



Full wwPDB NMR Structure Validation Report ⓘ

Feb 14, 2022 – 08:31 AM EST

PDB ID : 1IVT
Title : NMR structures of the C-terminal globular domain of human lamin A/C
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Deposited on : 2002-03-29

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<https://www.wwpdb.org/validation/2017/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:

MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
ShiftChecker : 2.26
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.26

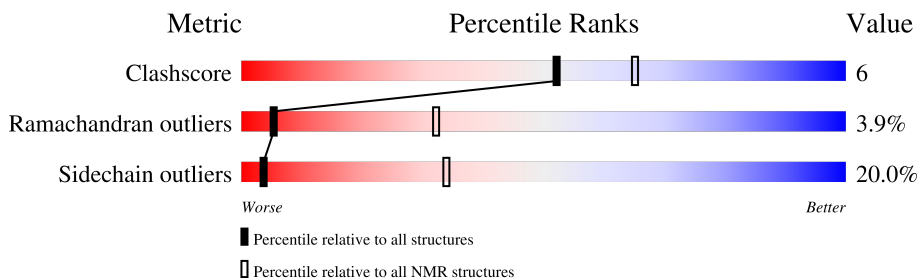
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment was not calculated.

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	158937	12864
Ramachandran outliers	154571	11451
Sidechain outliers	154315	11428

The table below summarises the geometric issues observed across the polymeric chains and their fit to the experimental data. The red, orange, yellow and green segments indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A cyan segment indicates the fraction of residues that are not part of the well-defined cores, and a grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	122	

2 Ensemble composition and analysis i

This entry contains 15 models. Model 5 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:434-A:446, A:451-A:472, A:477-A:517, A:527-A:543 (93)	0.27	5

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 3 clusters and 5 single-model clusters were found.

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

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 1886 atoms, of which 937 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Lamin A/C.

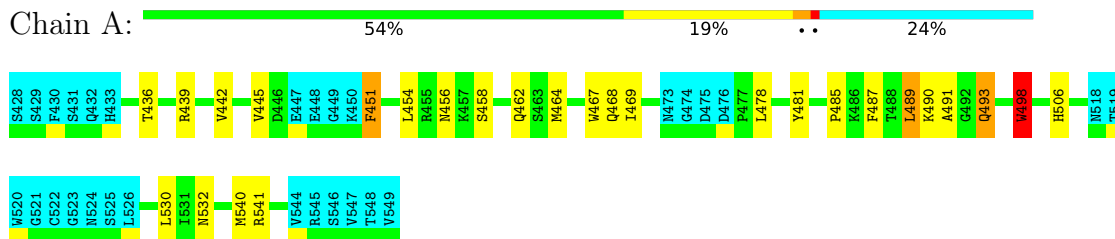
Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	122	1886	589	937	177	180	3	0

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: Lamin A/C

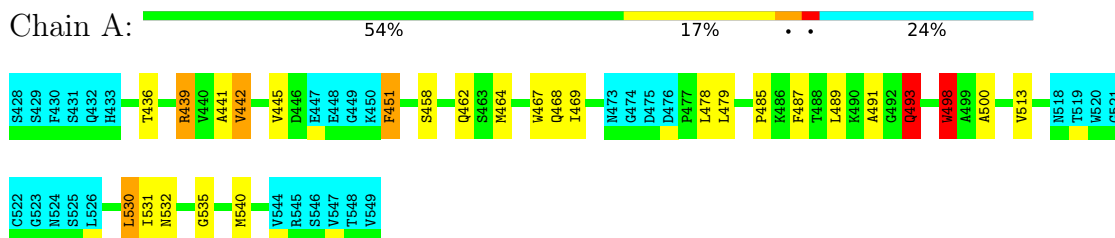


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

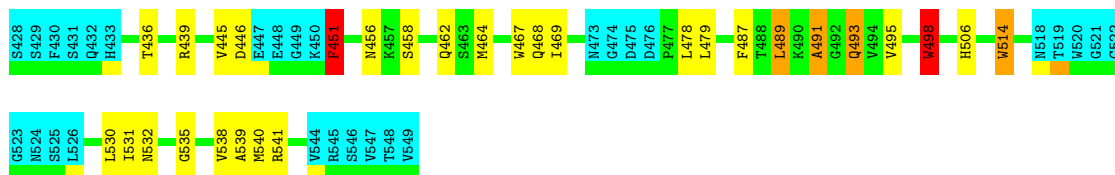
- Molecule 1: Lamin A/C



4.2.2 Score per residue for model 2

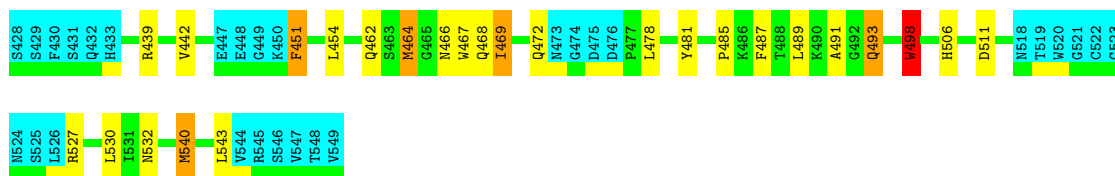
- Molecule 1: Lamin A/C





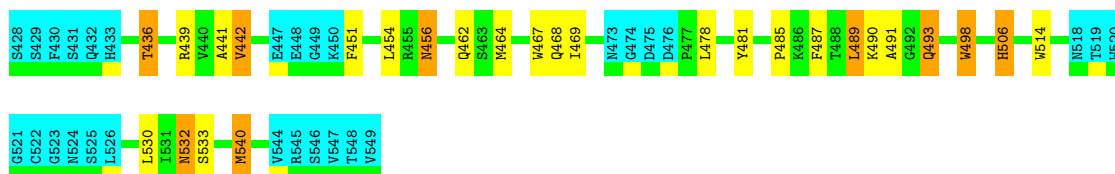
4.2.3 Score per residue for model 3

- Molecule 1: Lamin A/C



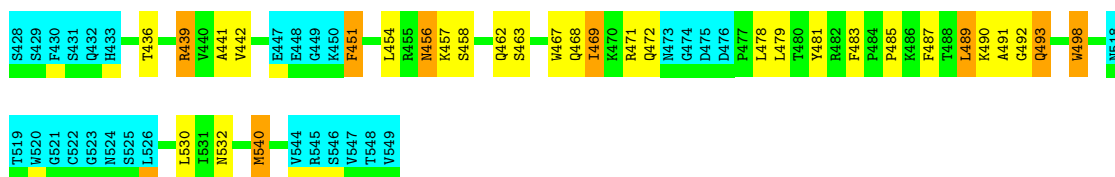
4.2.4 Score per residue for model 4

- Molecule 1: Lamin A/C



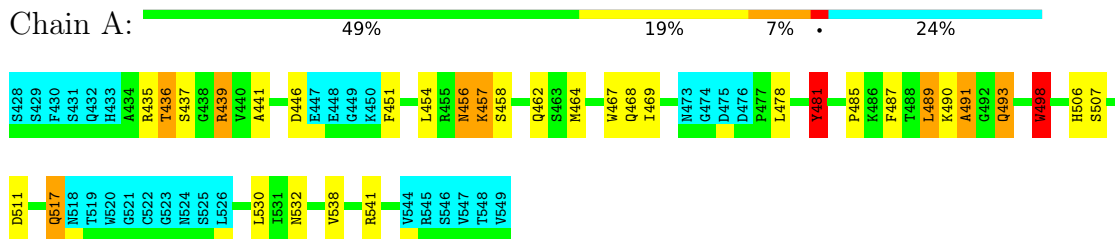
4.2.5 Score per residue for model 5 (medoid)

- Molecule 1: Lamin A/C



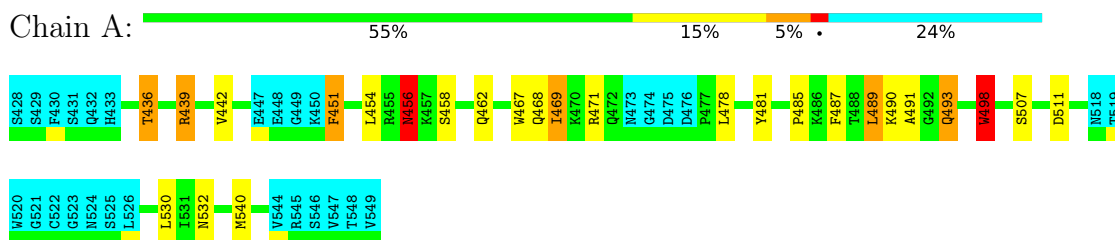
4.2.6 Score per residue for model 6

- Molecule 1: Lamin A/C



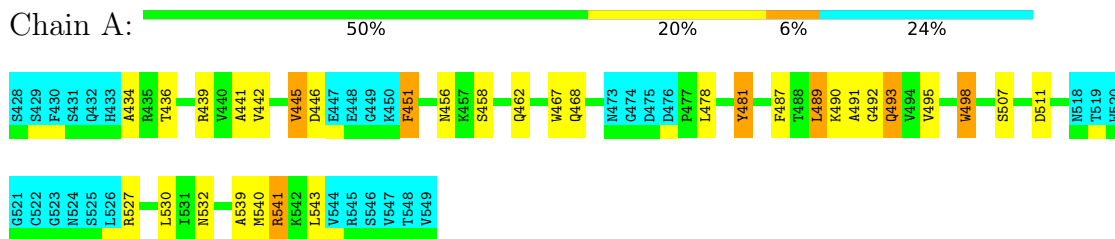
4.2.7 Score per residue for model 7

- Molecule 1: Lamin A/C



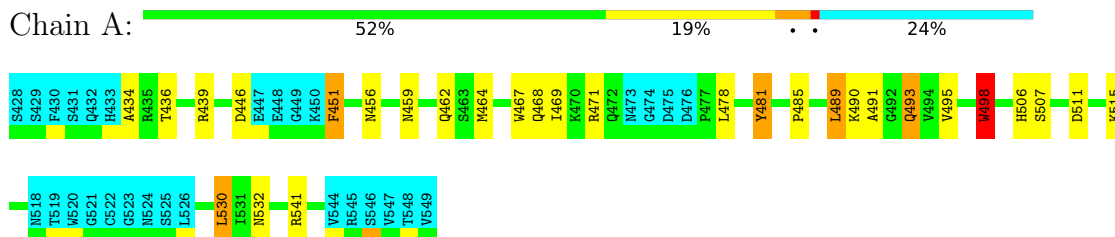
4.2.8 Score per residue for model 8

- Molecule 1: Lamin A/C



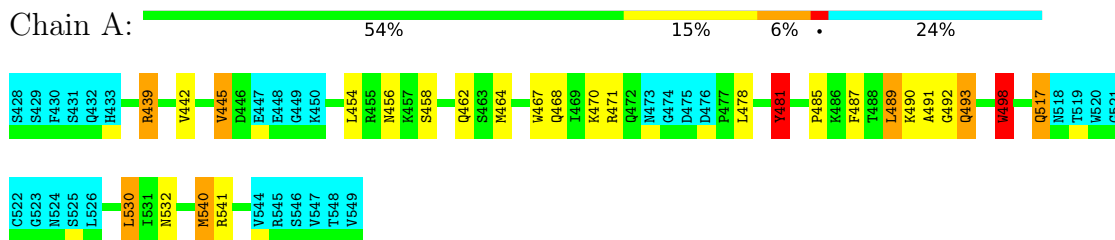
4.2.9 Score per residue for model 9

- Molecule 1: Lamin A/C



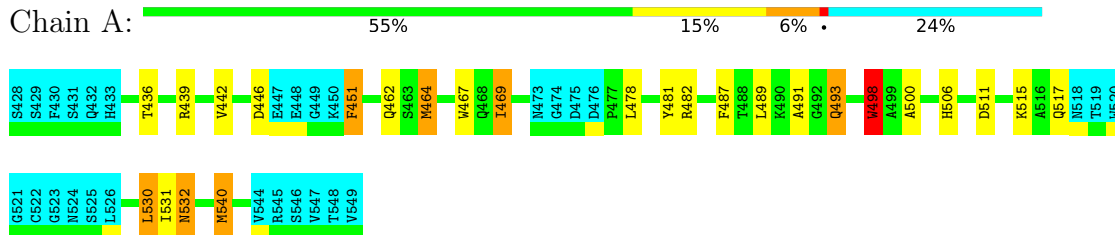
4.2.10 Score per residue for model 10

- Molecule 1: Lamin A/C



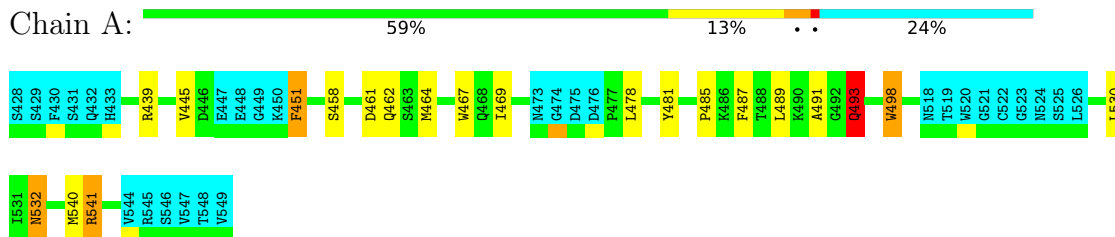
4.2.11 Score per residue for model 11

- Molecule 1: Lamin A/C



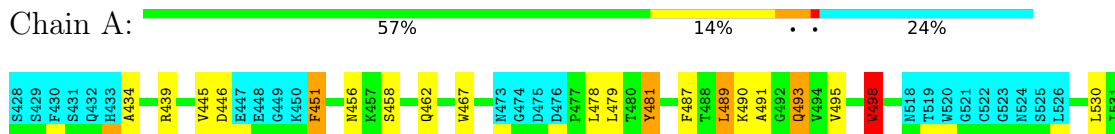
4.2.12 Score per residue for model 12

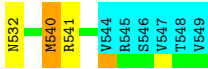
- Molecule 1: Lamin A/C



4.2.13 Score per residue for model 13

- Molecule 1: Lamin A/C

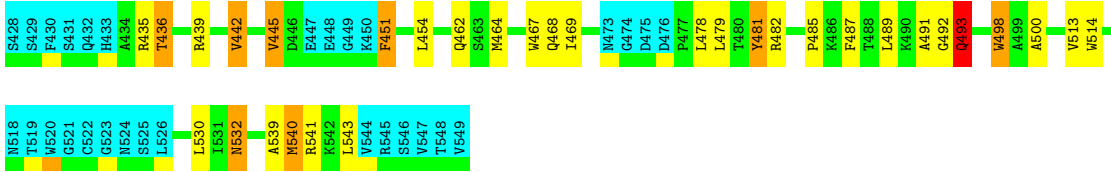




4.2.14 Score per residue for model 14

- Molecule 1: Lamin A/C

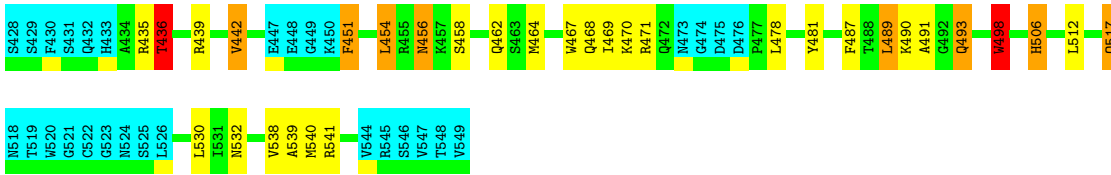
Chain A: 50% 19% 7% 24%



4.2.15 Score per residue for model 15

- Molecule 1: Lamin A/C

Chain A: 50% 18% 7% 24%



5 Refinement protocol and experimental data overview

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

Of the 500 calculated structures, 15 were deposited, based on the following criterion: *structures with acceptable covalent geometry, structures with favorable non-bond energy, structures with the least restraint violations, structures with the lowest energy*.

The authors did not provide any information on software used for structure solution, optimization or refinement.

No chemical shift data was provided.

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	1.06±0.01	0±0/748 (0.0± 0.0%)	1.60±0.03	8±2/1014 (0.8± 0.2%)
All	All	1.06	0/11220 (0.0%)	1.60	124/15210 (0.8%)

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	0.9±0.7
All	All	0	14

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	481	TYR	CB-CG-CD2	-10.55	114.67	121.00	14	7
1	A	481	TYR	CB-CG-CD1	10.03	127.02	121.00	14	8
1	A	458	SER	N-CA-CB	7.28	121.41	110.50	8	10
1	A	468	GLN	N-CA-CB	6.43	122.18	110.60	10	12
1	A	493	GLN	N-CA-CB	6.20	121.76	110.60	14	4
1	A	451	PHE	N-CA-CB	6.15	121.66	110.60	13	8
1	A	540	MET	CA-CB-CG	6.13	123.72	113.30	4	6
1	A	487	PHE	CB-CG-CD1	6.12	125.08	120.80	4	7
1	A	454	LEU	CB-CG-CD1	6.08	121.33	111.00	7	4
1	A	479	LEU	N-CA-CB	-6.06	98.28	110.40	5	4
1	A	487	PHE	CB-CG-CD2	-6.04	116.57	120.80	4	13
1	A	436	THR	CA-CB-CG2	-5.99	104.02	112.40	9	5
1	A	492	GLY	N-CA-C	5.77	127.53	113.10	14	2
1	A	470	LYS	N-CA-CB	-5.68	100.38	110.60	15	1
1	A	436	THR	CA-CB-OG1	5.67	120.90	109.00	15	3

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	442	VAL	CG1-CB-CG2	-5.67	101.84	110.90	4	1
1	A	514	TRP	CB-CG-CD1	-5.58	119.75	127.00	2	1
1	A	517	GLN	N-CA-C	-5.49	96.17	111.00	15	3
1	A	491	ALA	C-N-CA	5.48	133.81	122.30	6	2
1	A	498	TRP	N-CA-C	5.46	125.75	111.00	13	5
1	A	464	MET	N-CA-CB	5.46	120.43	110.60	4	3
1	A	506	HIS	CA-CB-CG	5.46	122.88	113.60	15	2
1	A	514	TRP	CB-CG-CD2	5.40	133.62	126.60	2	1
1	A	434	ALA	CB-CA-C	5.34	118.11	110.10	8	2
1	A	533	SER	N-CA-CB	-5.31	102.53	110.50	4	1
1	A	539	ALA	N-CA-CB	5.16	117.33	110.10	14	1
1	A	539	ALA	CB-CA-C	5.14	117.81	110.10	8	1
1	A	456	ASN	CA-CB-CG	5.13	124.69	113.40	4	1
1	A	493	GLN	CA-CB-CG	5.13	124.69	113.40	14	1
1	A	454	LEU	CB-CA-C	5.13	119.95	110.20	4	1
1	A	456	ASN	CB-CA-C	5.12	120.64	110.40	7	1
1	A	454	LEU	N-CA-CB	-5.12	100.17	110.40	4	1
1	A	540	MET	CG-SD-CE	-5.09	92.06	100.20	14	1
1	A	479	LEU	CB-CG-CD2	-5.01	102.48	111.00	5	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	451	PHE	Sidechain	5
1	A	481	TYR	Sidechain	5
1	A	541	ARG	Sidechain	2
1	A	487	PHE	Sidechain	1
1	A	483	PHE	Sidechain	1

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	732	745	745	8±2

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Mol	Chain	Non-H	H(model)	H(added)	Clashes
All	All	10980	11175	11175	127

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:456:ASN:HB2	1:A:489:LEU:HD11	0.77	1.56	10	8
1:A:489:LEU:HD13	1:A:493:GLN:NE2	0.77	1.95	8	10
1:A:456:ASN:CB	1:A:489:LEU:HD11	0.73	2.13	5	9
1:A:467:TRP:CD2	1:A:530:LEU:HD21	0.67	2.25	1	10
1:A:456:ASN:HB3	1:A:489:LEU:HD11	0.64	1.70	6	3
1:A:489:LEU:CD1	1:A:493:GLN:HE22	0.64	2.06	11	2
1:A:467:TRP:CE2	1:A:530:LEU:HD11	0.57	2.35	3	7
1:A:469:ILE:HG13	1:A:530:LEU:HD23	0.55	1.76	12	1
1:A:469:ILE:HD12	1:A:530:LEU:HD23	0.53	1.80	11	4
1:A:489:LEU:HD12	1:A:493:GLN:HE22	0.53	1.63	14	2
1:A:498:TRP:HA	1:A:498:TRP:CE3	0.53	2.39	7	11
1:A:489:LEU:HD12	1:A:490:LYS:N	0.50	2.21	5	9
1:A:436:THR:HG22	1:A:441:ALA:HA	0.50	1.84	1	4
1:A:469:ILE:HD13	1:A:530:LEU:HD23	0.50	1.83	9	5
1:A:464:MET:HB3	1:A:467:TRP:CD2	0.48	2.44	3	1
1:A:464:MET:HG2	1:A:467:TRP:CE2	0.47	2.44	12	3
1:A:467:TRP:CZ2	1:A:530:LEU:HD11	0.47	2.44	12	4
1:A:493:GLN:C	1:A:493:GLN:HE21	0.46	2.14	2	2
1:A:442:VAL:CG1	1:A:445:VAL:HG13	0.45	2.41	8	2
1:A:464:MET:SD	1:A:489:LEU:HD13	0.44	2.52	3	3
1:A:442:VAL:HG12	1:A:445:VAL:HG13	0.44	1.88	14	1
1:A:500:ALA:HB2	1:A:514:TRP:O	0.43	2.12	14	1
1:A:538:VAL:HG23	1:A:539:ALA:H	0.43	1.73	2	2
1:A:489:LEU:HD12	1:A:493:GLN:NE2	0.42	2.29	14	1
1:A:493:GLN:HE21	1:A:493:GLN:CA	0.42	2.27	12	1
1:A:435:ARG:HE	1:A:436:THR:H	0.42	1.57	15	2
1:A:442:VAL:HG12	1:A:445:VAL:CG1	0.42	2.43	1	1
1:A:530:LEU:HD22	1:A:531:ILE:N	0.42	2.29	11	1
1:A:467:TRP:CE3	1:A:530:LEU:HD21	0.42	2.49	12	6
1:A:437:SER:N	1:A:538:VAL:O	0.42	2.52	6	1
1:A:531:ILE:CG2	1:A:535:GLY:HA2	0.41	2.45	1	2
1:A:442:VAL:HA	1:A:454:LEU:HD23	0.41	1.92	15	1
1:A:493:GLN:HE21	1:A:493:GLN:C	0.41	2.19	12	2
1:A:434:ALA:HB2	1:A:541:ARG:HE	0.41	1.76	9	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:498:TRP:CE3	1:A:498:TRP:HA	0.41	2.51	15	1
1:A:441:ALA:HB2	1:A:457:LYS:HB2	0.41	1.92	6	1
1:A:456:ASN:O	1:A:492:GLY:HA2	0.41	2.16	10	2

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	93/122 (76%)	80±2 (86±2%)	10±3 (10±3%)	4±1 (4±1%)	5	32
All	All	1395/1830 (76%)	1198 (86%)	143 (10%)	54 (4%)	5	32

All 6 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	491	ALA	15
1	A	532	ASN	13
1	A	485	PRO	10
1	A	498	TRP	8
1	A	439	ARG	6
1	A	500	ALA	2

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	77/102 (75%)	62±3 (80±4%)	15±3 (20±4%)	4	34
All	All	1155/1530 (75%)	924 (80%)	231 (20%)	4	34

All 42 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	462	GLN	15
1	A	478	LEU	15
1	A	493	GLN	15
1	A	498	TRP	15
1	A	439	ARG	14
1	A	451	PHE	14
1	A	540	MET	13
1	A	489	LEU	10
1	A	442	VAL	8
1	A	541	ARG	8
1	A	481	TYR	8
1	A	506	HIS	7
1	A	445	VAL	6
1	A	446	ASP	6
1	A	469	ILE	6
1	A	511	ASP	6
1	A	532	ASN	6
1	A	464	MET	5
1	A	471	ARG	5
1	A	530	LEU	4
1	A	495	VAL	4
1	A	456	ASN	4
1	A	507	SER	4
1	A	454	LEU	3
1	A	436	THR	3
1	A	517	GLN	3
1	A	513	VAL	2
1	A	514	TRP	2
1	A	472	GLN	2
1	A	527	ARG	2
1	A	543	LEU	2
1	A	457	LYS	2
1	A	515	LYS	2
1	A	482	ARG	2
1	A	466	ASN	1
1	A	463	SER	1
1	A	435	ARG	1
1	A	459	ASN	1
1	A	470	LYS	1
1	A	461	ASP	1
1	A	479	LEU	1

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Mol	Chain	Res	Type	Models (Total)
1	A	512	LEU	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 monosaccharides 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

No chemical shift data were provided