



Full wwPDB NMR Structure Validation Report ⓘ

Mar 9, 2026 – 05:26 AM UTC

PDB ID : 6XXU / pdb_00006xxu
BMRB ID : 28028
Title : Solution NMR structure of the native form of UbcH7 (UBE2L3)
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Deposited on : 2020-01-28

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

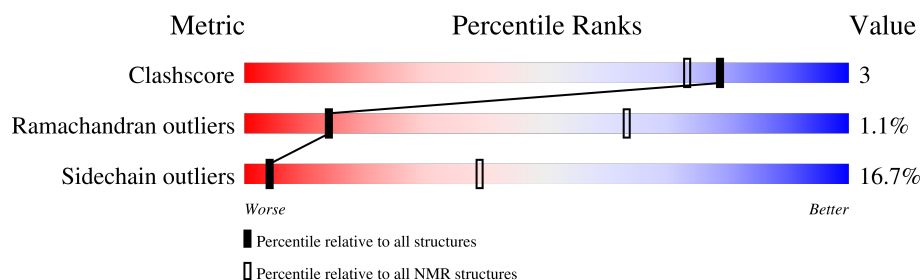
1 Overall quality at a glance

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	154	

2 Ensemble composition and analysis

This entry contains 21 models. Model 1 is the overall representative, medoid model (most similar to other models).

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:3-A:151 (149)	0.26	1

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 1 clusters. No single-model clusters were found.

Cluster number	Models
1	1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21

3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 2529 atoms, of which 1271 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Ubiquitin-conjugating enzyme E2 L3.

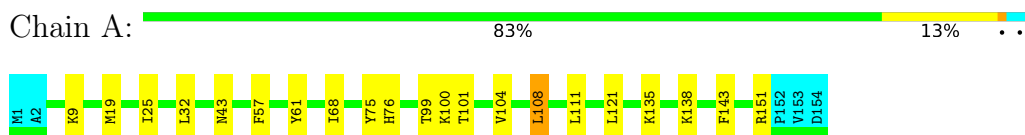
Mol	Chain	Residues	Atoms						Trace
1	A	154	Total	C	H	N	O	S	0
			2529	804	1271	217	231	6	

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: Ubiquitin-conjugating enzyme E2 L3

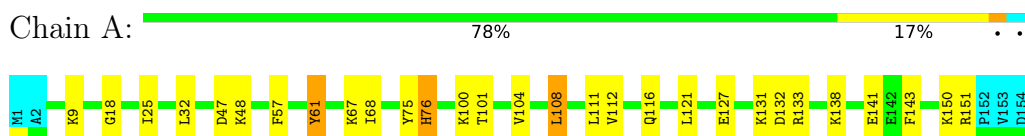


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

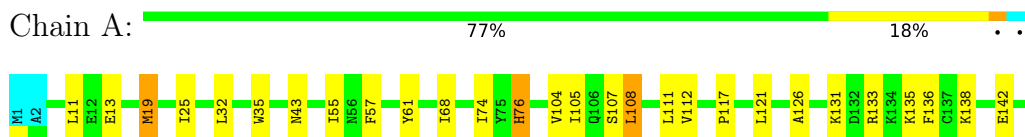
4.2.1 Score per residue for model 1 (medoid)

- Molecule 1: Ubiquitin-conjugating enzyme E2 L3



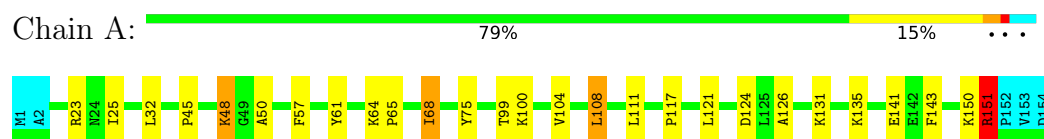
4.2.2 Score per residue for model 2

- Molecule 1: Ubiquitin-conjugating enzyme E2 L3



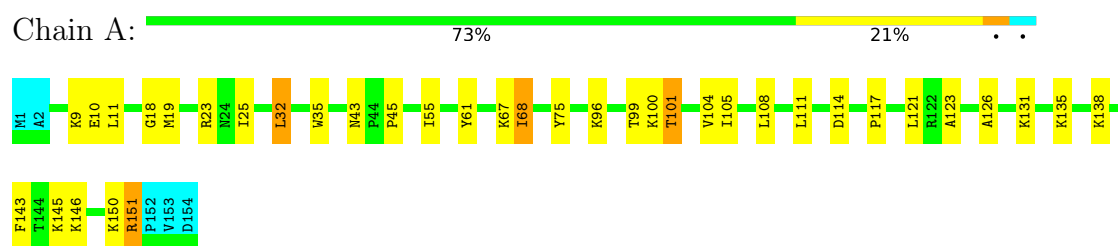
4.2.3 Score per residue for model 3

- Molecule 1: Ubiquitin-conjugating enzyme E2 L3



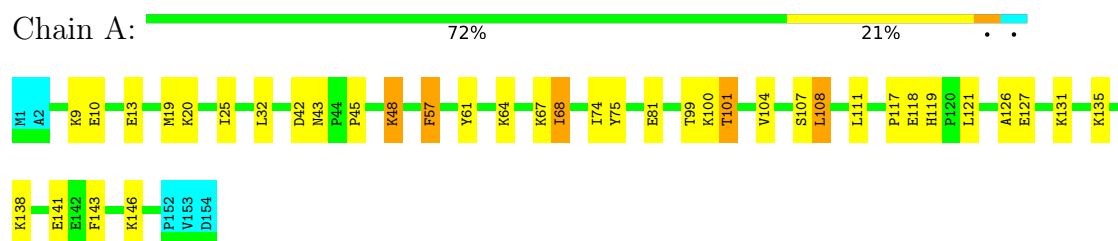
4.2.4 Score per residue for model 4

- Molecule 1: Ubiquitin-conjugating enzyme E2 L3



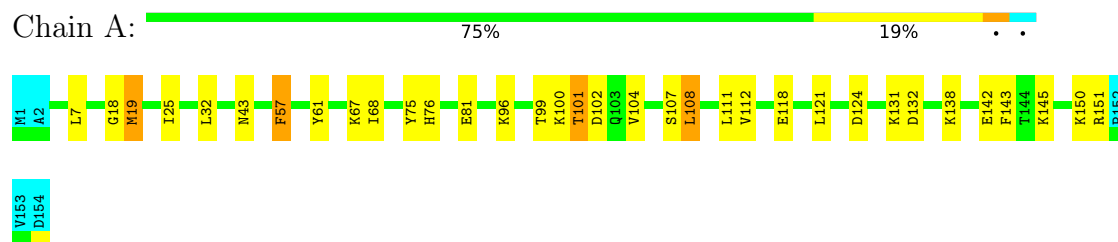
4.2.5 Score per residue for model 5

- Molecule 1: Ubiquitin-conjugating enzyme E2 L3



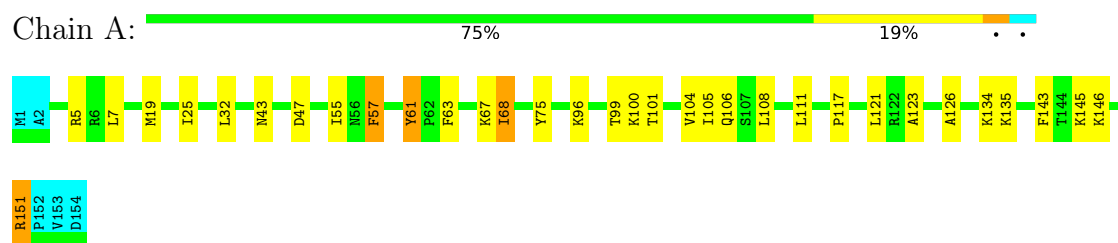
4.2.6 Score per residue for model 6

- Molecule 1: Ubiquitin-conjugating enzyme E2 L3



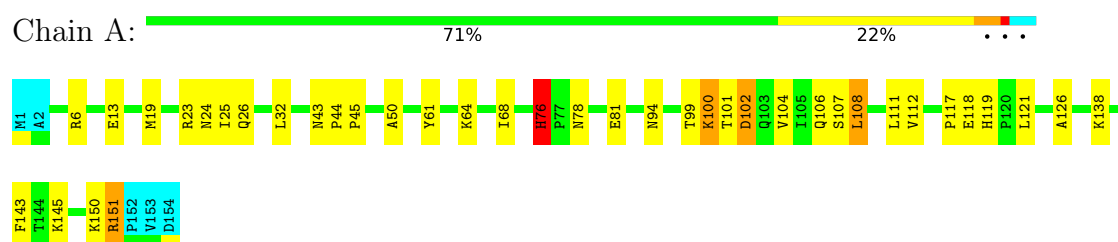
4.2.7 Score per residue for model 7

- Molecule 1: Ubiquitin-conjugating enzyme E2 L3



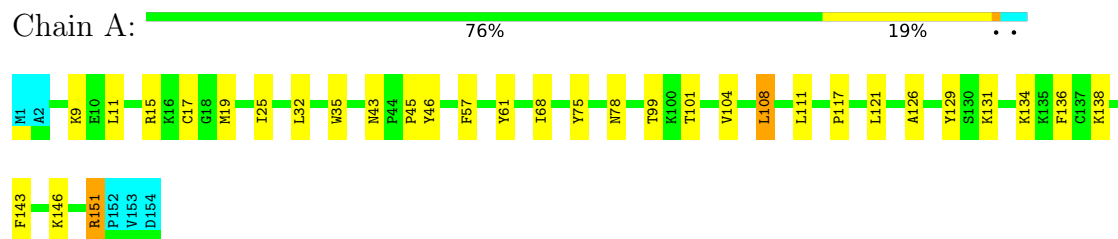
4.2.8 Score per residue for model 8

- Molecule 1: Ubiquitin-conjugating enzyme E2 L3



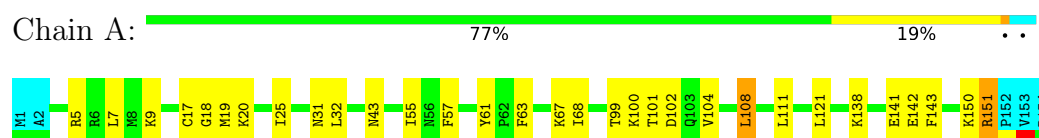
4.2.9 Score per residue for model 9

- Molecule 1: Ubiquitin-conjugating enzyme E2 L3



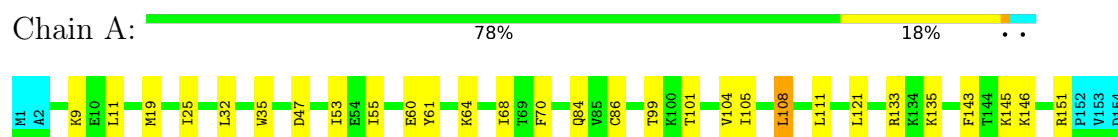
4.2.10 Score per residue for model 10

- Molecule 1: Ubiquitin-conjugating enzyme E2 L3



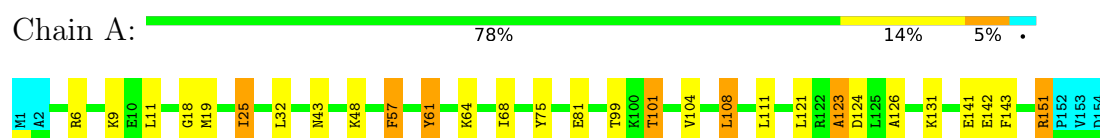
4.2.11 Score per residue for model 11

- Molecule 1: Ubiquitin-conjugating enzyme E2 L3



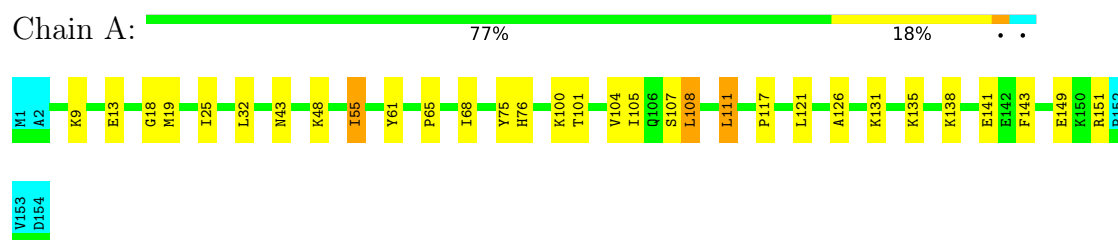
4.2.12 Score per residue for model 12

- Molecule 1: Ubiquitin-conjugating enzyme E2 L3



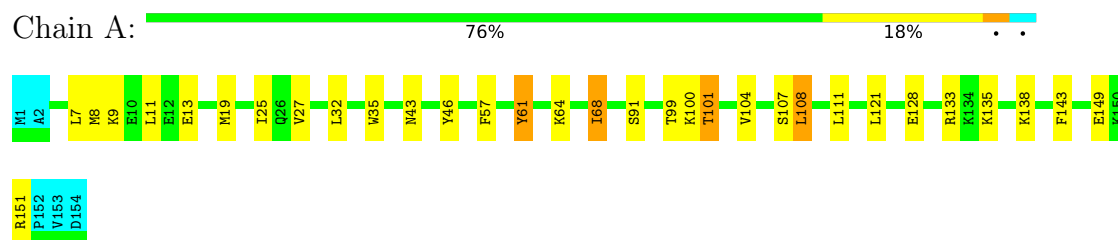
4.2.13 Score per residue for model 13

- Molecule 1: Ubiquitin-conjugating enzyme E2 L3



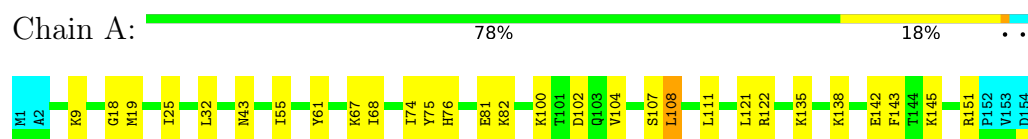
4.2.14 Score per residue for model 14

- Molecule 1: Ubiquitin-conjugating enzyme E2 L3



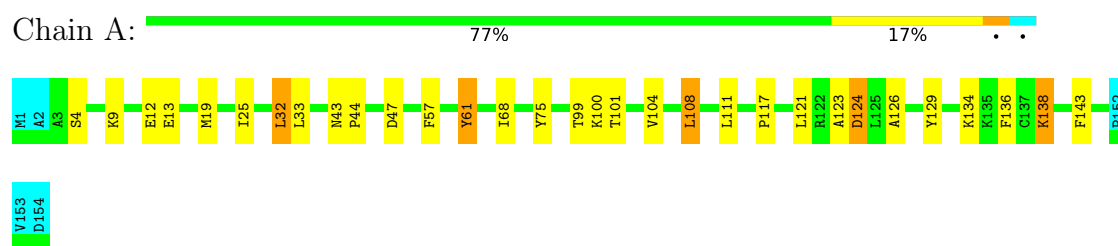
4.2.15 Score per residue for model 15

- Molecule 1: Ubiquitin-conjugating enzyme E2 L3



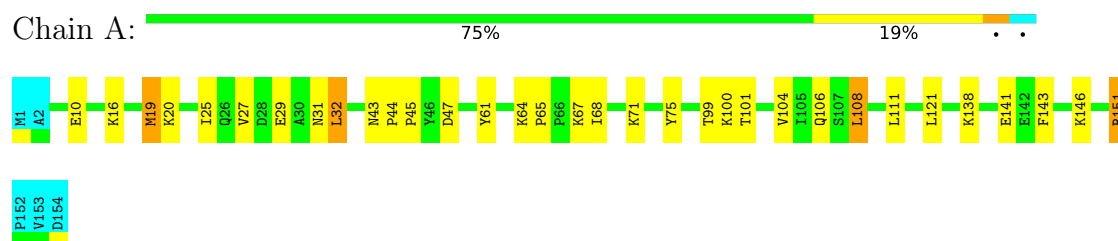
4.2.16 Score per residue for model 16

- Molecule 1: Ubiquitin-conjugating enzyme E2 L3



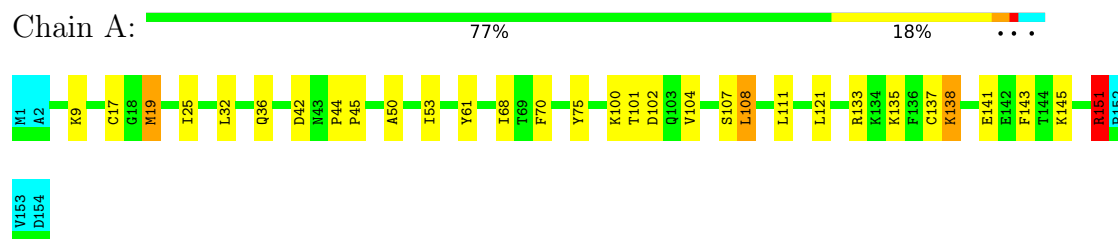
4.2.17 Score per residue for model 17

- Molecule 1: Ubiquitin-conjugating enzyme E2 L3



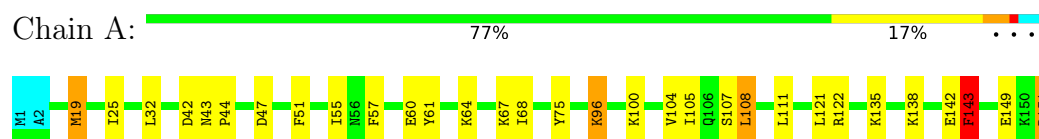
4.2.18 Score per residue for model 18

- Molecule 1: Ubiquitin-conjugating enzyme E2 L3



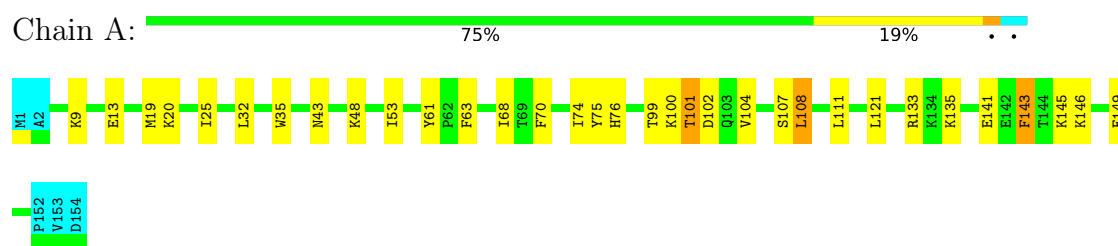
4.2.19 Score per residue for model 19

- Molecule 1: Ubiquitin-conjugating enzyme E2 L3



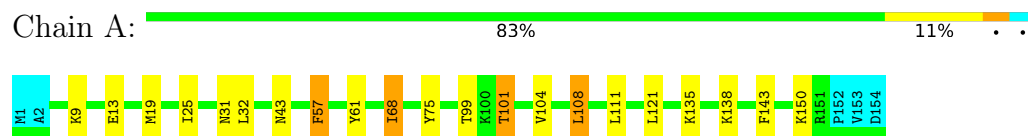
4.2.20 Score per residue for model 20

- Molecule 1: Ubiquitin-conjugating enzyme E2 L3



4.2.21 Score per residue for model 21

- Molecule 1: Ubiquitin-conjugating enzyme E2 L3



5 Refinement protocol and experimental data overview

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

Of the 21 calculated structures, 21 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
DYANA	structure calculation	
Amber	refinement	5.0

The following table shows chemical shift validation statistics as aggregates over all chemical shift files. Detailed validation can be found in section 7 of this report.

Chemical shift file(s)	working_cs.cif
Number of chemical shift lists	1
Total number of shifts	1957
Number of shifts mapped to atoms	1957
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	90%

6 Model quality

6.1 Standard geometry

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	0.64±0.01	0±0/1253 (0.0± 0.0%)	1.22±0.02	2±2/1694 (0.1± 0.1%)
All	All	0.64	0/26313 (0.0%)	1.22	37/35574 (0.1%)

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	0.7±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	76	HIS	CB-CG-CD2	-6.20	123.14	131.20	8	7
1	A	44	PRO	CA-C-N	6.02	127.37	119.84	8	5
1	A	44	PRO	C-N-CA	6.02	127.37	119.84	8	5
1	A	65	PRO	CA-C-N	5.94	125.91	120.21	3	3
1	A	65	PRO	C-N-CA	5.94	125.91	120.21	3	3
1	A	123	ALA	CA-C-N	5.75	128.78	120.79	16	2
1	A	123	ALA	C-N-CA	5.75	128.78	120.79	16	2
1	A	132	ASP	CA-CB-CG	-5.47	107.13	112.60	1	2
1	A	76	HIS	CA-C-N	5.37	124.99	119.56	8	1
1	A	76	HIS	C-N-CA	5.37	124.99	119.56	8	1
1	A	112	VAL	CA-C-N	5.30	127.84	120.63	6	1
1	A	112	VAL	C-N-CA	5.30	127.84	120.63	6	1
1	A	6	ARG	CA-C-N	5.25	127.32	120.28	12	1
1	A	6	ARG	C-N-CA	5.25	127.32	120.28	12	1
1	A	124	ASP	CA-CB-CG	5.18	117.78	112.60	16	1

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	31	ASN	CA-CB-CG	5.02	117.62	112.60	21	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	151	ARG	Sidechain	9
1	A	46	TYR	Sidechain	2
1	A	6	ARG	Sidechain	1
1	A	23	ARG	Sidechain	1
1	A	143	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	1222	1235	1234	7±2
All	All	25662	25935	25914	145

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 3.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:68:ILE:HD13	1:A:108:LEU:HD21	0.71	1.63	20	21
1:A:55:ILE:HD11	1:A:105:ILE:HD11	0.59	1.74	7	6
1:A:68:ILE:CD1	1:A:108:LEU:HD21	0.59	2.27	9	5
1:A:32:LEU:C	1:A:32:LEU:HD12	0.58	2.22	16	1
1:A:4:SER:HA	1:A:32:LEU:HD11	0.56	1.75	16	1
1:A:7:LEU:HD21	1:A:57:PHE:CD1	0.56	2.35	7	3
1:A:48:LYS:HE3	1:A:141:GLU:CG	0.55	2.31	1	1
1:A:68:ILE:HD11	1:A:104:VAL:HG13	0.55	1.77	11	21
1:A:11:LEU:HD12	1:A:35:TRP:CE3	0.51	2.40	4	5
1:A:68:ILE:HD11	1:A:104:VAL:CG1	0.51	2.35	19	6

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:50:ALA:HB2	1:A:151:ARG:HB3	0.51	1.83	18	3
1:A:35:TRP:CE2	1:A:101:THR:HG21	0.50	2.41	20	2
1:A:57:PHE:CE1	1:A:101:THR:HG23	0.50	2.41	21	3
1:A:57:PHE:CE2	1:A:101:THR:HG23	0.50	2.41	14	3
1:A:76:HIS:CE1	1:A:112:VAL:HG13	0.49	2.42	2	3
1:A:48:LYS:HE2	1:A:141:GLU:OE1	0.49	2.07	5	1
1:A:117:PRO:CB	1:A:126:ALA:HB1	0.49	2.37	16	4
1:A:32:LEU:HD12	1:A:32:LEU:O	0.48	2.09	4	1
1:A:117:PRO:HB3	1:A:126:ALA:HB1	0.48	1.86	2	7
1:A:74:ILE:HD12	1:A:74:ILE:O	0.47	2.09	5	2
1:A:100:LYS:HE3	1:A:102:ASP:OD2	0.47	2.10	8	1
1:A:143:PHE:C	1:A:143:PHE:CD1	0.46	2.93	19	2
1:A:7:LEU:HD21	1:A:57:PHE:CD2	0.46	2.45	6	1
1:A:61:TYR:CD2	1:A:61:TYR:C	0.45	2.94	16	4
1:A:48:LYS:HE3	1:A:141:GLU:OE1	0.44	2.13	13	1
1:A:129:TYR:CZ	1:A:136:PHE:CD1	0.44	3.05	9	2
1:A:48:LYS:CE	1:A:141:GLU:OE1	0.44	2.66	3	4
1:A:127:GLU:OE1	1:A:131:LYS:NZ	0.44	2.51	1	2
1:A:53:ILE:HG22	1:A:70:PHE:CG	0.44	2.48	11	3
1:A:104:VAL:O	1:A:108:LEU:HD22	0.43	2.13	7	4
1:A:11:LEU:HD12	1:A:35:TRP:CZ3	0.43	2.49	11	2
1:A:51:PHE:CZ	1:A:143:PHE:CZ	0.43	3.06	19	1
1:A:138:LYS:HE2	1:A:141:GLU:OE2	0.43	2.13	17	1
1:A:27:VAL:HG22	1:A:32:LEU:HA	0.43	1.91	17	1
1:A:74:ILE:C	1:A:74:ILE:HD12	0.42	2.39	2	1
1:A:123:ALA:O	1:A:126:ALA:HB3	0.42	2.14	7	3
1:A:61:TYR:CD1	1:A:61:TYR:C	0.42	2.97	7	1
1:A:86:CYS:H	1:A:121:LEU:HD11	0.42	1.74	11	1
1:A:138:LYS:HA	1:A:138:LYS:HE2	0.42	1.91	8	1
1:A:96:LYS:N	1:A:96:LYS:CD	0.42	2.83	19	1
1:A:11:LEU:HD21	1:A:25:ILE:CG2	0.42	2.45	12	1
1:A:74:ILE:HA	1:A:143:PHE:CZ	0.42	2.50	20	1
1:A:57:PHE:CD1	1:A:101:THR:HG23	0.42	2.50	12	1
1:A:107:SER:O	1:A:111:LEU:HD22	0.41	2.14	13	1
1:A:4:SER:CA	1:A:32:LEU:HD11	0.41	2.43	16	1
1:A:136:PHE:CD1	1:A:136:PHE:C	0.41	2.99	9	1
1:A:138:LYS:HE3	1:A:138:LYS:N	0.40	2.30	16	1
1:A:10:GLU:OE1	1:A:100:LYS:HE2	0.40	2.16	5	1
1:A:138:LYS:CE	1:A:141:GLU:OE2	0.40	2.69	18	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	149/154 (97%)	136±2 (91±1%)	12±2 (8±1%)	2±1 (1±0%)	14	63
All	All	3129/3234 (97%)	2852 (91%)	242 (8%)	35 (1%)	14	63

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	19	MET	18
1	A	18	GLY	7
1	A	45	PRO	7
1	A	60	GLU	2
1	A	47	ASP	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	134/138 (97%)	112±3 (83±2%)	22±3 (17±2%)	4	39
All	All	2814/2898 (97%)	2344 (83%)	470 (17%)	4	39

All 73 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	25	ILE	21
1	A	32	LEU	21
1	A	61	TYR	21
1	A	111	LEU	21
1	A	121	LEU	20

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Mol	Chain	Res	Type	Models (Total)
1	A	143	PHE	20
1	A	108	LEU	19
1	A	151	ARG	17
1	A	43	ASN	17
1	A	75	TYR	16
1	A	101	THR	16
1	A	100	LYS	15
1	A	99	THR	15
1	A	9	LYS	14
1	A	138	LYS	14
1	A	135	LYS	13
1	A	57	PHE	11
1	A	67	LYS	9
1	A	107	SER	9
1	A	13	GLU	8
1	A	146	LYS	8
1	A	64	LYS	8
1	A	145	LYS	8
1	A	150	LYS	7
1	A	131	LYS	7
1	A	133	ARG	6
1	A	19	MET	6
1	A	142	GLU	6
1	A	68	ILE	6
1	A	102	ASP	6
1	A	47	ASP	5
1	A	81	GLU	5
1	A	124	ASP	4
1	A	96	LYS	4
1	A	20	LYS	4
1	A	149	GLU	4
1	A	42	ASP	3
1	A	118	GLU	3
1	A	63	PHE	3
1	A	106	GLN	3
1	A	134	LYS	3
1	A	17	CYS	3
1	A	55	ILE	3
1	A	23	ARG	2
1	A	48	LYS	2
1	A	10	GLU	2
1	A	119	HIS	2

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Mol	Chain	Res	Type	Models (Total)
1	A	5	ARG	2
1	A	78	ASN	2
1	A	31	ASN	2
1	A	122	ARG	2
1	A	116	GLN	1
1	A	136	PHE	1
1	A	114	ASP	1
1	A	24	ASN	1
1	A	26	GLN	1
1	A	76	HIS	1
1	A	94	ASN	1
1	A	15	ARG	1
1	A	141	GLU	1
1	A	84	GLN	1
1	A	8	MET	1
1	A	27	VAL	1
1	A	91	SER	1
1	A	128	GLU	1
1	A	82	LYS	1
1	A	12	GLU	1
1	A	33	LEU	1
1	A	16	LYS	1
1	A	29	GLU	1
1	A	71	LYS	1
1	A	36	GLN	1
1	A	137	CYS	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 ⓘ

There are no oligosaccharides in this entry.

6.6 Ligand geometry

There are no ligands in this entry.

6.7 Other polymers

There are no such molecules in this entry.

6.8 Polymer linkage issues

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	1957
Number of shifts mapped to atoms	1957
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	8

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	154	-0.22 ± 0.11	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	149	0.17 ± 0.09	None needed (< 0.5 ppm)
$^{13}\text{C}'$	148	0.13 ± 0.13	None needed (< 0.5 ppm)
^{15}N	139	-0.10 ± 0.26	None needed (< 0.5 ppm)

7.1.3 Completeness of resonance assignments

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 90%, i.e. 1904 atoms were assigned a chemical shift out of a possible 2124. 0 out of 16 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	718/724 (99%)	290/290 (100%)	292/298 (98%)	136/136 (100%)
Sidechain	1109/1246 (89%)	751/799 (94%)	343/390 (88%)	15/57 (26%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	77/154 (50%)	45/75 (60%)	29/74 (39%)	3/5 (60%)
Overall	1904/2124 (90%)	1086/1164 (93%)	664/762 (87%)	154/198 (78%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 90%, i.e. 1957 atoms were assigned a chemical shift out of a possible 2184. 0 out of 17 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	739/747 (99%)	298/299 (100%)	302/308 (98%)	139/140 (99%)
Sidechain	1141/1283 (89%)	773/824 (94%)	353/402 (88%)	15/57 (26%)
Aromatic	77/154 (50%)	45/75 (60%)	29/74 (39%)	3/5 (60%)
Overall	1957/2184 (90%)	1116/1198 (93%)	684/784 (87%)	157/202 (78%)

7.1.4 Statistically unusual chemical shifts ⓘ

The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	51	PHE	CD1	117.78	125.33 – 137.83	-11.0
1	A	49	GLY	C	187.57	164.92 – 182.89	7.6
1	A	65	PRO	HA	2.70	2.78 – 6.00	-5.2
1	A	74	ILE	HD11	-0.74	-0.72 – 2.09	-5.1
1	A	74	ILE	HD12	-0.74	-0.72 – 2.09	-5.1
1	A	74	ILE	HD13	-0.74	-0.72 – 2.09	-5.1
1	A	78	ASN	H	11.39	5.28 – 11.36	5.0
1	A	57	PHE	CD1	125.32	125.33 – 137.83	-5.0

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. 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:

