



Full wwPDB NMR Structure Validation Report ⓘ

Apr 27, 2016 – 04:27 AM BST

PDB ID : 2N93
Title : Solution structure of lcFABP
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Deposited on : 2015-11-05

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
<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
Mogul : unknown
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
ShiftChecker : rb-20027457
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20027457

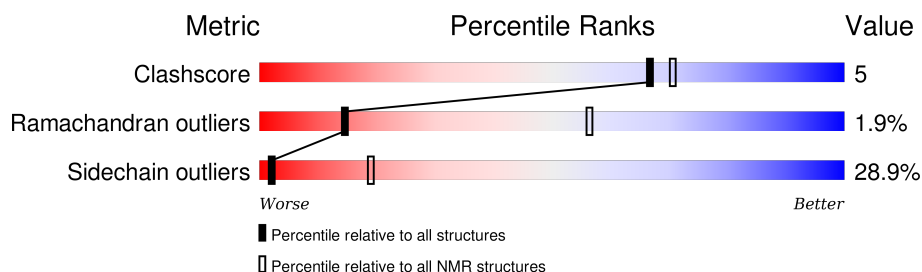
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR


The overall completeness of chemical shifts assignment is 86%.

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	114402	11133
Ramachandran outliers	111179	9975
Sidechain outliers	111093	9958

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	130	 62% 36% ..

2 Ensemble composition and analysis

This entry contains 10 models. Model 8 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:2-A:130 (129)	0.40	8

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 1 single-model cluster was found.

Cluster number	Models
1	1, 5, 6, 7, 8, 9, 10
2	3, 4
Single-model clusters	2

3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 2033 atoms, of which 1022 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Fatty acid-binding protein.

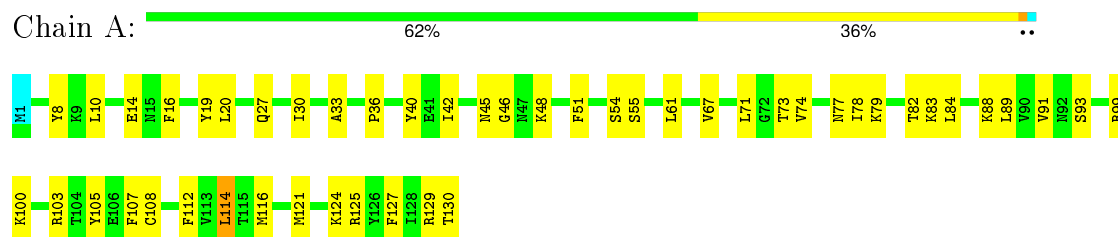
Mol	Chain	Residues	Atoms						Trace
1	A	130	Total	C	H	N	O	S	0
			2033	640	1022	166	198	7	

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: Fatty acid-binding protein

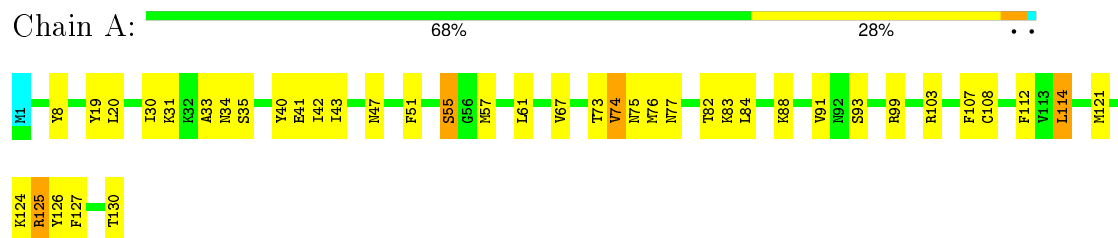


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

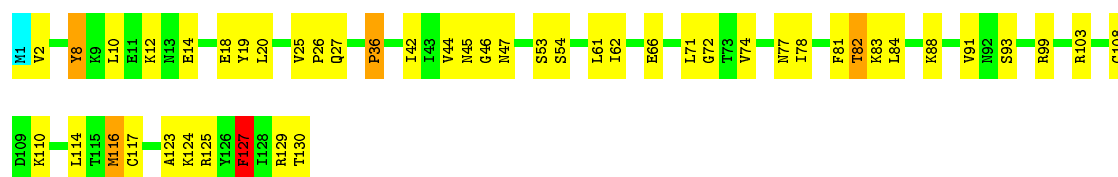
- Molecule 1: Fatty acid-binding protein



4.2.2 Score per residue for model 2

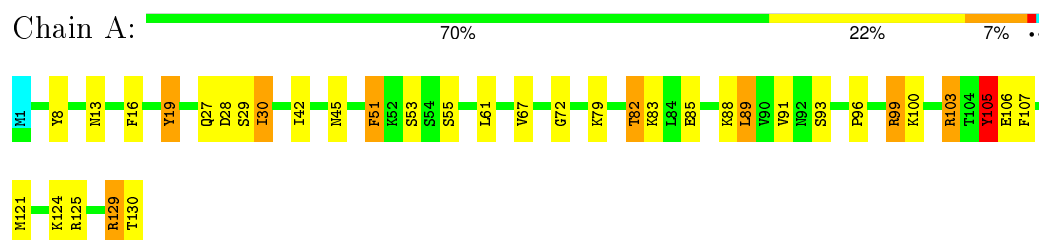
- Molecule 1: Fatty acid-binding protein





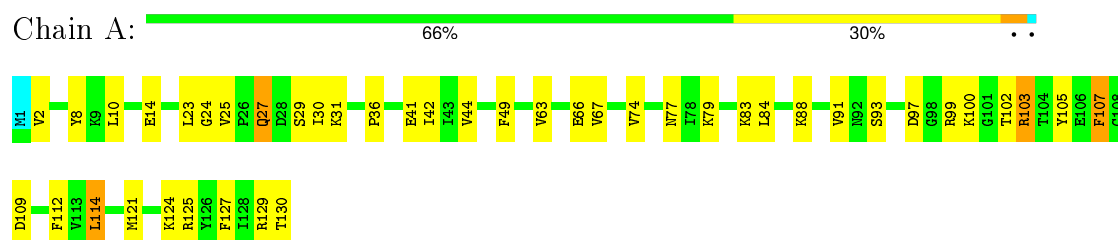
4.2.3 Score per residue for model 3

- Molecule 1: Fatty acid-binding protein



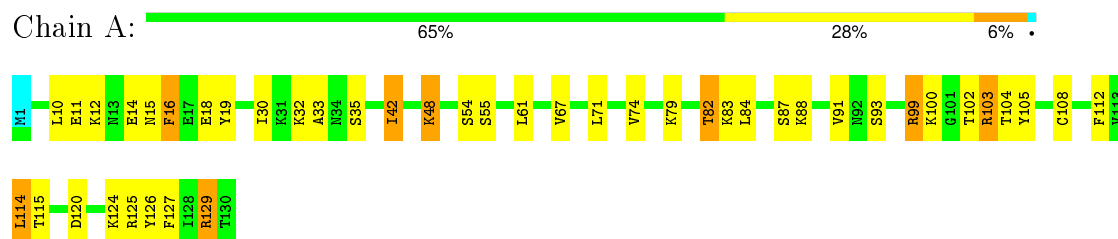
4.2.4 Score per residue for model 4

- Molecule 1: Fatty acid-binding protein



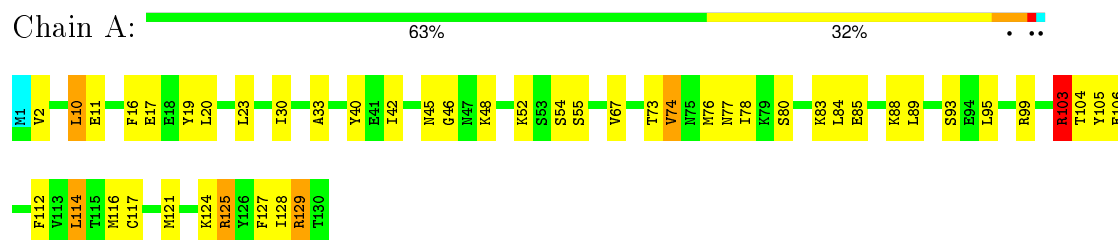
4.2.5 Score per residue for model 5

- Molecule 1: Fatty acid-binding protein



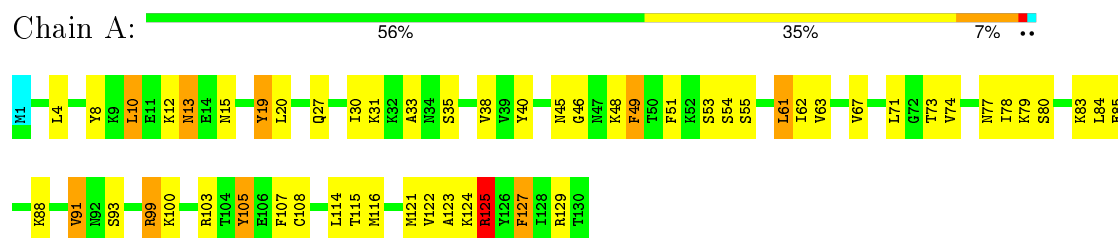
4.2.6 Score per residue for model 6

- Molecule 1: Fatty acid-binding protein



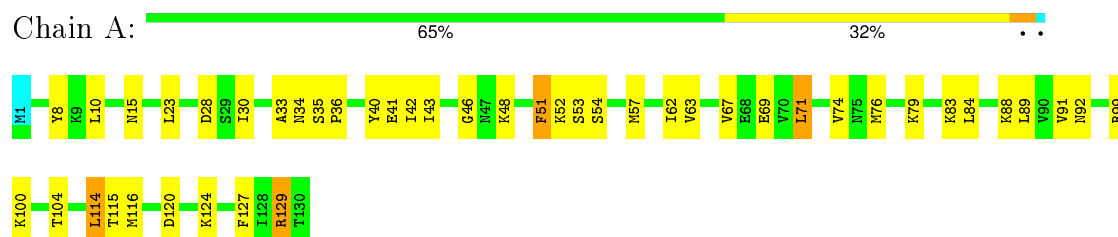
4.2.7 Score per residue for model 7

- Molecule 1: Fatty acid-binding protein



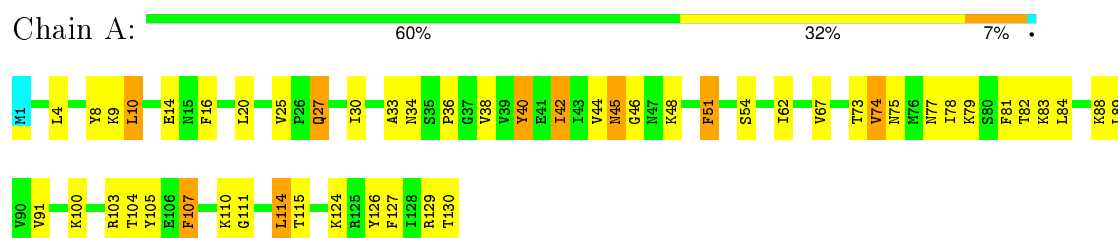
4.2.8 Score per residue for model 8 (medoid)

- Molecule 1: Fatty acid-binding protein



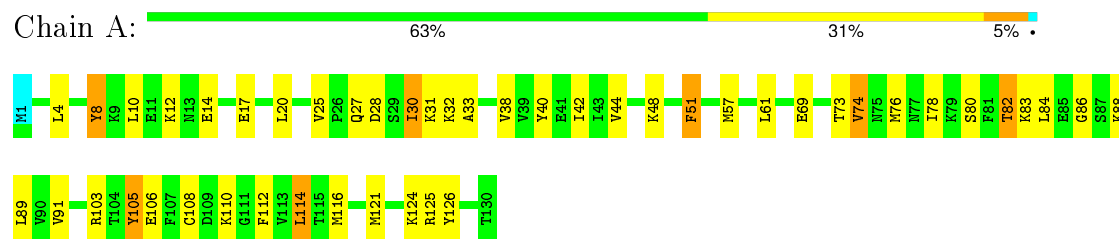
4.2.9 Score per residue for model 9

- Molecule 1: Fatty acid-binding protein



4.2.10 Score per residue for model 10

- Molecule 1: Fatty acid-binding protein



5 Refinement protocol and experimental data overview

The models were refined using the following method: *DGSA-distance geometry simulated annealing*.

Of the 200 calculated structures, 10 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	structure solution	1.1
AMBER	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)	2n93_cs.str
Number of chemical shift lists	1
Total number of shifts	1501
Number of shifts mapped to atoms	1501
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	86%

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

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	0.67±0.01	0±0/1017 (0.0±0.0%)	1.20±0.05	3±2/1366 (0.2±0.2%)
All	All	0.67	0/10170 (0.0%)	1.20	29/13660 (0.2%)

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	2.4±1.1
All	All	0	24

There are no bond-length outliers.

All unique angle 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(°)	Ideal(°)	Models	
								Worst	Total
1	A	103	ARG	NE-CZ-NH1	8.52	124.56	120.30	9	7
1	A	125	ARG	NE-CZ-NH1	8.32	124.46	120.30	7	2
1	A	129	ARG	NE-CZ-NH1	8.16	124.38	120.30	5	4
1	A	99	ARG	NE-CZ-NH1	7.65	124.12	120.30	7	2
1	A	19	TYR	CB-CG-CD1	-7.26	116.65	121.00	3	2
1	A	127	PHE	CB-CG-CD2	-6.78	116.06	120.80	7	1
1	A	127	PHE	CB-CG-CD1	6.70	125.49	120.80	7	1
1	A	91	VAL	CG1-CB-CG2	-6.66	100.25	110.90	7	1
1	A	105	TYR	CB-CG-CD2	-6.56	117.07	121.00	10	1
1	A	10	LEU	CB-CG-CD1	6.29	121.69	111.00	7	1
1	A	74	VAL	CG1-CB-CG2	-5.86	101.53	110.90	10	2
1	A	74	VAL	CA-CB-CG2	5.67	119.40	110.90	1	1
1	A	44	VAL	CA-CB-CG1	5.43	119.04	110.90	2	1
1	A	91	VAL	CA-CB-CG2	5.31	118.87	110.90	8	2
1	A	107	PHE	CB-CG-CD2	-5.17	117.18	120.80	1	1

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	126	TYR	Sidechain	4
1	A	103	ARG	Sidechain	4
1	A	19	TYR	Sidechain	3
1	A	105	TYR	Sidechain	2
1	A	8	TYR	Sidechain	2
1	A	129	ARG	Sidechain	1
1	A	111	GLY	Peptide	1
1	A	34	ASN	Peptide	1
1	A	99	ARG	Sidechain	1
1	A	15	ASN	Peptide	1
1	A	107	PHE	Sidechain	1
1	A	49	PHE	Sidechain	1
1	A	16	PHE	Sidechain	1
1	A	127	PHE	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	1003	1011	1011	10±4
All	All	10030	10110	10110	99

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:51:PHE:CZ	1:A:89:LEU:HD13	0.75	2.17	10	3
1:A:33:ALA:HB1	1:A:74:VAL:HG22	0.72	1.60	6	3
1:A:20:LEU:HD12	1:A:30:ILE:HD11	0.72	1.61	10	1
1:A:105:TYR:CE1	1:A:114:LEU:HD13	0.71	2.21	6	2
1:A:61:LEU:HD13	1:A:82:THR:HG21	0.68	1.64	3	5
1:A:114:LEU:HD11	1:A:127:PHE:CZ	0.66	2.25	5	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:71:LEU:HD23	1:A:74:VAL:CG1	0.64	2.22	8	1
1:A:105:TYR:CZ	1:A:114:LEU:HD13	0.61	2.30	3	1
1:A:42:ILE:HG21	1:A:112:PHE:CZ	0.61	2.31	5	1
1:A:51:PHE:CE1	1:A:89:LEU:HD13	0.56	2.36	10	2
1:A:10:LEU:HD23	1:A:127:PHE:CD2	0.56	2.36	2	1
1:A:20:LEU:HD13	1:A:30:ILE:HD11	0.55	1.77	7	1
1:A:49:PHE:HB2	1:A:63:VAL:HG22	0.55	1.77	7	1
1:A:33:ALA:HB1	1:A:74:VAL:HG12	0.54	1.79	7	3
1:A:33:ALA:CB	1:A:74:VAL:HG22	0.54	2.32	6	2
1:A:20:LEU:CD1	1:A:30:ILE:HD11	0.54	2.32	10	1
1:A:10:LEU:HD23	1:A:38:VAL:HB	0.52	1.79	7	2
1:A:103:ARG:CD	1:A:114:LEU:HD11	0.52	2.34	3	1
1:A:42:ILE:HD13	1:A:51:PHE:CD2	0.52	2.39	10	1
1:A:114:LEU:HD22	1:A:127:PHE:CZ	0.52	2.40	7	1
1:A:42:ILE:HG21	1:A:112:PHE:CE2	0.50	2.42	5	1
1:A:114:LEU:HB3	1:A:125:ARG:CZ	0.50	2.37	6	1
1:A:23:LEU:HD22	1:A:95:LEU:HG	0.50	1.84	6	1
1:A:61:LEU:CD1	1:A:82:THR:HG21	0.49	2.37	3	1
1:A:10:LEU:HD13	1:A:127:PHE:CD1	0.49	2.43	5	2
1:A:10:LEU:HD13	1:A:127:PHE:CE1	0.49	2.42	7	1
1:A:10:LEU:HD12	1:A:38:VAL:HB	0.48	1.83	9	1
1:A:71:LEU:HD23	1:A:74:VAL:HG11	0.48	1.84	8	1
1:A:25:VAL:HG11	1:A:74:VAL:HG12	0.48	1.84	9	1
1:A:103:ARG:NE	1:A:114:LEU:HD11	0.48	2.23	6	1
1:A:16:PHE:HA	1:A:19:TYR:CE1	0.47	2.44	6	2
1:A:27:GLN:HA	1:A:30:ILE:CG2	0.47	2.40	9	1
1:A:40:TYR:CD1	1:A:127:PHE:CE2	0.47	3.03	9	1
1:A:61:LEU:CD2	1:A:67:VAL:HG21	0.47	2.40	7	1
1:A:42:ILE:HD11	1:A:44:VAL:HG13	0.46	1.85	9	2
1:A:114:LEU:HD21	1:A:127:PHE:CE1	0.46	2.45	9	1
1:A:27:GLN:HA	1:A:30:ILE:HG22	0.46	1.88	4	3
1:A:40:TYR:CD2	1:A:127:PHE:CZ	0.46	3.04	1	3
1:A:44:VAL:HG12	1:A:49:PHE:CD2	0.45	2.47	4	1
1:A:25:VAL:CG1	1:A:74:VAL:HG23	0.45	2.42	2	1
1:A:71:LEU:HD22	1:A:76:MET:O	0.44	2.12	8	1
1:A:16:PHE:CE1	1:A:30:ILE:HG23	0.44	2.47	3	1
1:A:33:ALA:HB1	1:A:74:VAL:CG2	0.44	2.39	1	2
1:A:25:VAL:HG11	1:A:74:VAL:HG23	0.44	1.89	10	2
1:A:105:TYR:HB3	1:A:112:PHE:CE2	0.44	2.47	5	2
1:A:105:TYR:HE1	1:A:114:LEU:HD13	0.44	1.71	6	1
1:A:105:TYR:CE1	1:A:114:LEU:CD1	0.43	3.00	7	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:116:MET:HB3	1:A:123:ALA:HB3	0.43	1.90	2	1
1:A:67:VAL:HG23	1:A:80:SER:HB2	0.43	1.91	7	1
1:A:61:LEU:HD12	1:A:61:LEU:C	0.43	2.34	5	1
1:A:13:ASN:HA	1:A:125:ARG:HB3	0.43	1.89	7	1
1:A:10:LEU:HD11	1:A:36:PRO:CB	0.43	2.44	2	1
1:A:105:TYR:CG	1:A:114:LEU:HD12	0.42	2.50	10	1
1:A:103:ARG:HD3	1:A:114:LEU:HD11	0.42	1.91	3	1
1:A:10:LEU:HD23	1:A:127:PHE:CE1	0.42	2.49	6	1
1:A:42:ILE:HD13	1:A:112:PHE:CD2	0.42	2.49	6	1
1:A:105:TYR:CE1	1:A:114:LEU:HD12	0.42	2.49	7	1
1:A:13:ASN:HA	1:A:125:ARG:CB	0.42	2.44	7	1
1:A:105:TYR:CE1	1:A:114:LEU:HB3	0.42	2.49	9	1
1:A:33:ALA:HB1	1:A:74:VAL:CG1	0.42	2.44	8	1
1:A:42:ILE:HD11	1:A:44:VAL:CG1	0.42	2.43	9	1
1:A:114:LEU:CD2	1:A:127:PHE:CZ	0.42	3.02	1	1
1:A:15:ASN:CB	1:A:123:ALA:HA	0.41	2.45	7	1
1:A:19:TYR:CE1	1:A:20:LEU:HG	0.41	2.50	1	1
1:A:17:GLU:OE2	1:A:31:LYS:HE3	0.41	2.16	10	1
1:A:71:LEU:HD23	1:A:74:VAL:HG13	0.41	1.89	8	1
1:A:40:TYR:CG	1:A:127:PHE:CE2	0.41	3.08	6	2
1:A:104:THR:CG2	1:A:115:THR:HG22	0.41	2.46	5	1
1:A:114:LEU:HD21	1:A:127:PHE:CE2	0.41	2.51	8	1
1:A:61:LEU:HD22	1:A:67:VAL:HG21	0.41	1.92	7	1
1:A:91:VAL:CG2	1:A:105:TYR:CZ	0.40	3.04	7	1
1:A:20:LEU:HD11	1:A:26:PRO:C	0.40	2.37	2	1
1:A:128:ILE:HG22	1:A:129:ARG:N	0.40	2.31	6	1

6.3 Torsion angles ⓘ

6.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all NMR entries. The Analysed column shows the number of residues for which the backbone conformation was analysed and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	128/130 (98%)	106±4 (82±3%)	20±3 (16±2%)	2±1 (2±1%)	14	56
All	All	1280/1300 (98%)	1055 (82%)	201 (16%)	24 (2%)	14	56

All 13 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	46	GLY	5
1	A	36	PRO	4
1	A	72	GLY	2
1	A	62	ILE	2
1	A	48	LYS	2
1	A	55	SER	2
1	A	107	PHE	1
1	A	45	ASN	1
1	A	24	GLY	1
1	A	86	GLY	1
1	A	47	ASN	1
1	A	109	ASP	1
1	A	112	PHE	1

6.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all NMR entries. The Analysed column shows the number of residues for which the sidechain conformation was analysed and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	112/113 (99%)	80±2 (71±2%)	32±2 (29±2%)	2	19
All	All	1120/1130 (99%)	796 (71%)	324 (29%)	2	19

All 87 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	124	LYS	10
1	A	83	LYS	10
1	A	88	LYS	10
1	A	84	LEU	9
1	A	99	ARG	8
1	A	114	LEU	8
1	A	8	TYR	8
1	A	125	ARG	8
1	A	67	VAL	7
1	A	93	SER	7
1	A	42	ILE	7

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Mol	Chain	Res	Type	Models (Total)
1	A	79	LYS	6
1	A	129	ARG	6
1	A	91	VAL	6
1	A	77	ASN	6
1	A	100	LYS	6
1	A	121	MET	6
1	A	30	ILE	6
1	A	54	SER	6
1	A	51	PHE	6
1	A	73	THR	5
1	A	130	THR	5
1	A	14	GLU	5
1	A	48	LYS	5
1	A	27	GLN	5
1	A	78	ILE	5
1	A	108	CYS	5
1	A	45	ASN	5
1	A	82	THR	5
1	A	116	MET	5
1	A	35	SER	4
1	A	55	SER	4
1	A	12	LYS	4
1	A	107	PHE	4
1	A	71	LEU	4
1	A	53	SER	4
1	A	10	LEU	4
1	A	106	GLU	3
1	A	76	MET	3
1	A	41	GLU	3
1	A	28	ASP	3
1	A	85	GLU	3
1	A	115	THR	3
1	A	31	LYS	3
1	A	57	MET	3
1	A	2	VAL	3
1	A	104	THR	3
1	A	110	LYS	3
1	A	40	TYR	3
1	A	112	PHE	3
1	A	4	LEU	3
1	A	102	THR	2
1	A	20	LEU	2

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Mol	Chain	Res	Type	Models (Total)
1	A	69	GLU	2
1	A	80	SER	2
1	A	34	ASN	2
1	A	52	LYS	2
1	A	89	LEU	2
1	A	117	CYS	2
1	A	32	LYS	2
1	A	81	PHE	2
1	A	29	SER	2
1	A	120	ASP	2
1	A	23	LEU	2
1	A	75	ASN	2
1	A	13	ASN	2
1	A	63	VAL	2
1	A	18	GLU	2
1	A	43	ILE	2
1	A	74	VAL	2
1	A	11	GLU	2
1	A	62	ILE	2
1	A	66	GLU	2
1	A	16	PHE	1
1	A	96	PRO	1
1	A	15	ASN	1
1	A	87	SER	1
1	A	9	LYS	1
1	A	105	TYR	1
1	A	122	VAL	1
1	A	17	GLU	1
1	A	127	PHE	1
1	A	92	ASN	1
1	A	61	LEU	1
1	A	47	ASN	1
1	A	103	ARG	1
1	A	97	ASP	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 86% for the well-defined parts and 85% for the entire structure.

7.1 Chemical shift list 1

File name: 2n93_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	1501
Number of shifts mapped to atoms	1501
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	130	-0.31 ± 0.08	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	119	-0.07 ± 0.12	None needed (< 0.5 ppm)
$^{13}\text{C}'$	130	0.08 ± 0.13	None needed (< 0.5 ppm)
^{15}N	124	-0.98 ± 0.38	Should be applied

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 86%, i.e. 1335 atoms were assigned a chemical shift out of a possible 1558. 0 out of 23 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	635/639 (99%)	253/255 (99%)	258/258 (100%)	124/126 (98%)
Sidechain	686/816 (84%)	423/475 (89%)	251/305 (82%)	12/36 (33%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	14/103 (14%)	14/55 (25%)	0/48 (0%)	0/0 (—%)
Overall	1335/1558 (86%)	690/785 (88%)	509/611 (83%)	136/162 (84%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 85%, i.e. 1341 atoms were assigned a chemical shift out of a possible 1571. 0 out of 23 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	638/644 (99%)	254/257 (99%)	260/260 (100%)	124/127 (98%)
Sidechain	689/824 (84%)	425/480 (89%)	252/308 (82%)	12/36 (33%)
Aromatic	14/103 (14%)	14/55 (25%)	0/48 (0%)	0/0 (—%)
Overall	1341/1571 (85%)	693/792 (88%)	512/616 (83%)	136/163 (83%)

7.1.4 Statistically unusual chemical shifts ⓘ

There are no statistically unusual chemical shifts.

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:

