text{C}'$	77	0.31 ± 0.18	None needed (< 0.5 ppm)
^{15}N	81	-1.78 ± 0.36	Should be applied

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 90%, i.e. 444 atoms were assigned a chemical shift out of a possible 495. 0 out of 2 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	188/190 (99%)	77/77 (100%)	74/76 (97%)	37/37 (100%)
Sidechain	224/259 (86%)	152/165 (92%)	68/78 (87%)	4/16 (25%)
Aromatic	32/46 (70%)	21/21 (100%)	11/25 (44%)	0/0 (—%)
Overall	444/495 (90%)	250/263 (95%)	153/179 (85%)	41/53 (77%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 90%, i.e. 536 atoms were assigned a chemical shift out of a possible 593. 0 out of 3 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	228/230 (99%)	93/93 (100%)	90/92 (98%)	45/45 (100%)
Sidechain	272/310 (88%)	185/198 (93%)	83/95 (87%)	4/17 (24%)
Aromatic	36/53 (68%)	23/25 (92%)	13/27 (48%)	0/1 (0%)
Overall	536/593 (90%)	301/316 (95%)	186/214 (87%)	49/63 (78%)

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.

List Id	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	32	ARG	NE	116.02	76.53 – 92.65	19.5
1	A	32	ARG	HD3	1.09	1.81 – 4.39	-7.8

7.1.5 Random Coil Index (RCI) plots [i](#)

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. If well-defined core and ill-defined regions are not identified then it is shown as gray bars.

Random coil index (RCI) for chain A:

