



Full wwPDB NMR Structure Validation Report ⓘ

Jan 5, 2021 – 08:43 AM GMT

PDB ID : 6QXZ
Title : Solution structure of the ASHH2 CW domain with the N-terminal histone H3 tail mimicking peptide monomethylated on lysine 4
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Deposited on : 2019-03-08

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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

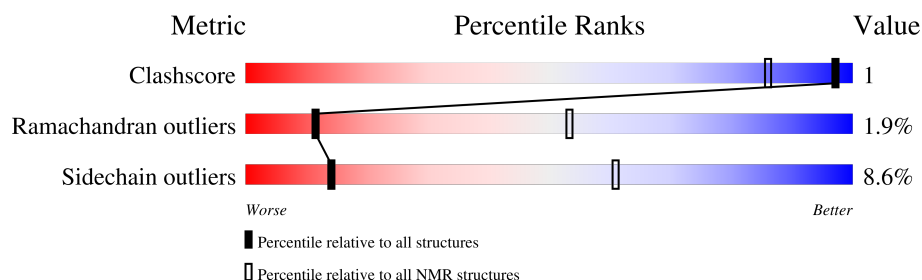
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	2.16
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.16

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 79%.

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	79	
2	B	9	

2 Ensemble composition and analysis

This entry contains 20 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:863-A:885, A:890-A:921, B:3-B:3, B:5-B:6 (58)	0.28	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 2 clusters and 1 single-model cluster was found.

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

3 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 1348 atoms, of which 650 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Histone-lysine N-methyltransferase ASHH2.

Mol	Chain	Residues	Atoms						Trace
1	A	79	Total	C	H	N	O	S	0
			1185	370	566	112	131	6	

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	850	GLY	-	expression tag	UNP Q2LAE1
A	851	SER	-	expression tag	UNP Q2LAE1
A	852	ARG	-	expression tag	UNP Q2LAE1
A	853	ARG	-	expression tag	UNP Q2LAE1
A	854	ALA	-	expression tag	UNP Q2LAE1
A	855	SER	-	expression tag	UNP Q2LAE1
A	856	VAL	-	expression tag	UNP Q2LAE1
A	857	GLY	-	expression tag	UNP Q2LAE1
A	858	SER	-	expression tag	UNP Q2LAE1
A	859	GLU	-	expression tag	UNP Q2LAE1
A	860	PHE	-	expression tag	UNP Q2LAE1

- Molecule 2 is a protein called ALA-ARG-THR-MLZ-GLN-THR-ALA-ARG-TYR.

Mol	Chain	Residues	Atoms					Trace
2	B	9	Total	C	H	N	O	0
			162	47	84	17	14	

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

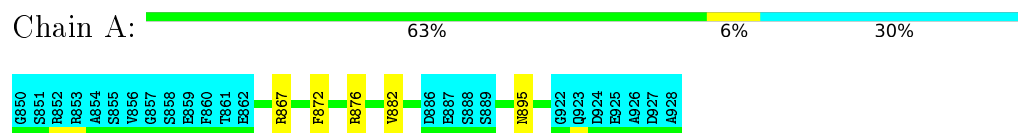
Mol	Chain	Residues	Atoms	
3	A	1	Total	Zn
			1	1

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: Histone-lysine N-methyltransferase ASHH2



- Molecule 2: ALA-ARG-THR-MLZ-GLN-THR-ALA-ARG-TYR

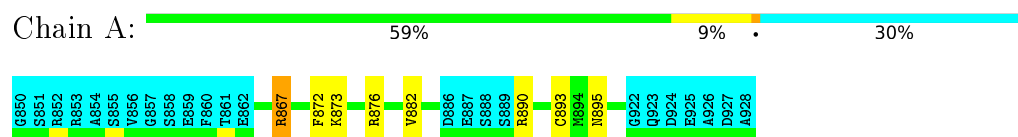


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1 (medoid)

- Molecule 1: Histone-lysine N-methyltransferase ASHH2

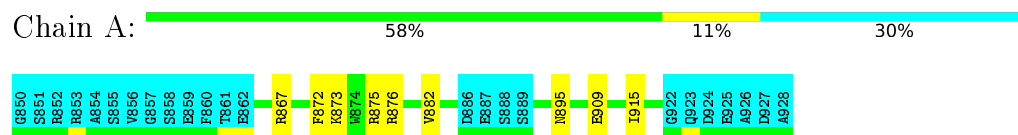


- Molecule 2: ALA-ARG-THR-MLZ-GLN-THR-ALA-ARG-TYR



4.2.2 Score per residue for model 2

- Molecule 1: Histone-lysine N-methyltransferase ASHH2

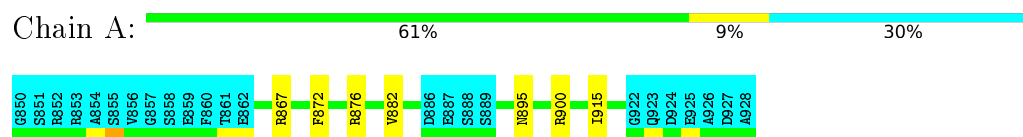


- Molecule 2: ALA-ARG-THR-MLZ-GLN-THR-ALA-ARG-TYR



4.2.3 Score per residue for model 3

- Molecule 1: Histone-lysine N-methyltransferase ASHH2

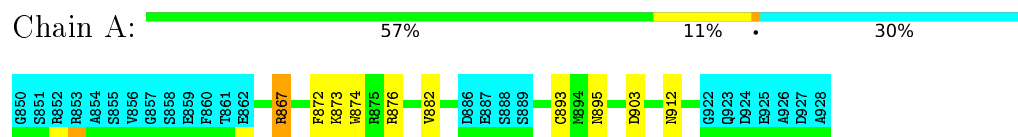


- Molecule 2: ALA-ARG-THR-MLZ-GLN-THR-ALA-ARG-TYR



4.2.4 Score per residue for model 4

- Molecule 1: Histone-lysine N-methyltransferase ASHH2

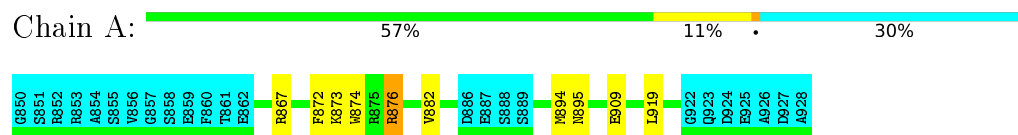


- Molecule 2: ALA-ARG-THR-MLZ-GLN-THR-ALA-ARG-TYR



4.2.5 Score per residue for model 5

- Molecule 1: Histone-lysine N-methyltransferase ASHH2

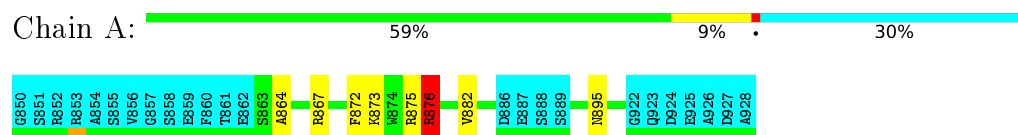


- Molecule 2: ALA-ARG-THR-MLZ-GLN-THR-ALA-ARG-TYR



4.2.6 Score per residue for model 6

- Molecule 1: Histone-lysine N-methyltransferase ASHH2

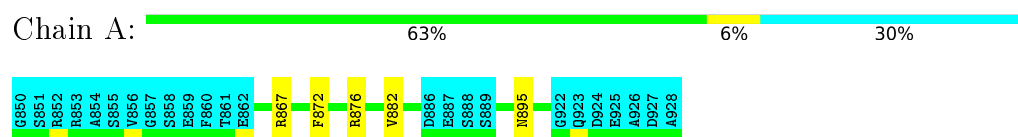


- Molecule 2: ALA-ARG-THR-MLZ-GLN-THR-ALA-ARG-TYR



4.2.7 Score per residue for model 7

- Molecule 1: Histone-lysine N-methyltransferase ASHH2

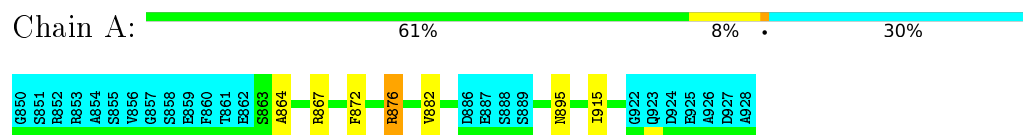


- Molecule 2: ALA-ARG-THR-MLZ-GLN-THR-ALA-ARG-TYR



4.2.8 Score per residue for model 8

- Molecule 1: Histone-lysine N-methyltransferase ASHH2

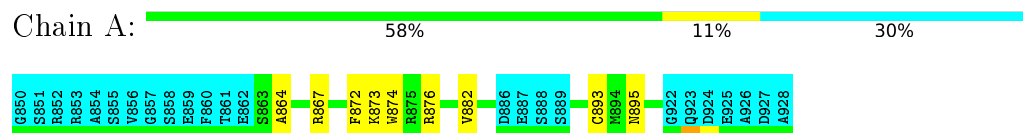


- Molecule 2: ALA-ARG-THR-MLZ-GLN-THR-ALA-ARG-TYR



4.2.9 Score per residue for model 9

- Molecule 1: Histone-lysine N-methyltransferase ASHH2

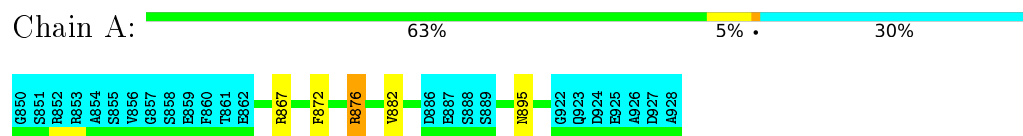


- Molecule 2: ALA-ARG-THR-MLZ-GLN-THR-ALA-ARG-TYR



4.2.10 Score per residue for model 10

- Molecule 1: Histone-lysine N-methyltransferase ASHH2

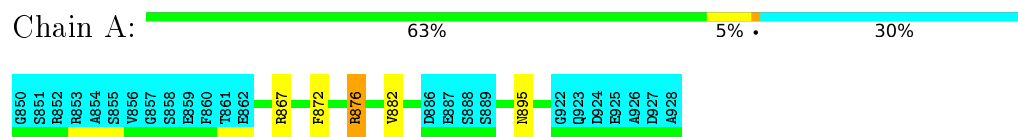


- Molecule 2: ALA-ARG-THR-MLZ-GLN-THR-ALA-ARG-TYR



4.2.11 Score per residue for model 11

- Molecule 1: Histone-lysine N-methyltransferase ASHH2

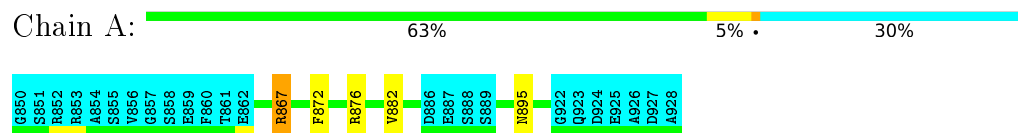


- Molecule 2: ALA-ARG-THR-MLZ-GLN-THR-ALA-ARG-TYR



4.2.12 Score per residue for model 12

- Molecule 1: Histone-lysine N-methyltransferase ASHH2

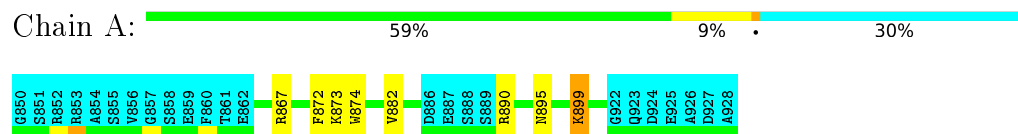


- Molecule 2: ALA-ARG-THR-MLZ-GLN-THR-ALA-ARG-TYR



4.2.13 Score per residue for model 13

- Molecule 1: Histone-lysine N-methyltransferase ASHH2

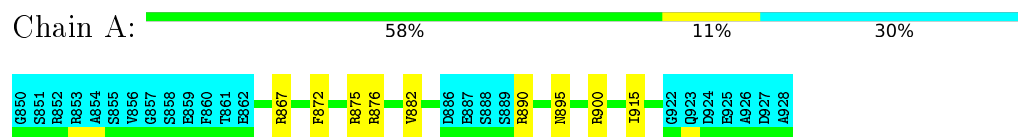


- Molecule 2: ALA-ARG-THR-MLZ-GLN-THR-ALA-ARG-TYR



4.2.14 Score per residue for model 14

- Molecule 1: Histone-lysine N-methyltransferase ASHH2

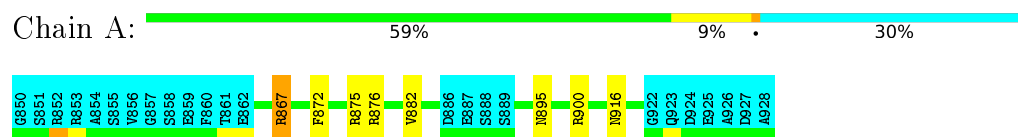


- Molecule 2: ALA-ARG-THR-MLZ-GLN-THR-ALA-ARG-TYR



4.2.15 Score per residue for model 15

- Molecule 1: Histone-lysine N-methyltransferase ASHH2

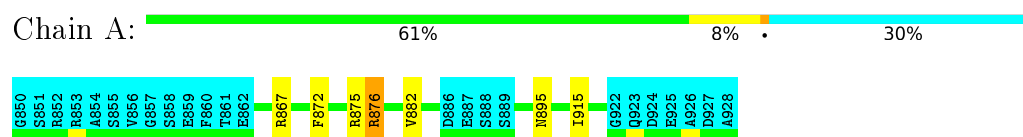


- Molecule 2: ALA-ARG-THR-MLZ-GLN-THR-ALA-ARG-TYR



4.2.16 Score per residue for model 16

- Molecule 1: Histone-lysine N-methyltransferase ASHH2

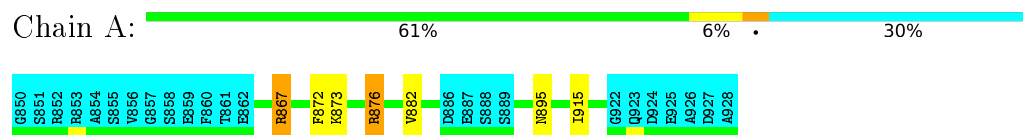


- Molecule 2: ALA-ARG-THR-MLZ-GLN-THR-ALA-ARG-TYR



4.2.17 Score per residue for model 17

- Molecule 1: Histone-lysine N-methyltransferase ASHH2

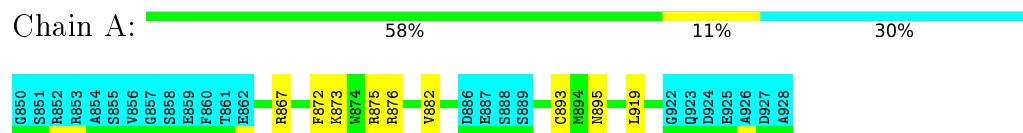


- Molecule 2: ALA-ARG-THR-MLZ-GLN-THR-ALA-ARG-TYR



4.2.18 Score per residue for model 18

- Molecule 1: Histone-lysine N-methyltransferase ASHH2

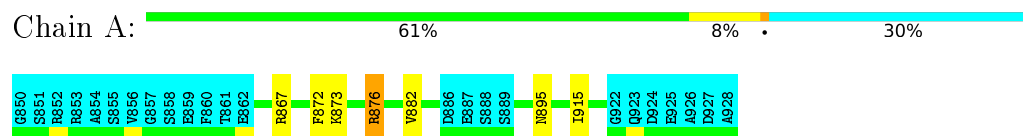


- Molecule 2: ALA-ARG-THR-MLZ-GLN-THR-ALA-ARG-TYR



4.2.19 Score per residue for model 19

- Molecule 1: Histone-lysine N-methyltransferase ASHH2

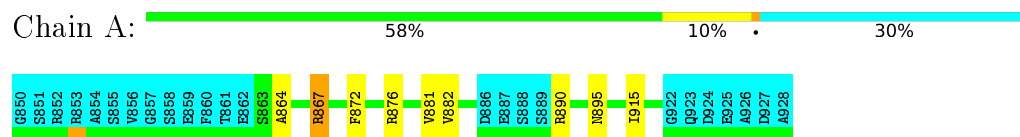


- Molecule 2: ALA-ARG-THR-MLZ-GLN-THR-ALA-ARG-TYR



4.2.20 Score per residue for model 20

- Molecule 1: Histone-lysine N-methyltransferase ASHH2



- Molecule 2: ALA-ARG-THR-MLZ-GLN-THR-ALA-ARG-TYR



5 Refinement protocol and experimental data overview ⓘ

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

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
Amber	refinement	
CYANA	structure calculation	

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	884
Number of shifts mapped to atoms	879
Number of unparsed shifts	4
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	1
Assignment completeness (well-defined parts)	79%

6 Model quality [i](#)

6.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MLZ, ZN

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	0.74±0.01	0±0/454 (0.0± 0.0%)	1.15±0.02	2±1/611 (0.3± 0.1%)
2	B	0.61±0.06	0±0/22 (0.0± 0.0%)	1.05±0.15	0±0/29 (0.0± 0.0%)
All	All	0.74	0/9520 (0.0%)	1.14	37/12800 (0.3%)

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	0.4±0.7
All	All	0	8

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	867	ARG	NE-CZ-NH1	8.02	124.31	120.30	8	12
1	A	876	ARG	NE-CZ-NH1	7.54	124.07	120.30	3	13
1	A	890	ARG	NE-CZ-NH1	6.84	123.72	120.30	20	4
1	A	900	ARG	NE-CZ-NH1	6.72	123.66	120.30	15	2
1	A	875	ARG	NE-CZ-NH1	6.22	123.41	120.30	14	6

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	867	ARG	Sidechain	4
1	A	876	ARG	Sidechain	4

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	445	420	420	1±1
2	B	23	22	22	0±0
All	All	9380	8840	8840	11

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:864:ALA:HB3	1:A:882:VAL:HG11	0.58	1.76	20	4
1:A:873:LYS:HE2	1:A:893:CYS:SG	0.53	2.43	18	4
1:A:899:LYS:CA	1:A:899:LYS:HE3	0.44	2.42	13	1
1:A:919:LEU:CD2	2:B:5:GLN:H	0.41	2.29	18	1
1:A:867:ARG:HB2	1:A:874:TRP:CZ3	0.40	2.50	4	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	55/79 (70%)	50±1 (90±2%)	5±1 (8±2%)	1±0 (2±0%)	12	54
2	B	3/9 (33%)	2±1 (68±20%)	1±1 (28±19%)	0±0 (3±10%)	6	37
All	All	1160/1760 (66%)	1031 (89%)	107 (9%)	22 (2%)	11	53

All 3 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	872	PHE	20
2	B	6	THR	1
2	B	3	THR	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	50/68 (74%)	46±1 (92±3%)	4±1 (8±3%)	16	64
2	B	3/6 (50%)	2±1 (78±22%)	1±1 (22±22%)	3	30
All	All	1060/1480 (72%)	969 (91%)	91 (9%)	14	61

All 17 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	895	ASN	20
1	A	882	VAL	16
1	A	876	ARG	11
2	B	6	THR	9
1	A	867	ARG	9
1	A	873	LYS	6
1	A	915	ILE	6
2	B	5	GLN	4
1	A	909	GLU	2
1	A	903	ASP	1
1	A	912	ASN	1
1	A	894	MET	1
1	A	900	ARG	1
1	A	916	ASN	1
1	A	899	LYS	1
1	A	881	VAL	1
1	A	919	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](#)

1 non-standard protein/DNA/RNA residue is modelled in this entry.

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.6 Ligand geometry [i](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

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 79% for the well-defined parts and 76% 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

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	884
Number of shifts mapped to atoms	879
Number of unparsed shifts	4
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	1
Number of shift outliers (ShiftChecker)	12

The following errors were found when reading this chemical shift list.

- Chemical shift has been reported more than once. All 4 occurrences are reported below.

Shift ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
841	B	4	MLZ	HB3	1.636	0.020	?
843	B	4	MLZ	HG3	1.262	0.020	?
845	B	4	MLZ	HD3	1.797	0.020	?
847	B	4	MLZ	HE3	3.116	0.020	?

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

- No matching atoms found in structure. The only occurrence is reported below.

Chain	Res	Type	Atom	Shift Data		
				Value	Uncertainty	Ambiguity
B	4	MLZ	HC	1.031	0.02	1

7.1.2 Chemical shift referencing ⓘ

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	80	2.38 ± 0.14	Should be applied
$^{13}\text{C}_\beta$	76	2.74 ± 0.13	Should be applied
$^{13}\text{C}'$	0	—	None (insufficient data)
^{15}N	80	-0.95 ± 0.34	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 79%, i.e. 574 atoms were assigned a chemical shift out of a possible 729. 4 out of 4 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	222/288 (77%)	114/115 (99%)	54/116 (47%)	54/57 (95%)
Sidechain	304/387 (79%)	193/229 (84%)	103/134 (77%)	8/24 (33%)
Aromatic	48/54 (89%)	26/28 (93%)	19/23 (83%)	3/3 (100%)
Overall	574/729 (79%)	333/372 (90%)	176/273 (64%)	65/84 (77%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 76%, i.e. 799 atoms were assigned a chemical shift out of a possible 1054. 5 out of 5 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	327/433 (76%)	167/173 (97%)	80/174 (46%)	80/86 (93%)
Sidechain	418/550 (76%)	267/325 (82%)	142/188 (76%)	9/37 (24%)
Aromatic	54/71 (76%)	30/37 (81%)	21/31 (68%)	3/3 (100%)
Overall	799/1054 (76%)	464/535 (87%)	243/393 (62%)	92/126 (73%)

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.

Mol	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	876	ARG	NE	132.31	92.63 – 76.73	30.0
1	A	875	ARG	NE	119.31	92.63 – 76.73	21.8
1	A	867	ARG	NE	118.83	92.63 – 76.73	21.5

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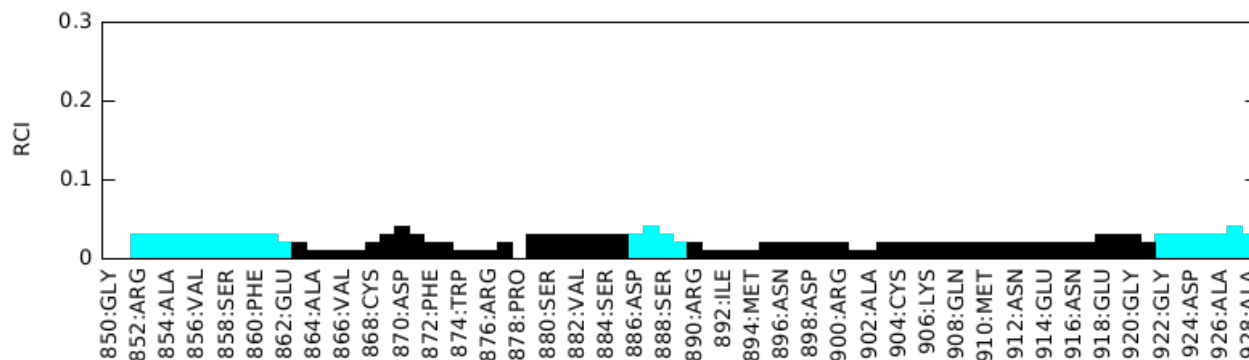
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Mol	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	915	ILE	HG12	-1.35	3.27 – -0.73	-6.6
1	A	866	VAL	HG22	-0.78	2.20 – -0.60	-5.6
1	A	866	VAL	HG21	-0.78	2.20 – -0.60	-5.6
1	A	866	VAL	HG23	-0.78	2.20 – -0.60	-5.6
1	A	915	ILE	HD13	-0.95	2.13 – -0.77	-5.6
1	A	915	ILE	HD12	-0.95	2.13 – -0.77	-5.6
1	A	915	ILE	HD11	-0.95	2.13 – -0.77	-5.6
1	A	876	ARG	HB2	0.33	3.15 – 0.45	-5.4
1	A	867	ARG	HG2	0.12	2.92 – 0.22	-5.4

7.1.5 Random Coil Index (RCI) plots [i](#)

The images below report *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:



Random coil index (RCI) for chain B:

