



Full wwPDB NMR Structure Validation Report ⓘ

Mar 26, 2026 – 11:19 PM UTC

PDB ID : 8ONG / pdb_00008ong
BMRB ID : 18045
Title : Structure of the endothelial monocyte activating polypeptide II (EMAP II) in solution
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Deposited on : 2023-04-02

This is a Full wwPDB NMR Structure Validation Report for a publicly released PDB entry.

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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

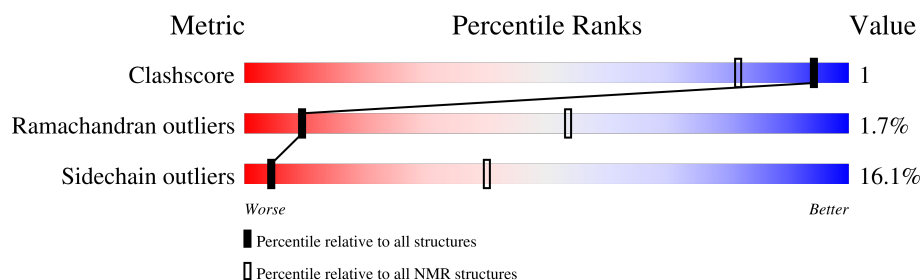
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR, SOLUTION SCATTERING

The overall completeness of chemical shifts assignment is 80%.

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	169	

2 Ensemble composition and analysis

This entry contains 19 models. Model 11 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:7-A:113, A:120-A:152, A:156-A:169 (154)	0.65	11

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. No single-model clusters were found.

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

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 2618 atoms, of which 1325 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Aminoacyl tRNA synthase complex-interacting multifunctional protein 1.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	169	2618	810	1325	226	245	12	0

There are 2 discrepancies between the modelled and reference sequences:

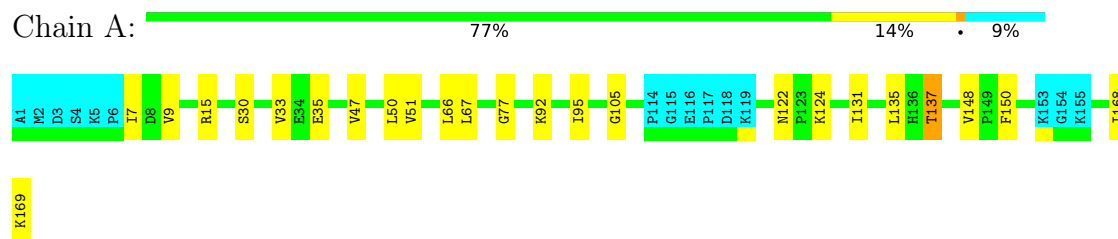
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	ALA	-	expression tag	UNP Q12904
A	2	MET	-	expression tag	UNP Q12904

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: Aminoacyl tRNA synthase complex-interacting multifunctional protein 1

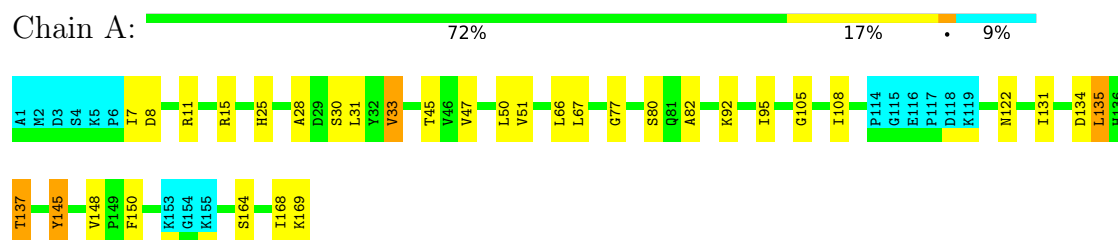


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

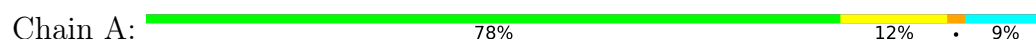
4.2.1 Score per residue for model 1

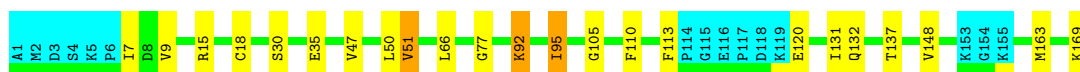
- Molecule 1: Aminoacyl tRNA synthase complex-interacting multifunctional protein 1



4.2.2 Score per residue for model 2

- Molecule 1: Aminoacyl tRNA synthase complex-interacting multifunctional protein 1





4.2.3 Score per residue for model 3

- Molecule 1: Aminoacyl tRNA synthase complex-interacting multifunctional protein 1

Chain A: 78% 11% 9%



4.2.4 Score per residue for model 4

- Molecule 1: Aminoacyl tRNA synthase complex-interacting multifunctional protein 1

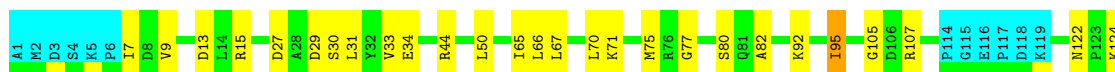
Chain A: 73% 17% 9%



4.2.5 Score per residue for model 5

- Molecule 1: Aminoacyl tRNA synthase complex-interacting multifunctional protein 1

Chain A: 69% 20% 9%



4.2.6 Score per residue for model 6

- Molecule 1: Aminoacyl tRNA synthase complex-interacting multifunctional protein 1

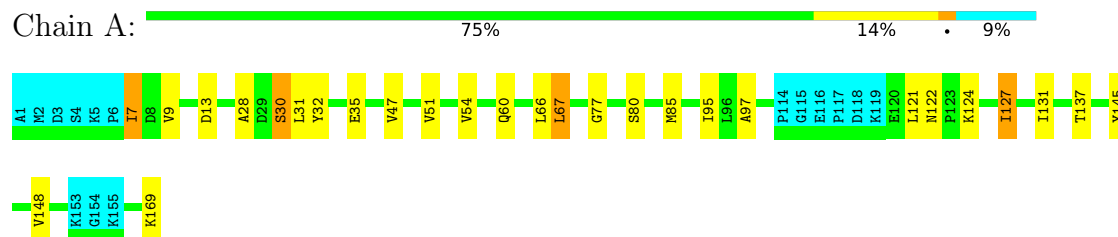
Chain A: 76% 14% 9%





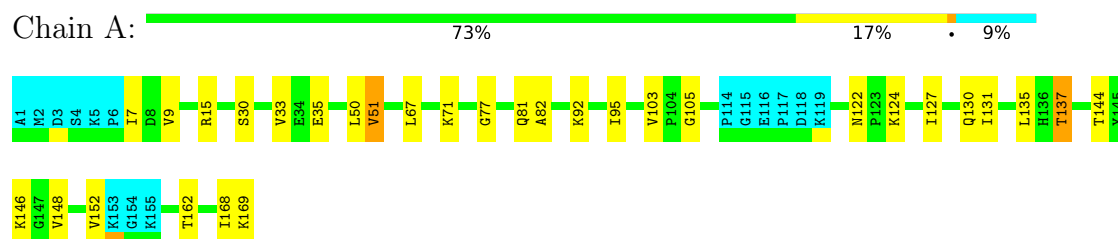
4.2.7 Score per residue for model 7

- Molecule 1: Aminoacyl tRNA synthase complex-interacting multifunctional protein 1



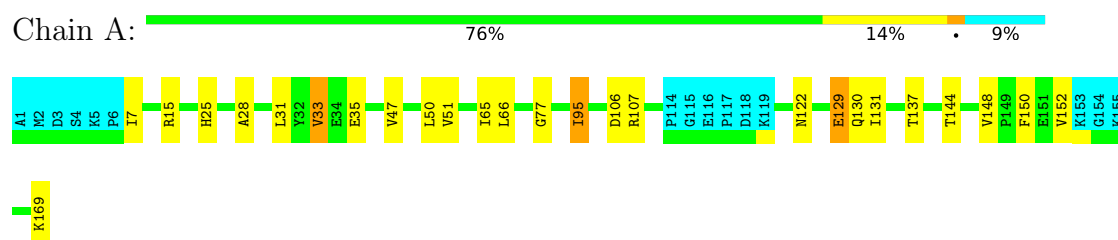
4.2.8 Score per residue for model 8

- Molecule 1: Aminoacyl tRNA synthase complex-interacting multifunctional protein 1



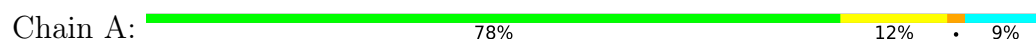
4.2.9 Score per residue for model 9

- Molecule 1: Aminoacyl tRNA synthase complex-interacting multifunctional protein 1



4.2.10 Score per residue for model 10

- Molecule 1: Aminoacyl tRNA synthase complex-interacting multifunctional protein 1

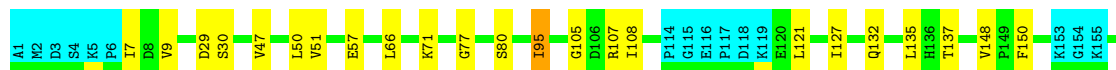




4.2.11 Score per residue for model 11 (medoid)

- Molecule 1: Aminoacyl tRNA synthase complex-interacting multifunctional protein 1

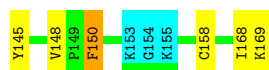
Chain A: 77% 14% 9%



4.2.12 Score per residue for model 12

- Molecule 1: Aminoacyl tRNA synthase complex-interacting multifunctional protein 1

Chain A: 72% 18% 9%



4.2.13 Score per residue for model 13

- Molecule 1: Aminoacyl tRNA synthase complex-interacting multifunctional protein 1

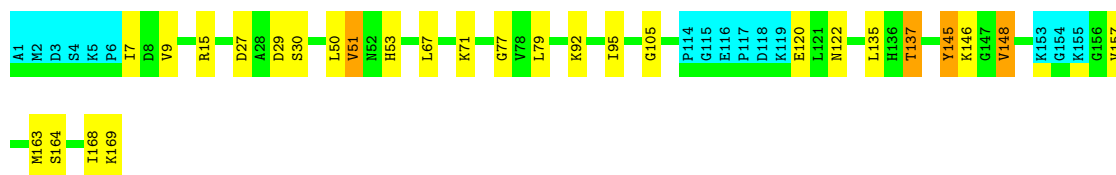
Chain A: 76% 13% 9%



4.2.14 Score per residue for model 14

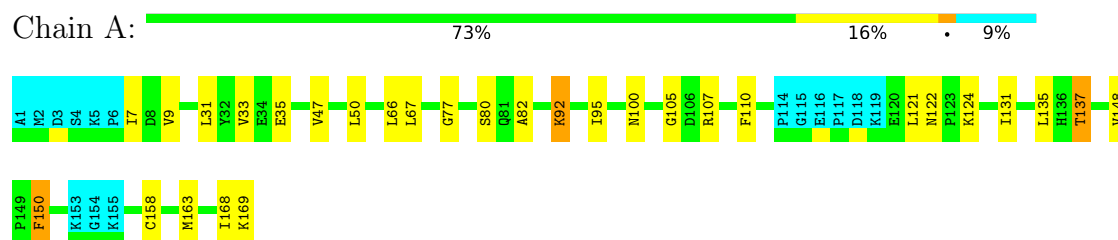
- Molecule 1: Aminoacyl tRNA synthase complex-interacting multifunctional protein 1

Chain A: 75% 14% 9%



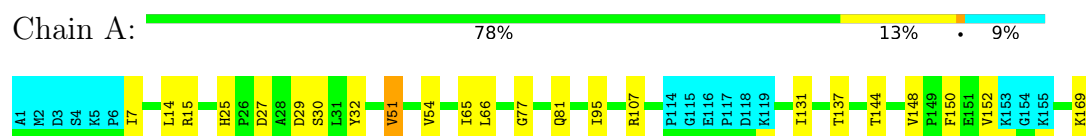
4.2.15 Score per residue for model 15

- Molecule 1: Aminoacyl tRNA synthase complex-interacting multifunctional protein 1



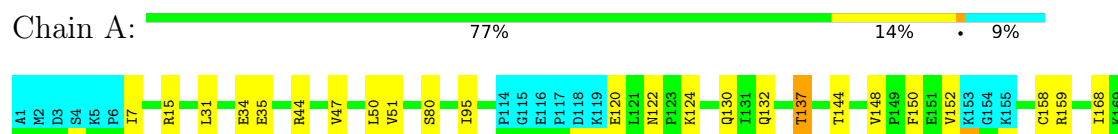
4.2.16 Score per residue for model 16

- Molecule 1: Aminoacyl tRNA synthase complex-interacting multifunctional protein 1



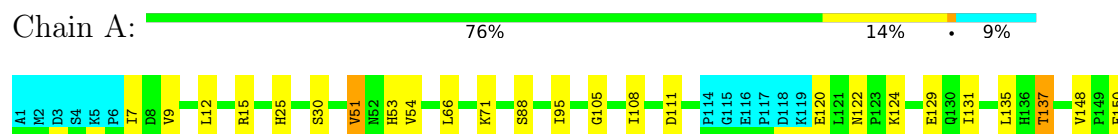
4.2.17 Score per residue for model 17

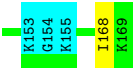
- Molecule 1: Aminoacyl tRNA synthase complex-interacting multifunctional protein 1



4.2.18 Score per residue for model 18

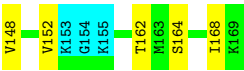
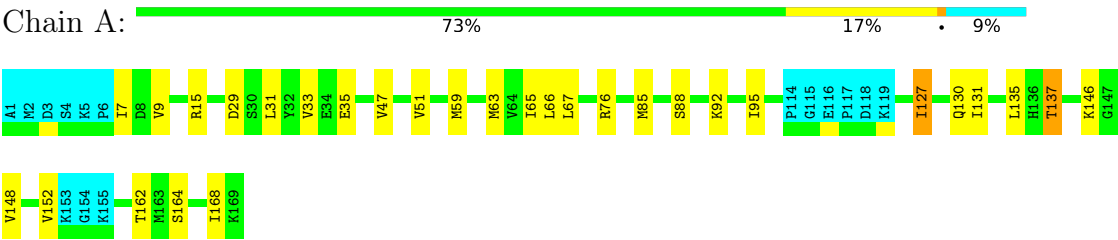
- Molecule 1: Aminoacyl tRNA synthase complex-interacting multifunctional protein 1





4.2.19 Score per residue for model 19

- Molecule 1: Aminoacyl tRNA synthase complex-interacting multifunctional protein 1



5 Refinement protocol and experimental data overview

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

Of the 200 calculated structures, 19 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
CYANA	structure calculation	
YASARA	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)	working_cs.cif
Number of chemical shift lists	1
Total number of shifts	1761
Number of shifts mapped to atoms	1761
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	80%

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	0.86±0.01	0±1/1204 (0.0± 0.0%)	0.87±0.03	1±1/1632 (0.0± 0.1%)
All	All	0.86	8/22876 (0.0%)	0.87	10/31008 (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	148	VAL	CA-CB	6.16	1.60	1.55	3	3
1	A	7	ILE	CA-CB	5.63	1.59	1.54	7	1
1	A	127	ILE	CA-CB	5.52	1.60	1.54	5	3
1	A	152	VAL	CA-CB	5.30	1.59	1.53	13	1

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	127	ILE	N-CA-C	5.54	116.18	110.36	7	1
1	A	132	GLN	CA-C-N	-5.52	114.13	119.87	2	1
1	A	132	GLN	C-N-CA	-5.52	114.13	119.87	2	1
1	A	152	VAL	N-CA-C	-5.51	101.95	109.55	17	1
1	A	32	TYR	N-CA-C	-5.31	102.05	109.69	12	2
1	A	97	ALA	CA-C-N	-5.28	115.86	119.66	7	1
1	A	97	ALA	C-N-CA	-5.28	115.86	119.66	7	1
1	A	145	TYR	CA-CB-CG	5.12	123.12	113.90	14	1
1	A	20	ILE	N-CA-C	-5.05	106.75	111.45	12	1

There are no chirality outliers.

There are no planarity outliers.

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	1184	1211	1211	3±1
All	All	22496	23009	23009	55

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 1.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:137:THR:HG23	1:A:168:ILE:HD11	0.60	1.74	8	12
1:A:30:SER:HB3	1:A:51:VAL:HG22	0.57	1.76	7	1
1:A:108:ILE:HG21	1:A:150:PHE:CD1	0.53	2.39	11	3
1:A:95:ILE:HD13	1:A:95:ILE:H	0.52	1.65	5	4
1:A:67:LEU:HD11	1:A:82:ALA:HA	0.50	1.82	13	6
1:A:92:LYS:HE2	1:A:162:THR:HG23	0.48	1.86	8	4
1:A:53:HIS:HB3	1:A:93:ILE:HD13	0.47	1.86	13	1
1:A:67:LEU:O	1:A:67:LEU:HD12	0.46	2.10	19	3
1:A:150:PHE:CE2	1:A:158:CYS:HB3	0.45	2.47	4	3
1:A:92:LYS:HE3	1:A:163:MET:SD	0.45	2.51	4	3
1:A:135:LEU:HD22	1:A:145:TYR:CB	0.44	2.41	1	1
1:A:67:LEU:HD23	1:A:67:LEU:O	0.43	2.13	7	1
1:A:25:HIS:CD2	1:A:33:VAL:HG23	0.43	2.48	9	3
1:A:25:HIS:CD2	1:A:25:HIS:H	0.43	2.31	18	1
1:A:150:PHE:CE1	1:A:158:CYS:HB3	0.43	2.49	17	1
1:A:108:ILE:HG21	1:A:150:PHE:CD2	0.42	2.49	6	2
1:A:67:LEU:HD13	1:A:70:LEU:O	0.41	2.15	5	1
1:A:95:ILE:H	1:A:95:ILE:HD13	0.41	1.75	3	1
1:A:53:HIS:O	1:A:54:VAL:C	0.40	2.64	18	1
1:A:129:GLU:CD	1:A:129:GLU:H	0.40	2.24	9	1
1:A:32:TYR:CD1	1:A:32:TYR:C	0.40	2.99	7	1
1:A:92:LYS:HE2	1:A:163:MET:SD	0.40	2.57	14	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	153/169 (91%)	137±2 (90±1%)	13±2 (8±1%)	3±1 (2±1%)	9	53
All	All	2907/3211 (91%)	2612 (90%)	246 (8%)	49 (2%)	9	53

All 8 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	77	GLY	16
1	A	105	GLY	14
1	A	51	VAL	7
1	A	120	GLU	5
1	A	28	ALA	4
1	A	101	GLY	1
1	A	53	HIS	1
1	A	29	ASP	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	135/147 (92%)	113±3 (84±2%)	22±3 (16±2%)	4	40
All	All	2565/2793 (92%)	2153 (84%)	412 (16%)	4	40

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	7	ILE	19
1	A	95	ILE	19

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Mol	Chain	Res	Type	Models (Total)
1	A	137	THR	19
1	A	148	VAL	19
1	A	50	LEU	15
1	A	131	ILE	15
1	A	30	SER	14
1	A	122	ASN	14
1	A	66	LEU	13
1	A	169	LYS	13
1	A	15	ARG	12
1	A	47	VAL	12
1	A	51	VAL	12
1	A	9	VAL	11
1	A	124	LYS	11
1	A	135	LEU	10
1	A	35	GLU	10
1	A	31	LEU	9
1	A	33	VAL	8
1	A	80	SER	8
1	A	130	GLN	8
1	A	150	PHE	7
1	A	71	LYS	7
1	A	107	ARG	7
1	A	132	GLN	6
1	A	29	ASP	6
1	A	144	THR	6
1	A	92	LYS	5
1	A	145	TYR	5
1	A	65	ILE	5
1	A	127	ILE	5
1	A	164	SER	4
1	A	110	PHE	4
1	A	76	ARG	4
1	A	34	GLU	4
1	A	121	LEU	4
1	A	129	GLU	4
1	A	152	VAL	4
1	A	13	ASP	3
1	A	27	ASP	3
1	A	54	VAL	3
1	A	146	LYS	3
1	A	134	ASP	2
1	A	60	GLN	2

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Mol	Chain	Res	Type	Models (Total)
1	A	102	SER	2
1	A	44	ARG	2
1	A	111	ASP	2
1	A	67	LEU	2
1	A	85	MET	2
1	A	81	GLN	2
1	A	103	VAL	2
1	A	79	LEU	2
1	A	88	SER	2
1	A	8	ASP	1
1	A	11	ARG	1
1	A	45	THR	1
1	A	18	CYS	1
1	A	113	PHE	1
1	A	38	VAL	1
1	A	75	MET	1
1	A	106	ASP	1
1	A	57	GLU	1
1	A	139	ASP	1
1	A	53	HIS	1
1	A	157	VAL	1
1	A	100	ASN	1
1	A	14	LEU	1
1	A	25	HIS	1
1	A	32	TYR	1
1	A	159	ARG	1
1	A	12	LEU	1
1	A	59	MET	1
1	A	63	MET	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 80% for the well-defined parts and 77% 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	1761
Number of shifts mapped to atoms	1761
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	5

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	161	-0.09 ± 0.15	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	150	0.14 ± 0.08	None needed (< 0.5 ppm)
$^{13}\text{C}'$	0	—	None (insufficient data)
^{15}N	138	0.61 ± 0.35	None needed (imprecise)

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 80%, i.e. 1667 atoms were assigned a chemical shift out of a possible 2090. 0 out of 28 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	580/757 (77%)	295/306 (96%)	152/308 (49%)	133/143 (93%)
Sidechain	1083/1252 (87%)	746/818 (91%)	337/388 (87%)	0/46 (0%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	4/81 (5%)	3/41 (7%)	0/36 (0%)	1/4 (25%)
Overall	1667/2090 (80%)	1044/1165 (90%)	489/732 (67%)	134/193 (69%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 77%, i.e. 1758 atoms were assigned a chemical shift out of a possible 2272. 0 out of 28 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	611/828 (74%)	312/335 (93%)	161/338 (48%)	138/155 (89%)
Sidechain	1143/1363 (84%)	786/888 (89%)	357/425 (84%)	0/50 (0%)
Aromatic	4/81 (5%)	3/41 (7%)	0/36 (0%)	1/4 (25%)
Overall	1758/2272 (77%)	1101/1264 (87%)	518/799 (65%)	139/209 (67%)

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	9	VAL	HB	-0.82	0.43 – 3.54	-9.0
1	A	9	VAL	HG21	-0.68	-0.58 – 2.19	-5.4
1	A	9	VAL	HG22	-0.68	-0.58 – 2.19	-5.4
1	A	9	VAL	HG23	-0.68	-0.58 – 2.19	-5.4
1	A	146	LYS	HG3	-0.04	0.04 – 2.67	-5.3

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:

