



Full wwPDB NMR Structure Validation Report ⓘ

Mar 9, 2026 – 07:21 AM UTC

PDB ID : 8C8A / pdb_00008c8a
BMRB ID : 34782
Title : The NMR structure of the MAX28 effector from *Magnaporthe oryzae*
Authors : Lahfa, M.; Padilla, A.; de Guillen, K.; Kroj, T.; Roumestand, C.; Barthe, P.
Deposited on : 2023-01-19

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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

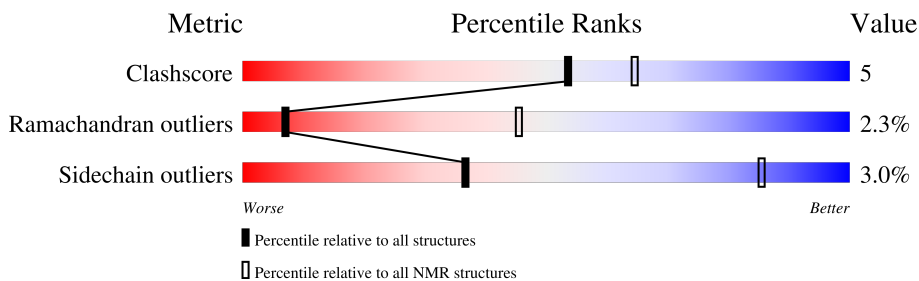
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 61%.

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	155	

2 Ensemble composition and analysis

This entry contains 20 models. Model 10 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:37-A:99 (63)	0.46	10

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 2 clusters and 3 single-model clusters were found.

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

3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 1308 atoms, of which 664 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called But2 domain-containing protein.

Mol	Chain	Residues	Atoms					Trace	
			Total	C	H	N	O		S
1	A	89	1308	411	664	104	125	4	0

There are 30 discrepancies between the modelled and reference sequences:

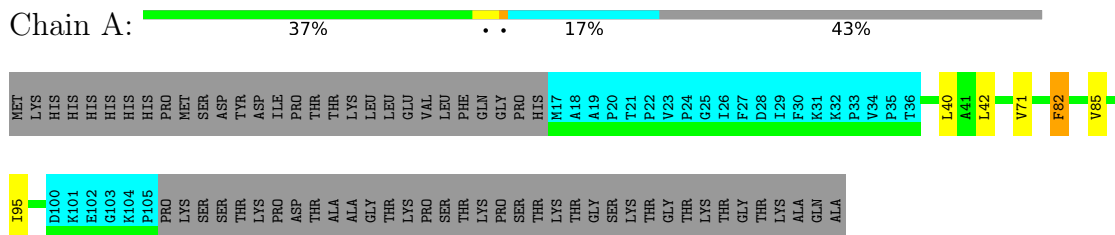
Chain	Residue	Modelled	Actual	Comment	Reference
A	-12	MET	-	initiating methionine	UNP G4MW19
A	-11	LYS	-	expression tag	UNP G4MW19
A	-10	HIS	-	expression tag	UNP G4MW19
A	-9	HIS	-	expression tag	UNP G4MW19
A	-8	HIS	-	expression tag	UNP G4MW19
A	-7	HIS	-	expression tag	UNP G4MW19
A	-6	HIS	-	expression tag	UNP G4MW19
A	-5	HIS	-	expression tag	UNP G4MW19
A	-4	PRO	-	expression tag	UNP G4MW19
A	-3	MET	-	expression tag	UNP G4MW19
A	-2	SER	-	expression tag	UNP G4MW19
A	-1	ASP	-	expression tag	UNP G4MW19
A	0	TYR	-	expression tag	UNP G4MW19
A	1	ASP	-	expression tag	UNP G4MW19
A	2	ILE	-	expression tag	UNP G4MW19
A	3	PRO	-	expression tag	UNP G4MW19
A	4	THR	-	expression tag	UNP G4MW19
A	5	THR	-	expression tag	UNP G4MW19
A	6	LYS	-	expression tag	UNP G4MW19
A	7	LEU	-	expression tag	UNP G4MW19
A	8	LEU	-	expression tag	UNP G4MW19
A	9	GLU	-	expression tag	UNP G4MW19
A	10	VAL	-	expression tag	UNP G4MW19
A	11	LEU	-	expression tag	UNP G4MW19
A	12	PHE	-	expression tag	UNP G4MW19
A	13	GLN	-	expression tag	UNP G4MW19
A	14	GLY	-	expression tag	UNP G4MW19
A	15	PRO	-	expression tag	UNP G4MW19
A	16	HIS	-	expression tag	UNP G4MW19
A	17	MET	-	expression tag	UNP G4MW19

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: But2 domain-containing protein

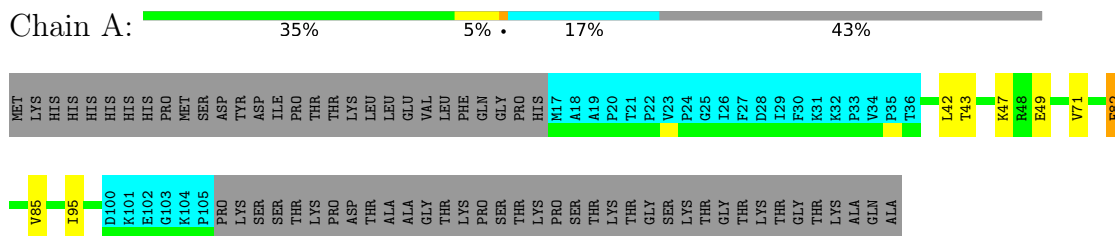


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

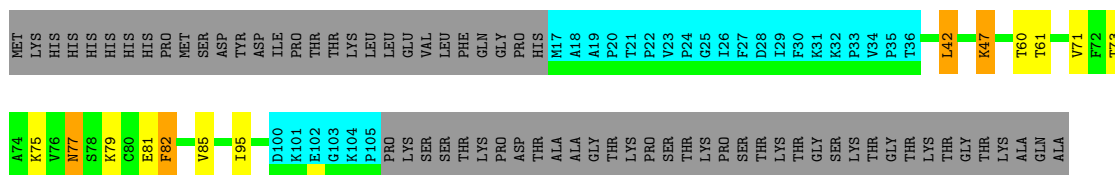
- Molecule 1: But2 domain-containing protein



4.2.2 Score per residue for model 2

- Molecule 1: But2 domain-containing protein

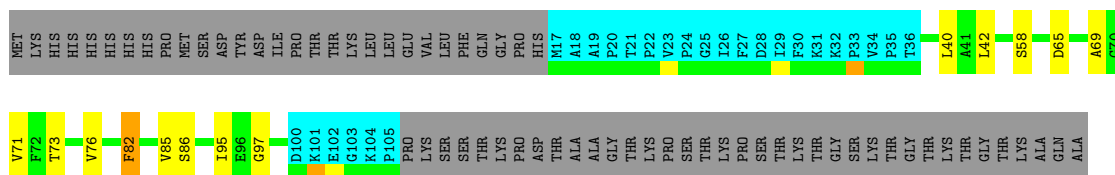




4.2.3 Score per residue for model 3

- Molecule 1: But2 domain-containing protein

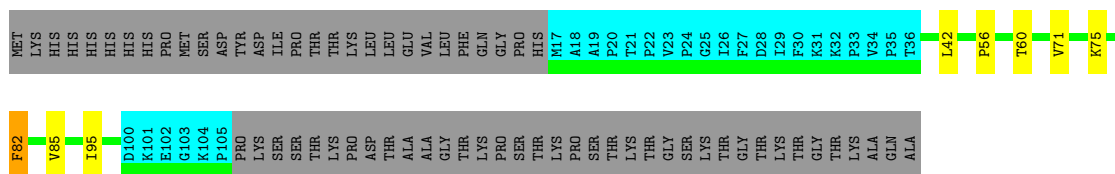
Chain A: 32% 8% 17% 43%



4.2.4 Score per residue for model 4

- Molecule 1: But2 domain-containing protein

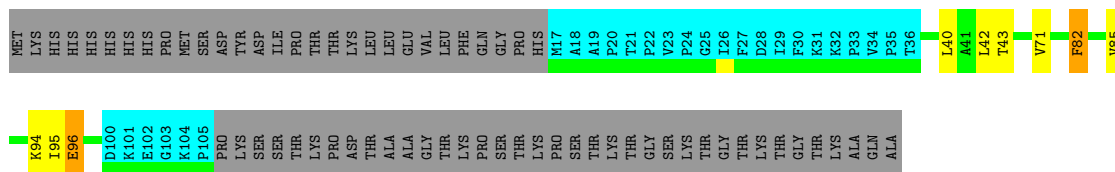
Chain A: 35% 5% 17% 43%



4.2.5 Score per residue for model 5

- Molecule 1: But2 domain-containing protein

Chain A: 35% 5% 17% 43%

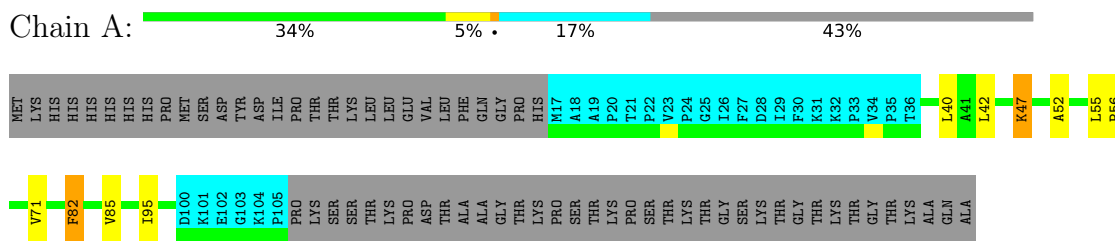


4.2.6 Score per residue for model 6

- Molecule 1: But2 domain-containing protein

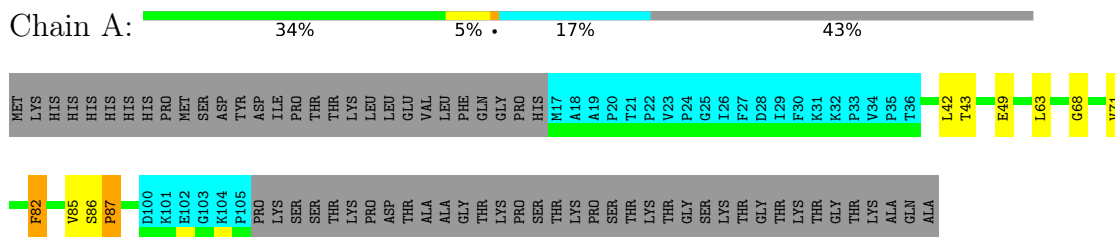
4.2.10 Score per residue for model 10 (medoid)

- Molecule 1: But2 domain-containing protein



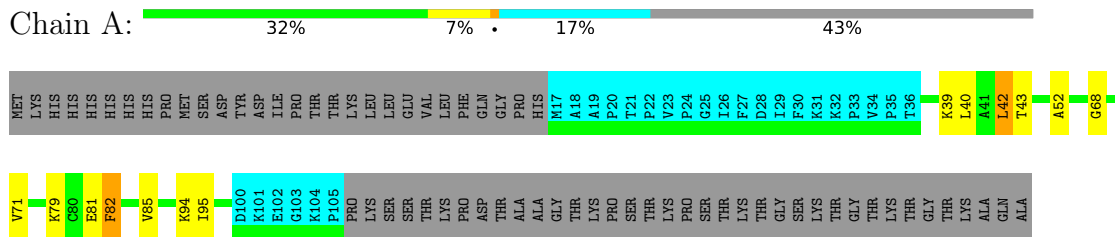
4.2.11 Score per residue for model 11

- Molecule 1: But2 domain-containing protein



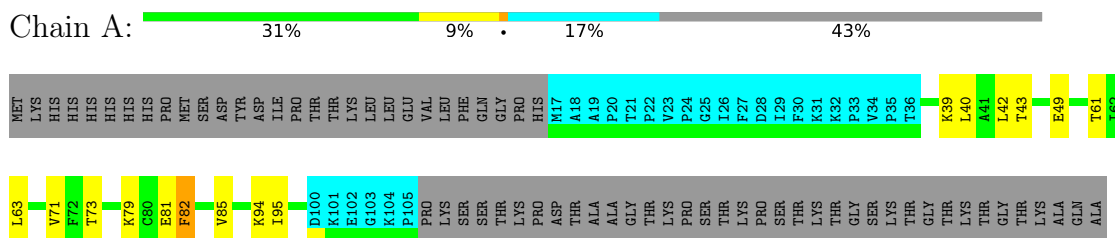
4.2.12 Score per residue for model 12

- Molecule 1: But2 domain-containing protein



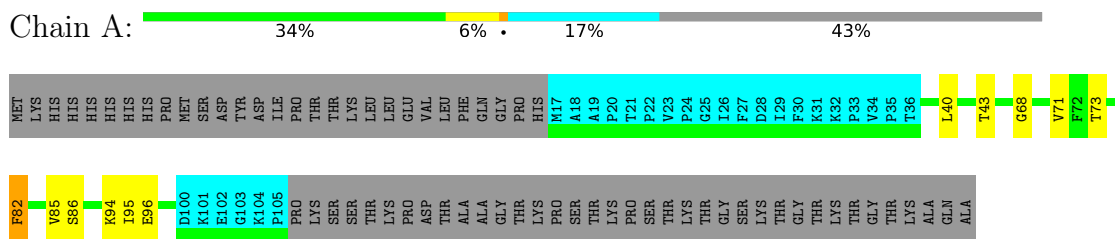
4.2.13 Score per residue for model 13

- Molecule 1: But2 domain-containing protein



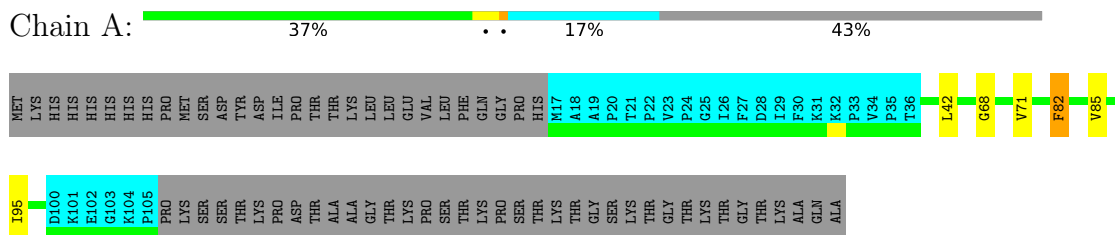
4.2.14 Score per residue for model 14

- Molecule 1: But2 domain-containing protein



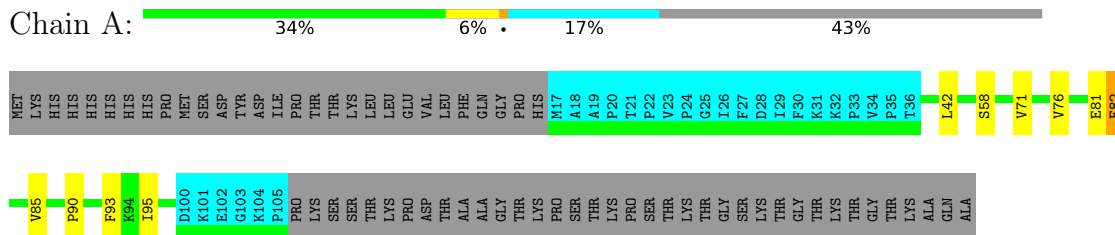
4.2.15 Score per residue for model 15

- Molecule 1: But2 domain-containing protein



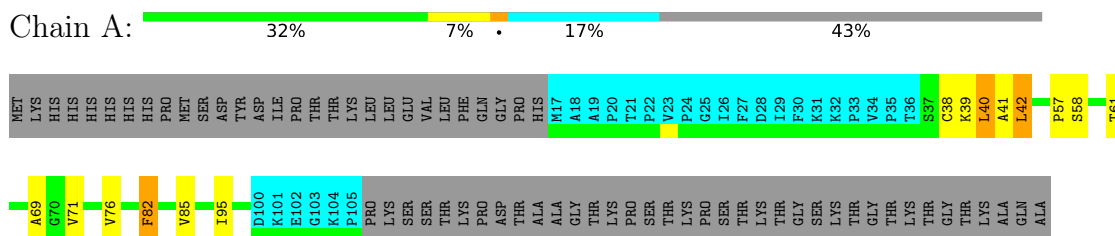
4.2.16 Score per residue for model 16

- Molecule 1: But2 domain-containing protein



4.2.17 Score per residue for model 17

- Molecule 1: But2 domain-containing protein



5 Refinement protocol and experimental data overview

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

Of the 20 calculated structures, 20 were deposited, based on the following criterion: *structures with the lowest energy*.

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

Software name	Classification	Version
CNS	refinement	1.2
CYANA	structure calculation	3.98.13

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	648
Number of shifts mapped to atoms	579
Number of unparsed shifts	0
Number of shifts with mapping errors	69
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	61%

6 Model quality [i](#)

6.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the (average) root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#Z>5	RMSZ	#Z>5
1	A	1.26±0.05	1±1/456 (0.1± 0.2%)	0.89±0.04	0±0/619 (0.0± 0.0%)
All	All	1.26	12/9120 (0.1%)	0.89	1/12380 (0.0%)

All unique bond outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
1	A	56	PRO	CA-C	7.03	1.55	1.51	10	4
1	A	39	LYS	C-N	-6.37	1.24	1.33	17	2
1	A	40	LEU	N-CA	-5.74	1.39	1.46	17	1
1	A	42	LEU	N-CA	-5.72	1.39	1.46	17	3
1	A	96	GLU	N-CA	-5.32	1.39	1.46	5	1
1	A	41	ALA	C-N	-5.17	1.26	1.33	17	1

All unique angle outliers are listed below.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	66	THR	N-CA-C	-5.33	106.73	113.18	6	1

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	449	459	459	5±2
All	All	8980	9180	9180	94

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 5.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:82:PHE:CE1	1:A:85:VAL:HG23	0.64	2.28	12	13
1:A:73:THR:HB	1:A:86:SER:OG	0.62	1.94	3	2
1:A:82:PHE:CE2	1:A:85:VAL:HG23	0.61	2.31	20	7
1:A:42:LEU:HB2	1:A:63:LEU:HD13	0.55	1.77	9	5
1:A:94:LYS:HG2	1:A:95:ILE:N	0.54	2.18	5	2
1:A:77:ASN:ND2	1:A:81:GLU:H	0.53	2.01	2	1
1:A:61:THR:O	1:A:73:THR:HA	0.52	2.05	2	5
1:A:40:LEU:O	1:A:52:ALA:HA	0.52	2.05	10	7
1:A:40:LEU:HD12	1:A:61:THR:OG1	0.51	2.05	17	1
1:A:40:LEU:HB2	1:A:61:THR:HG21	0.49	1.84	9	2
1:A:38:CYS:SG	1:A:57:PRO:HA	0.48	2.49	17	1
1:A:42:LEU:HD13	1:A:95:ILE:CD1	0.47	2.40	10	9
1:A:43:THR:OG1	1:A:94:LYS:HB3	0.47	2.09	9	5
1:A:58:SER:HA	1:A:76:VAL:O	0.46	2.11	7	4
1:A:79:LYS:HE2	1:A:81:GLU:OE2	0.46	2.11	13	1
1:A:60:THR:HG22	1:A:75:LYS:HG2	0.45	1.87	2	2
1:A:43:THR:HG22	1:A:49:GLU:HA	0.45	1.87	13	5
1:A:47:LYS:HE3	1:A:47:LYS:HA	0.45	1.88	2	2
1:A:82:PHE:CD1	1:A:85:VAL:HG23	0.44	2.47	7	1
1:A:41:ALA:O	1:A:95:ILE:HA	0.43	2.12	19	1
1:A:40:LEU:HD13	1:A:97:GLY:HA2	0.43	1.91	3	1
1:A:50:VAL:CG1	1:A:65:ASP:HA	0.43	2.44	9	1
1:A:42:LEU:HD23	1:A:95:ILE:CD1	0.43	2.44	5	6
1:A:90:PRO:HG2	1:A:93:PHE:CD1	0.42	2.49	16	1
1:A:79:LYS:HD3	1:A:81:GLU:OE1	0.42	2.13	12	1
1:A:86:SER:HA	1:A:87:PRO:C	0.42	2.40	9	2
1:A:39:LYS:HD2	1:A:39:LYS:C	0.41	2.40	13	1
1:A:40:LEU:HA	1:A:96:GLU:O	0.41	2.14	14	2
1:A:77:ASN:ND2	1:A:79:LYS:HB2	0.41	2.30	2	1
1:A:55:LEU:HG	1:A:61:THR:OG1	0.40	2.16	20	1
1:A:65:ASP:O	1:A:69:ALA:HA	0.40	2.16	3	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	63/155 (41%)	56±1 (89±2%)	6±1 (9±2%)	1±1 (2±1%)	7	45
All	All	1260/3100 (41%)	1120 (89%)	111 (9%)	29 (2%)	7	45

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

Mol	Chain	Res	Type	Models (Total)
1	A	71	VAL	20
1	A	68	GLY	6
1	A	70	GLY	1
1	A	87	PRO	1
1	A	69	ALA	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	52/131 (40%)	50±1 (97±1%)	2±1 (3±1%)	37	85
All	All	1040/2620 (40%)	1009 (97%)	31 (3%)	37	85

All 7 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	82	PHE	20
1	A	47	LYS	3
1	A	55	LEU	3
1	A	81	GLU	2
1	A	77	ASN	1

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Mol	Chain	Res	Type	Models (Total)
1	A	79	LYS	1
1	A	91	THR	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](#)

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 61% for the well-defined parts and 52% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *starch_output*

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	648
Number of shifts mapped to atoms	579
Number of unparsed shifts	0
Number of shifts with mapping errors	69
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	1

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

- No matching atom found in the structure. All 69 occurrences are reported below.

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	134	THR	H	8.031	0.000	1
1	A	134	THR	HA	4.293	0.000	1
1	A	134	THR	HB	4.162	0.000	1
1	A	134	THR	HG21	1.137	0.000	1
1	A	134	THR	HG22	1.137	0.000	1
1	A	134	THR	HG23	1.137	0.000	1
1	A	134	THR	N	114.04	0.000	1
1	A	135	LYS	H	8.277	0.000	1
1	A	135	LYS	HA	4.584	0.000	1
1	A	135	LYS	HB2	1.774	0.000	.
1	A	135	LYS	HB3	1.67	0.000	.
1	A	135	LYS	HD2	1.64	0.000	.
1	A	135	LYS	HD3	1.62	0.000	.
1	A	135	LYS	HE2	2.953	0.000	.

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	135	LYS	HE3	2.953	0.000	.
1	A	135	LYS	HG2	1.428	0.000	.
1	A	135	LYS	HG3	1.406	0.000	.
1	A	135	LYS	N	125.18	0.000	1
1	A	136	THR	H	8.022	0.000	1
1	A	136	THR	HA	4.222	0.000	1
1	A	136	THR	HB	4.18	0.000	1
1	A	136	THR	HG21	1.156	0.000	1
1	A	136	THR	HG22	1.156	0.000	1
1	A	136	THR	HG23	1.156	0.000	1
1	A	136	THR	N	114.5	0.000	1
1	A	137	GLY	H	8.249	0.000	1
1	A	137	GLY	HA2	3.949	0.000	.
1	A	137	GLY	HA3	3.925	0.000	.
1	A	137	GLY	N	107.79	0.000	1
1	A	138	THR	H	7.923	0.000	1
1	A	138	THR	HA	4.275	0.000	1
1	A	138	THR	HB	4.123	0.000	1
1	A	138	THR	HG21	1.133	0.000	1
1	A	138	THR	HG22	1.133	0.000	1
1	A	138	THR	HG23	1.133	0.000	1
1	A	138	THR	N	113.82	0.000	1
1	A	139	LYS	H	8.312	0.000	1
1	A	139	LYS	HA	4.587	0.000	1
1	A	139	LYS	HB2	1.782	0.000	.
1	A	139	LYS	HB3	1.679	0.000	.
1	A	139	LYS	HD2	1.65	0.000	.
1	A	139	LYS	HD3	1.63	0.000	.
1	A	139	LYS	HE2	2.946	0.000	.
1	A	139	LYS	HE3	2.946	0.000	.
1	A	139	LYS	HG2	1.437	0.000	.
1	A	139	LYS	HG3	1.406	0.000	.
1	A	139	LYS	N	125.3	0.000	1
1	A	140	ALA	H	8.138	0.000	1
1	A	140	ALA	HA	4.239	0.000	1
1	A	140	ALA	HB1	1.351	0.000	1
1	A	140	ALA	HB2	1.351	0.000	1
1	A	140	ALA	HB3	1.351	0.000	1
1	A	140	ALA	N	123.28	0.000	1
1	A	141	GLN	H	8.228	0.000	1
1	A	141	GLN	HA	4.249	0.000	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	141	GLN	HB2	2.069	0.000	.
1	A	141	GLN	HB3	1.922	0.000	.
1	A	141	GLN	HE21	7.549	0.000	.
1	A	141	GLN	HE22	6.786	0.000	.
1	A	141	GLN	HG2	2.336	0.000	.
1	A	141	GLN	HG3	2.3	0.000	.
1	A	141	GLN	N	120.16	0.000	1
1	A	141	GLN	NE2	112.73	0.000	1
1	A	142	ALA	H	7.934	0.000	1
1	A	142	ALA	HA	4.058	0.000	1
1	A	142	ALA	HB1	1.274	0.000	1
1	A	142	ALA	HB2	1.274	0.000	1
1	A	142	ALA	HB3	1.274	0.000	1
1	A	142	ALA	N	131.35	0.000	1

7.1.2 Chemical shift referencing [i](#)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	0	—	None (insufficient data)
$^{13}\text{C}_\beta$	0	—	None (insufficient data)
$^{13}\text{C}'$	0	—	None (insufficient data)
^{15}N	81	0.03 \pm 0.27	None needed (< 0.5 ppm)

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 61%, i.e. 472 atoms were assigned a chemical shift out of a possible 777. 0 out of 11 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	183/313 (58%)	125/128 (98%)	0/126 (0%)	58/59 (98%)
Sidechain	274/434 (63%)	270/286 (94%)	0/137 (0%)	4/11 (36%)
Aromatic	15/30 (50%)	15/15 (100%)	0/15 (0%)	0/0 (—%)
Overall	472/777 (61%)	410/429 (96%)	0/278 (0%)	62/70 (89%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 52%, i.e. 579 atoms were assigned a chemical shift out of a possible 1120. 0 out of 13 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	229/433 (53%)	157/176 (89%)	0/178 (0%)	72/79 (91%)
Sidechain	333/637 (52%)	329/419 (79%)	0/203 (0%)	4/15 (27%)
Aromatic	17/50 (34%)	17/25 (68%)	0/25 (0%)	0/0 (—%)
Overall	579/1120 (52%)	503/620 (81%)	0/406 (0%)	76/94 (81%)

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	95	ILE	HB	0.03	0.35 – 3.22	-6.1

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:

