



Full wwPDB NMR Structure Validation Report ⓘ

Mar 5, 2026 – 02:01 PM UTC

PDB ID : 6G99 / pdb_00006g99
BMRB ID : 34258
Title : Solution structure of FUS-ZnF bound to UGGUG
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Deposited on : 2018-04-10

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

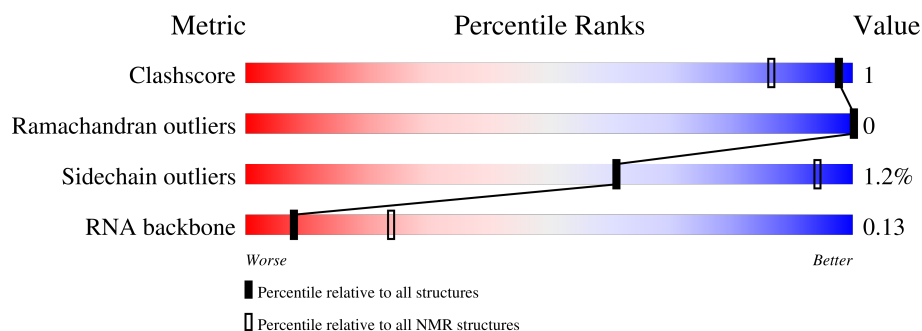
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 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	229148	14424
Ramachandran outliers	224038	12848
Sidechain outliers	223484	12823
RNA backbone	8273	777

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	B	41	
2	A	5	

2 Ensemble composition and analysis

This entry contains 20 models. Model 19 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	B:426-B:452 (27)	0.12	19

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

3 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 756 atoms, of which 336 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called RNA-binding protein FUS.

Mol	Chain	Residues	Atoms						Trace
1	B	41	Total	C	H	N	O	S	0
			596	188	283	60	60	5	

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	414	GLY	-	expression tag	UNP P35637
B	415	PRO	-	expression tag	UNP P35637
B	416	LEU	-	expression tag	UNP P35637
B	417	GLY	-	expression tag	UNP P35637
B	418	SER	-	expression tag	UNP P35637

- Molecule 2 is a RNA chain called RNA (5'-R(*UP*GP*GP*UP*G)-3').

Mol	Chain	Residues	Atoms						Trace
2	A	5	Total	C	H	N	O	P	0
			159	48	53	19	35	4	

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

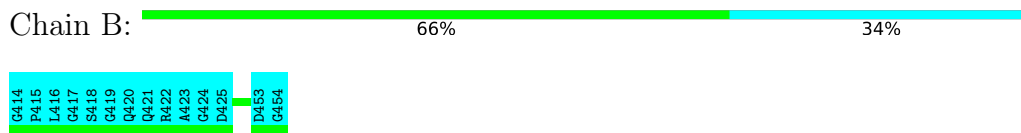
Mol	Chain	Residues	Atoms	
3	B	1	Total	Zn
			1	1

4 Residue-property plots [i](#)

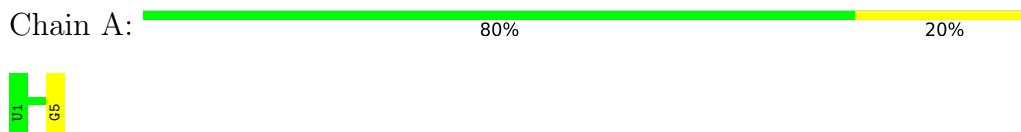
4.1 Average score per residue in the NMR ensemble

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: RNA-binding protein FUS



- Molecule 2: RNA (5'-R(*UP*GP*GP*UP*G)-3')

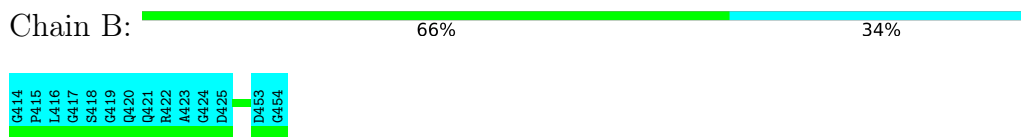


4.2 Scores per residue for each member of the ensemble

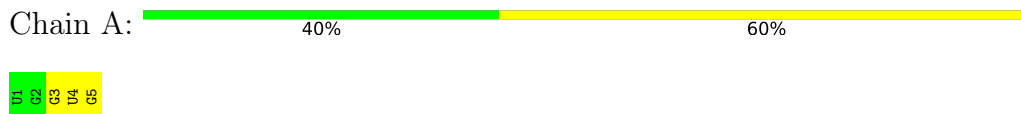
Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

- Molecule 1: RNA-binding protein FUS



- Molecule 2: RNA (5'-R(*UP*GP*GP*UP*G)-3')



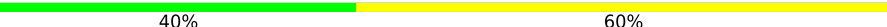
4.2.2 Score per residue for model 2

- Molecule 1: RNA-binding protein FUS

Chain B:  61% 5% 34%



- Molecule 2: RNA (5'-R(*UP*GP*GP*UP*G)-3')

Chain A:  40% 60%



4.2.3 Score per residue for model 3

- Molecule 1: RNA-binding protein FUS

Chain B:  63% 34%



- Molecule 2: RNA (5'-R(*UP*GP*GP*UP*G)-3')

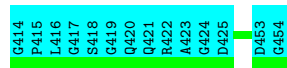
Chain A:  80% 20%



4.2.4 Score per residue for model 4

- Molecule 1: RNA-binding protein FUS

Chain B:  66% 34%



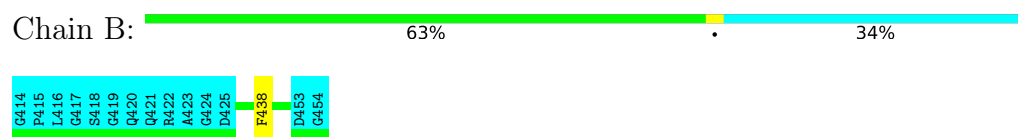
- Molecule 2: RNA (5'-R(*UP*GP*GP*UP*G)-3')

Chain A:  60% 40%



4.2.5 Score per residue for model 5

- Molecule 1: RNA-binding protein FUS



- Molecule 2: RNA (5'-R(*UP*GP*GP*UP*G)-3')



4.2.6 Score per residue for model 6

- Molecule 1: RNA-binding protein FUS

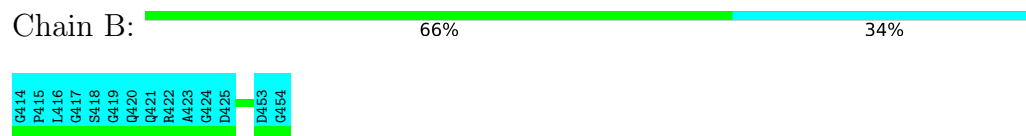


- Molecule 2: RNA (5'-R(*UP*GP*GP*UP*G)-3')



4.2.7 Score per residue for model 7

- Molecule 1: RNA-binding protein FUS



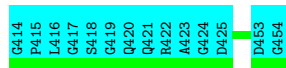
- Molecule 2: RNA (5'-R(*UP*GP*GP*UP*G)-3')



4.2.8 Score per residue for model 8

- Molecule 1: RNA-binding protein FUS

Chain B:  66% 34%



- Molecule 2: RNA (5'-R(*UP*GP*GP*UP*G)-3')

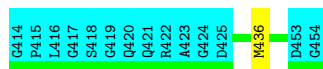
Chain A:  80% 20%



4.2.9 Score per residue for model 9

- Molecule 1: RNA-binding protein FUS

Chain B:  63% 34%



- Molecule 2: RNA (5'-R(*UP*GP*GP*UP*G)-3')

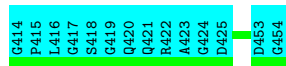
Chain A:  60% 40%



4.2.10 Score per residue for model 10

- Molecule 1: RNA-binding protein FUS

Chain B:  66% 34%



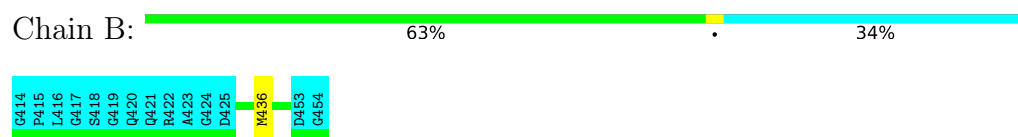
- Molecule 2: RNA (5'-R(*UP*GP*GP*UP*G)-3')

Chain A:  80% 20%

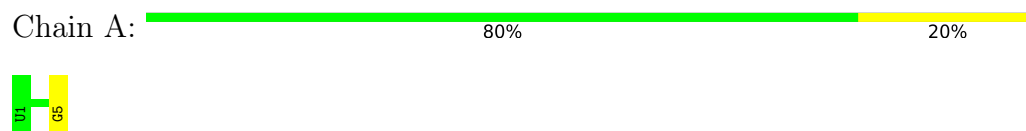


4.2.11 Score per residue for model 11

- Molecule 1: RNA-binding protein FUS

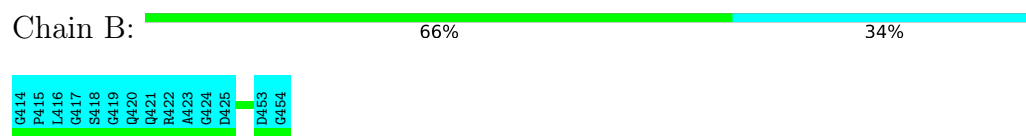


- Molecule 2: RNA (5'-R(*UP*GP*GP*UP*G)-3')



4.2.12 Score per residue for model 12

- Molecule 1: RNA-binding protein FUS

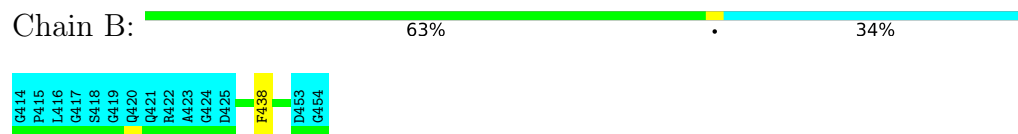


- Molecule 2: RNA (5'-R(*UP*GP*GP*UP*G)-3')



4.2.13 Score per residue for model 13

- Molecule 1: RNA-binding protein FUS

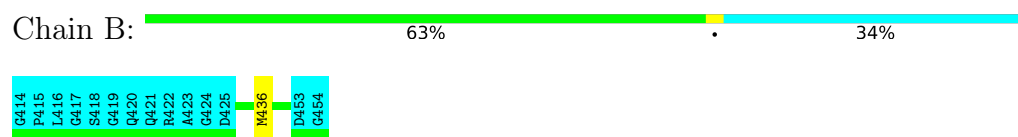


- Molecule 2: RNA (5'-R(*UP*GP*GP*UP*G)-3')

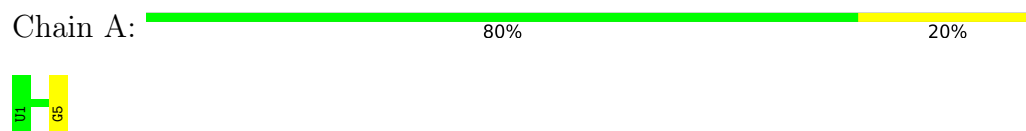


4.2.14 Score per residue for model 14

- Molecule 1: RNA-binding protein FUS

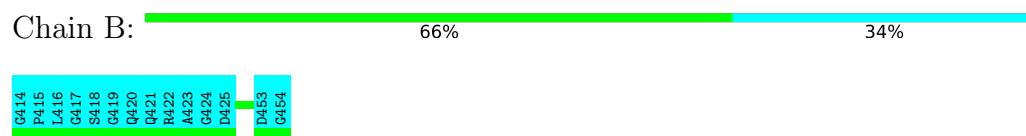


- Molecule 2: RNA (5'-R(*UP*GP*GP*UP*G)-3')

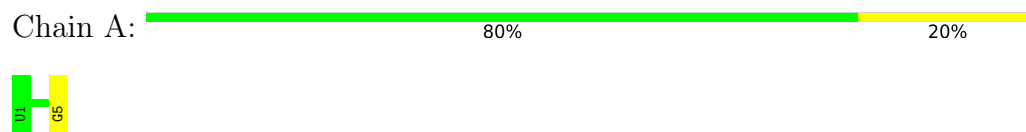


4.2.15 Score per residue for model 15

- Molecule 1: RNA-binding protein FUS

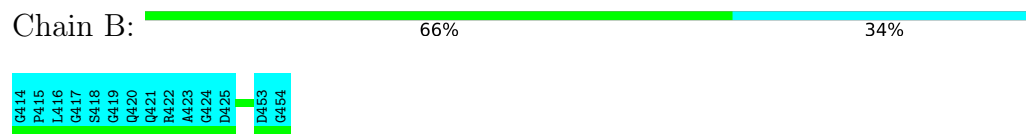


- Molecule 2: RNA (5'-R(*UP*GP*GP*UP*G)-3')



4.2.16 Score per residue for model 16

- Molecule 1: RNA-binding protein FUS

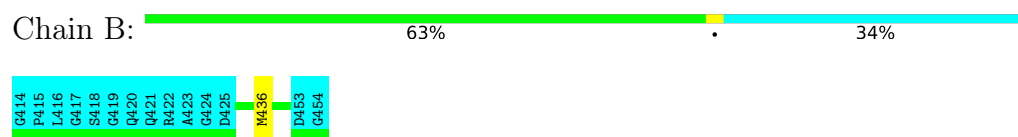


- Molecule 2: RNA (5'-R(*UP*GP*GP*UP*G)-3')



4.2.17 Score per residue for model 17

- Molecule 1: RNA-binding protein FUS

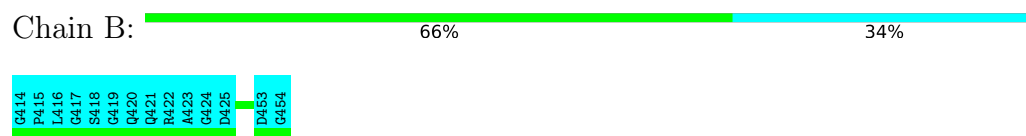


- Molecule 2: RNA (5'-R(*UP*GP*GP*UP*G)-3')



4.2.18 Score per residue for model 18

- Molecule 1: RNA-binding protein FUS

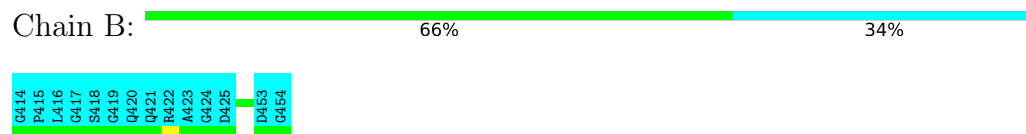


- Molecule 2: RNA (5'-R(*UP*GP*GP*UP*G)-3')



4.2.19 Score per residue for model 19 (medoid)

- Molecule 1: RNA-binding protein FUS



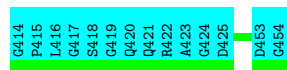
- Molecule 2: RNA (5'-R(*UP*GP*GP*UP*G)-3')



4.2.20 Score per residue for model 20

- Molecule 1: RNA-binding protein FUS

Chain B: 66% 34%



- Molecule 2: RNA (5'-R(*UP*GP*GP*UP*G)-3')

Chain A: 80% 20%



5 Refinement protocol and experimental data overview

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

Of the 500 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
CYANA	structure calculation	
Amber	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	2
Total number of shifts	499
Number of shifts mapped to atoms	499
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](#)

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

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	B	222	201	201	0±1
2	A	106	53	55	0±1
All	All	6580	5080	5120	6

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:B:438:PHE:CD2	2:A:2:G:C2	0.47	3.03	6	2
1:B:438:PHE:CE1	2:A:3:G:C5	0.45	3.04	6	1
1:B:438:PHE:CE2	2:A:3:G:C5	0.43	3.06	5	1
1:B:438:PHE:CE2	2:A:3:G:C4	0.40	3.08	13	1
1:B:440:TRP:CZ2	2:A:1:U:H1'	0.40	2.52	6	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	B	27/41 (66%)	24±0 (89±0%)	3±0 (11±0%)	0±0 (0±0%)	100	100
All	All	540/820 (66%)	480 (89%)	60 (11%)	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	B	26/34 (76%)	26±0 (99±2%)	0±0 (1±2%)	61	94
All	All	520/680 (76%)	514 (99%)	6 (1%)	61	94

All 1 unique residues with a non-rotameric sidechain are listed below.

Mol	Chain	Res	Type	Models (Total)
1	B	436	MET	6

6.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers	Suiteness
2	A	4/5 (80%)	1±0 (25±0%)	0±1 (12±15%)	0.23±0.00
All	All	80/100 (80%)	20 (25%)	10 (12%)	0.23

The overall RNA backbone suiteness is 0.13.

All unique RNA backbone outliers are listed below:

Mol	Chain	Res	Type	Models (Total)
2	A	5	G	20

All unique RNA pucker outliers are listed below:

Mol	Chain	Res	Type	Models (Total)
2	A	4	U	7
2	A	3	G	3

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 oligosaccharides 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 83% for the well-defined parts and 82% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *632uggug_starch_STAR_ambig*

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	430
Number of shifts mapped to atoms	430
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	3

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	41	-0.04 ± 0.31	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	36	0.33 ± 0.32	None needed (< 0.5 ppm)
$^{13}\text{C}'$	0	—	None (insufficient data)
^{15}N	36	-1.76 ± 0.73	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 69%, i.e. 309 atoms were assigned a chemical shift out of a possible 451. 0 out of 0 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	100/127 (79%)	50/50 (100%)	27/54 (50%)	23/23 (100%)
Sidechain	178/196 (91%)	119/123 (97%)	52/61 (85%)	7/12 (58%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	31/34 (91%)	17/17 (100%)	12/15 (80%)	2/2 (100%)
Sugar	0/55 (0%)	0/30 (0%)	0/25 (0%)	0/0 (—%)
Base	0/39 (0%)	0/24 (0%)	0/7 (0%)	0/8 (0%)
Overall	309/451 (69%)	186/244 (76%)	91/162 (56%)	32/45 (71%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 72%, i.e. 429 atoms were assigned a chemical shift out of a possible 599. 0 out of 1 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	158/200 (79%)	81/82 (99%)	41/82 (50%)	36/36 (100%)
Sidechain	240/271 (89%)	161/170 (95%)	70/84 (83%)	9/17 (53%)
Aromatic	31/34 (91%)	17/17 (100%)	12/15 (80%)	2/2 (100%)
Sugar	0/55 (0%)	0/30 (0%)	0/25 (0%)	0/0 (—%)
Base	0/39 (0%)	0/24 (0%)	0/7 (0%)	0/8 (0%)
Overall	429/599 (72%)	259/323 (80%)	123/213 (58%)	47/63 (75%)

7.1.4 Statistically unusual chemical shifts [i](#)

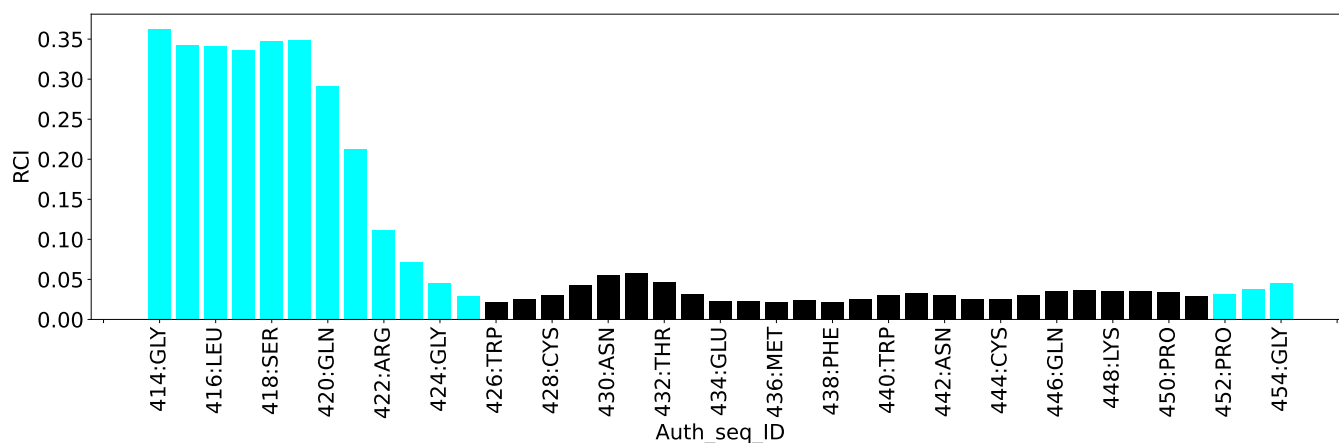
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	B	451	LYS	HG2	-0.85	0.13 – 2.61	-9.0
1	B	437	ASN	HB2	0.39	1.27 – 4.34	-7.9
1	B	437	ASN	HD21	4.30	4.94 – 9.72	-6.3

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 B:



7.2 Chemical shift list 2

File name: working_cs.cif

Chemical shift list name: *uggug632_manual_STAR_copy*

7.2.1 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	69
Number of shifts mapped to atoms	69
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

7.2.2 Chemical shift referencing [i](#)

No chemical shift referencing corrections were calculated (not enough data).

7.2.3 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 14%, i.e. 65 atoms were assigned a chemical shift out of a possible 451. 0 out of 0 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	0/127 (0%)	0/50 (0%)	0/54 (0%)	0/23 (0%)

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	Total	¹H	¹³C	¹⁵N
Sidechain	0/196 (0%)	0/123 (0%)	0/61 (0%)	0/12 (0%)
Aromatic	0/34 (0%)	0/17 (0%)	0/15 (0%)	0/2 (0%)
Sugar	55/55 (100%)	30/30 (100%)	25/25 (100%)	0/0 (—%)
Base	10/39 (26%)	5/24 (21%)	5/7 (71%)	0/8 (0%)
Overall	65/451 (14%)	35/244 (14%)	30/162 (19%)	0/45 (0%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 11%, i.e. 65 atoms were assigned a chemical shift out of a possible 599. 0 out of 1 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Backbone	0/200 (0%)	0/82 (0%)	0/82 (0%)	0/36 (0%)
Sidechain	0/271 (0%)	0/170 (0%)	0/84 (0%)	0/17 (0%)
Aromatic	0/34 (0%)	0/17 (0%)	0/15 (0%)	0/2 (0%)
Sugar	55/55 (100%)	30/30 (100%)	25/25 (100%)	0/0 (—%)
Base	10/39 (26%)	5/24 (21%)	5/7 (71%)	0/8 (0%)
Overall	65/599 (11%)	35/323 (11%)	30/213 (14%)	0/63 (0%)

7.2.4 Statistically unusual chemical shifts [i](#)

There are no statistically unusual chemical shifts.

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

No *random coil index*(RCI) plot could be generated from the current chemical shift list. RCI is only applicable to proteins