Full wwPDB NMR Structure Validation Report (i)

Dec 20, 2022 – 12:31 pm GMT

PDB ID	:	7Z07
BMRB ID	:	34711
Title	:	Solution NMR structure of N-acetylglucosaminyltransferase V (GnTV) G26P mutant TMD
Authors	:	Silber, M.; Muhle-Goll, C.
Deposited on	:	2022-02-22

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 (i) 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 (i)) were used in the production of this report:

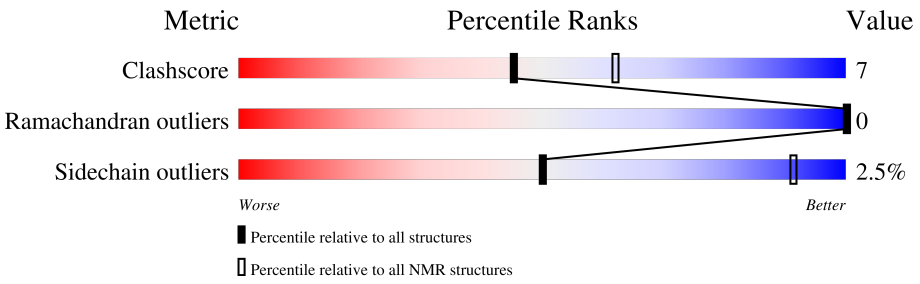
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	2.31.3
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.3

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
SOLUTION NMR

The overall completeness of chemical shifts assignment is 83%.

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 <=5%

Mol	Chain	Length	Quality of chain
1	A	29	21% 7% 72%

2 Ensemble composition and analysis (i)

This entry contains 50 models. Model 49 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:23-A:30 (8)	0.18	49

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 6 clusters and 7 single-model clusters were found.

Cluster number	Models
1	1, 7, 9, 12, 13, 18, 20, 26, 28, 33, 36, 38, 40, 42, 45, 47, 48
2	2, 8, 11, 19, 22, 27, 30, 31, 32, 37, 44, 49
3	4, 6, 10, 14, 24, 25, 46, 50
4	5, 34
5	17, 41
6	3, 39
Single-model clusters	15; 16; 21; 23; 29; 35; 43

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 533 atoms, of which 279 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyl transferase A.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	29	533	176	279	42	34	2	0

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	11	LYS	-	expression tag	UNP Q09328
A	12	LYS	-	expression tag	UNP Q09328
A	26	PRO	GLY	engineered mutation	UNP Q09328
A	38	LYS	-	expression tag	UNP Q09328
A	39	LYS	-	expression tag	UNP Q09328

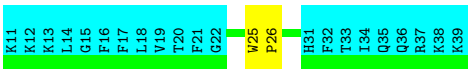
4 Residue-property plots (i)

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: Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase A

Chain A: 21% 7% 72%



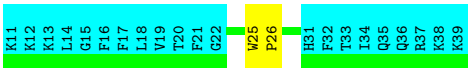
4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

• Molecule 1: Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase A

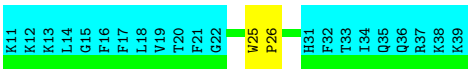
Chain A: 21% 7% 72%



4.2.2 Score per residue for model 2

• Molecule 1: Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase A

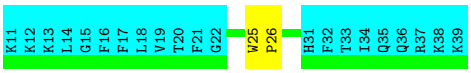
Chain A: 21% 7% 72%



4.2.3 Score per residue for model 3

• Molecule 1: Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase A

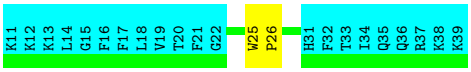
Chain A: 21% 7% 72%



4.2.4 Score per residue for model 4

• Molecule 1: Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase A

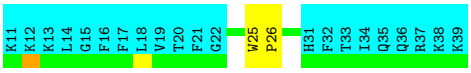
Chain A: 21% 7% 72%



4.2.5 Score per residue for model 5

• Molecule 1: Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase A

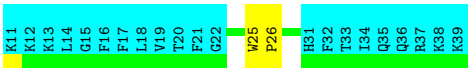
Chain A: 21% 7% 72%



4.2.6 Score per residue for model 6

• Molecule 1: Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase A

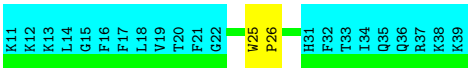
Chain A: 21% 7% 72%



4.2.7 Score per residue for model 7

• Molecule 1: Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase A

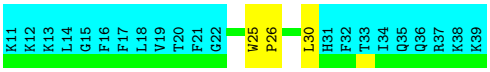
Chain A: 21% 7% 72%



4.2.8 Score per residue for model 8

• Molecule 1: Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase A

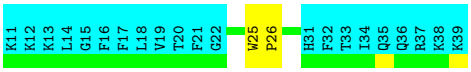
Chain A: 17% 10% 72%



4.2.9 Score per residue for model 9

• Molecule 1: Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase A

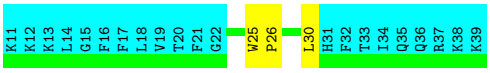
Chain A: 21% 7% 72%



4.2.10 Score per residue for model 10

• Molecule 1: Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase A

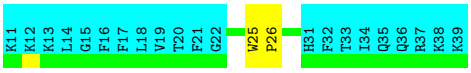
Chain A: 17% 10% 72%



4.2.11 Score per residue for model 11

• Molecule 1: Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase A

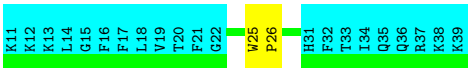
Chain A: 21% 7% 72%



4.2.12 Score per residue for model 12

• Molecule 1: Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase A

Chain A: 21% 7% 72%



4.2.13 Score per residue for model 13

• Molecule 1: Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase A

Chain A: 21% 7% 72%

K11 K12 K13 L14 G15 F16 F17 L18 V19 T20 F21 G22 W25 P26 H31 F32 T33 I34 Q35 Q36 R37 K38 K39

4.2.14 Score per residue for model 14

• Molecule 1: Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase A

Chain A: 21% 7% 72%

K11 K12 K13 L14 G15 F16 F17 L18 V19 T20 F21 G22 W25 P26 H31 F32 T33 I34 Q35 Q36 R37 K38 K39

4.2.15 Score per residue for model 15

• Molecule 1: Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase A

Chain A: 21% 7% 72%

K11 K12 K13 L14 G15 F16 F17 L18 V19 T20 F21 G22 W25 P26 H31 F32 T33 I34 Q35 Q36 R37 K38 K39

4.2.16 Score per residue for model 16

• Molecule 1: Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase A

Chain A: 28% 72%

K11 K12 K13 L14 G15 F16 F17 L18 V19 T20 F21 G22 H31 F32 T33 I34 Q35 Q36 R37 K38 K39

4.2.17 Score per residue for model 17

• Molecule 1: Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase A

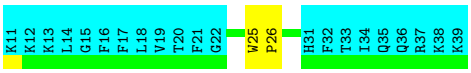
Chain A: 21% 7% 72%

K11 K12 K13 L14 G15 F16 F17 L18 V19 T20 F21 G22 W25 P26 H31 F32 T33 I34 Q35 Q36 R37 K38 K39

4.2.18 Score per residue for model 18

• Molecule 1: Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase A

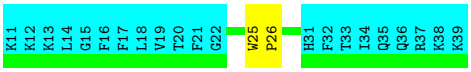
Chain A: 21% 7% 72%



4.2.19 Score per residue for model 19

• Molecule 1: Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase A

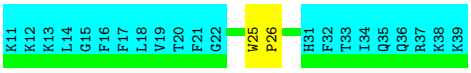
Chain A: 21% 7% 72%



4.2.20 Score per residue for model 20

• Molecule 1: Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase A

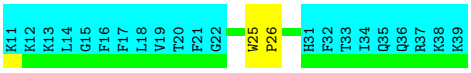
Chain A: 21% 7% 72%



4.2.21 Score per residue for model 21

• Molecule 1: Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase A

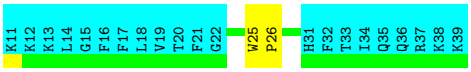
Chain A: 21% 7% 72%



4.2.22 Score per residue for model 22

• Molecule 1: Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase A

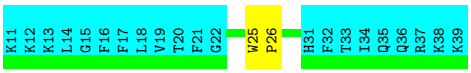
Chain A: 21% 7% 72%



4.2.23 Score per residue for model 23

• Molecule 1: Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase A

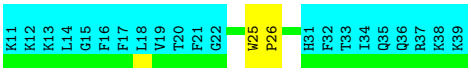
Chain A: 21% 7% 72%



4.2.24 Score per residue for model 24

• Molecule 1: Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase A

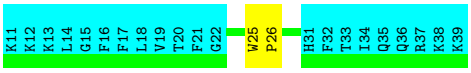
Chain A: 21% 7% 72%



4.2.25 Score per residue for model 25

• Molecule 1: Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase A

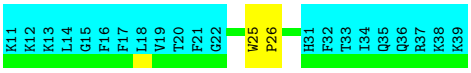
Chain A: 21% 7% 72%



4.2.26 Score per residue for model 26

• Molecule 1: Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase A

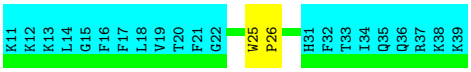
Chain A: 21% 7% 72%



4.2.27 Score per residue for model 27

• Molecule 1: Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase A

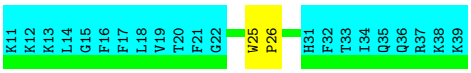
Chain A: 21% 7% 72%



4.2.28 Score per residue for model 28

• Molecule 1: Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase A

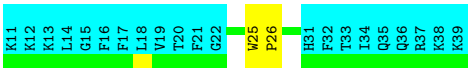
Chain A: 21% 7% 72%



4.2.29 Score per residue for model 29

• Molecule 1: Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase A

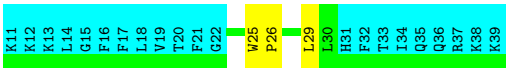
Chain A: 21% 7% 72%



4.2.30 Score per residue for model 30

• Molecule 1: Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase A

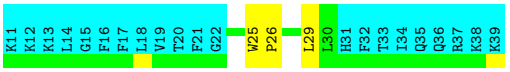
Chain A: 17% 10% 72%



4.2.31 Score per residue for model 31

• Molecule 1: Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase A

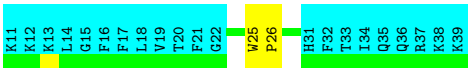
Chain A: 17% 10% 72%



4.2.32 Score per residue for model 32

• Molecule 1: Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase A

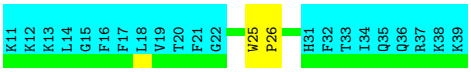
Chain A: 21% 7% 72%



4.2.33 Score per residue for model 33

• Molecule 1: Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase A

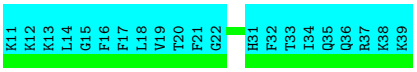
Chain A: 21% 7% 72%



4.2.34 Score per residue for model 34

• Molecule 1: Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase A

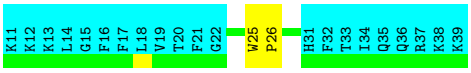
Chain A: 28% 72%



4.2.35 Score per residue for model 35

• Molecule 1: Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase A

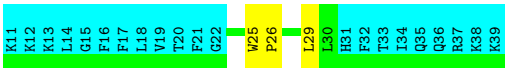
Chain A: 21% 7% 72%



4.2.36 Score per residue for model 36

• Molecule 1: Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase A

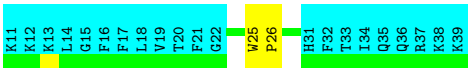
Chain A: 17% 10% 72%



4.2.37 Score per residue for model 37

• Molecule 1: Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase A

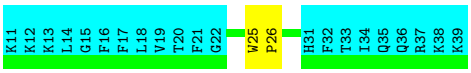
Chain A: 21% 7% 72%



4.2.38 Score per residue for model 38

• Molecule 1: Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase A

Chain A: 21% 7% 72%



4.2.39 Score per residue for model 39

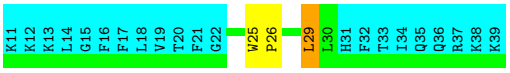
• Molecule 1: Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase A

Chain A: 21% 7% 72%

4.2.40 Score per residue for model 40

• Molecule 1: Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase A

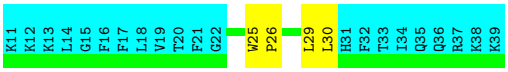
Chain A: 17% 7% • 72%



4.2.41 Score per residue for model 41

• Molecule 1: Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase A

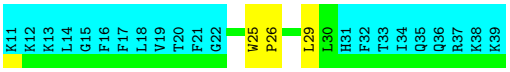
Chain A: 14% 14% 72%



4.2.42 Score per residue for model 42

• Molecule 1: Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase A

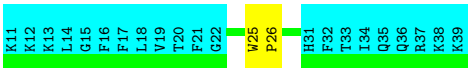
Chain A: 17% 10% 72%



4.2.43 Score per residue for model 43

• Molecule 1: Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase A

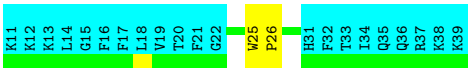
Chain A: 21% 7% 72%



4.2.44 Score per residue for model 44

• Molecule 1: Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase A

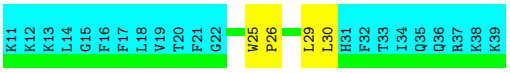
Chain A: 21% 7% 72%



4.2.45 Score per residue for model 45

• Molecule 1: Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase A

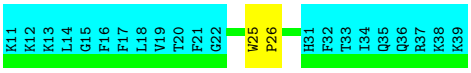
Chain A: 14% 14% 72%



4.2.46 Score per residue for model 46

• Molecule 1: Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase A

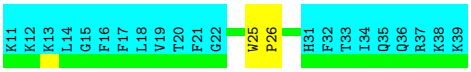
Chain A: 21% 7% 72%



4.2.47 Score per residue for model 47

• Molecule 1: Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase A

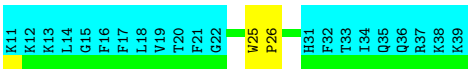
Chain A: 21% 7% 72%



4.2.48 Score per residue for model 48

• Molecule 1: Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase A

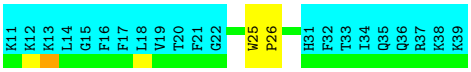
Chain A: 21% 7% 72%



4.2.49 Score per residue for model 49 (medoid)

• Molecule 1: Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase A

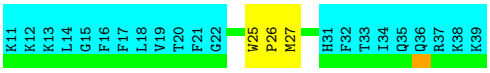
Chain A: 21% 7% 72%



4.2.50 Score per residue for model 50

• Molecule 1: Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase A

Chain A: 17% 10% 72%



5 Refinement protocol and experimental data overview (i)

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

Of the 400 calculated structures, 50 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	refinement	
ARIA	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	345
Number of shifts mapped to atoms	345
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	83%

6 Model quality (i)

6.1 Standard geometry (i)

There are no covalent bond-length or bond-angle outliers.

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	72	77	77	1±0
All	All	3600	3850	3850	50

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 7.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:25:TRP:HB3	1:A:26:PRO:HD3	0.51	1.82	3	42
1:A:25:TRP:N	1:A:26:PRO:HD2	0.48	2.24	11	6
1:A:29:LEU:O	1:A:29:LEU:HD13	0.42	2.14	31	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	8/29 (28%)	8±0 (100±0%)	0±0 (0±0%)	0±0 (0±0%)	100	100
All	All	400/1450 (28%)	400 (100%)	0 (0%)	0 (0%)	100	100

There are no Ramachandran outliers.

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	8/27 (30%)	8±0 (98±6%)	0±0 (2±6%)	50	91
All	All	400/1350 (30%)	390 (98%)	10 (2%)	50	91

All 3 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	29	LEU	6
1	A	30	LEU	3
1	A	27	MET	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 (i)

The completeness of assignment taking into account all chemical shift lists is 83% for the well-defined parts and 73% 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 (i)

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	345
Number of shifts mapped to atoms	345
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	1

7.1.2 Chemical shift referencing (i)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	28	-0.11 ± 0.09	None needed (< 0.5 ppm)
$^{13}C_{\beta}$	26	0.90 ± 0.07	Should be applied
$^{13}C'$	0	—	None (insufficient data)
^{15}N	27	0.71 ± 0.57	None needed (imprecise)

7.1.3 Completeness of resonance assignments (i)

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 83%, i.e. 97 atoms were assigned a chemical shift out of a possible 117. 2 out of 2 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	30/38 (79%)	15/15 (100%)	8/16 (50%)	7/7 (100%)
Sidechain	52/58 (90%)	32/35 (91%)	20/23 (87%)	0/0 (—%)

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	Total	^{1}H	^{13}C	^{15}N
Aromatic	15/21 (71%)	8/11 (73%)	6/9 (67%)	1/1 (100%)
Overall	97/117 (83%)	55/61 (90%)	34/48 (71%)	8/8 (100%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 73%, i.e. 309 atoms were assigned a chemical shift out of a possible 425. 4 out of 5 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

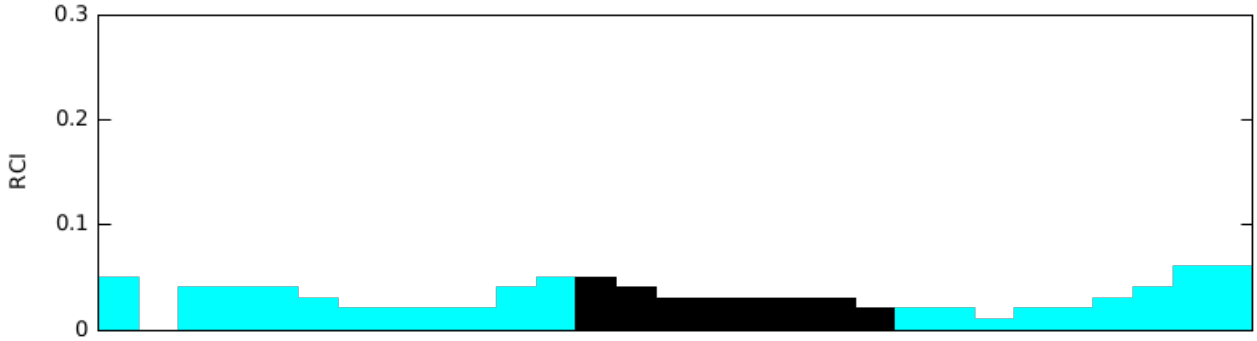
	Total	^{1}H	^{13}C	^{15}N
Backbone	109/143 (76%)	54/57 (95%)	28/58 (48%)	27/28 (96%)
Sidechain	171/217 (79%)	107/130 (82%)	64/77 (83%)	0/10 (0%)
Aromatic	29/65 (45%)	17/35 (49%)	11/27 (41%)	1/3 (33%)
Overall	309/425 (73%)	178/222 (80%)	103/162 (64%)	28/41 (68%)

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.

Mol	Chain	Res	Type	Atom	Shift, *ppm*	Expected range, *ppm*	Z-score
1	A	11	LYS	HD3	8.36	2.75 – 0.45	29.4

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.

Random coil index (RCI) for chain A: