



# wwPDB NMR Structure Validation Summary Report ⓘ

Apr 20, 2024 – 08:40 AM EDT

PDB ID : 5JTM  
BMRB ID : 30081  
Title : The structure of chaperone SecB in complex with unstructured PhoA binding site a  
Authors : Huang, C.; Saio, T.; Rossi, P.; Kalodimos, C.G.  
Deposited on : 2016-05-09

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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The following versions of software and data (see [references ⓘ](#)) 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)  
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) : 2.36.2

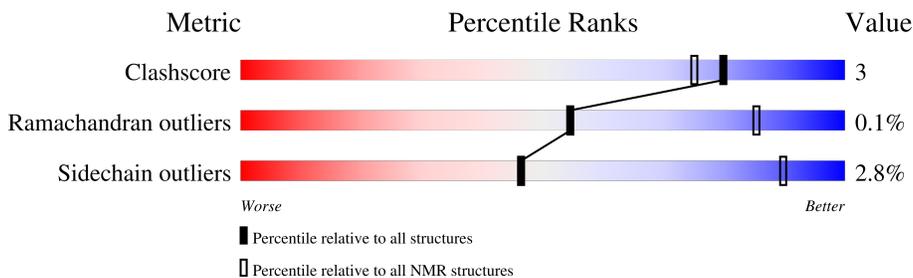
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*SOLUTION NMR*

The overall completeness of chemical shifts assignment is 13%.

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  $\geq 3$ , 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	155	71% 26%
1	B	155	79% 19%
1	C	155	75% 20%
1	D	155	77% 21%
2	E	25	100%
2	F	25	100%
2	G	25	100%
2	H	25	100%

## 2 Ensemble composition and analysis i

This entry contains 20 models. Model 20 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:11-A:86, A:95-A:133, B:9-B:134, C:11-C:134, D:10-D:131 (487)	0.76	20

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 4 clusters and 2 single-model clusters were found.

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

### 3 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 11104 atoms, of which 5488 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Protein-export protein SecB.

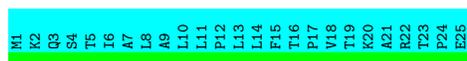
Mol	Chain	Residues	Atoms						Trace
1	A	155	Total	C	H	N	O	S	0
			2367	762	1155	198	243	9	
1	B	155	Total	C	H	N	O	S	0
			2367	762	1155	198	243	9	
1	C	155	Total	C	H	N	O	S	0
			2367	762	1155	198	243	9	
1	D	155	Total	C	H	N	O	S	0
			2367	762	1155	198	243	9	

- Molecule 2 is a protein called Alkaline phosphatase.

Mol	Chain	Residues	Atoms						Trace
2	E	25	Total	C	H	N	O	S	0
			409	126	217	31	34	1	
2	F	25	Total	C	H	N	O	S	0
			409	126	217	31	34	1	
2	G	25	Total	C	H	N	O	S	0
			409	126	217	31	34	1	
2	H	25	Total	C	H	N	O	S	0
			409	126	217	31	34	1	

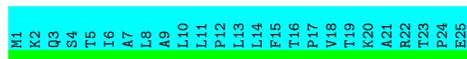


Chain F:  100%



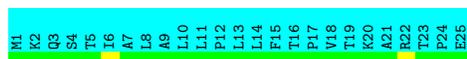
- Molecule 2: Alkaline phosphatase

Chain G:  100%



- Molecule 2: Alkaline phosphatase

Chain H:  100%

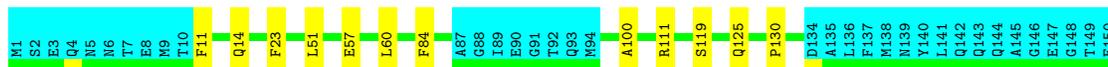


## 4.2 Residue scores for the representative (medoid) model from the NMR ensemble

The representative model is number 20. Colouring as in section 4.1 above.

- Molecule 1: Protein-export protein SecB

Chain A:  66% 8% 26%



- Molecule 1: Protein-export protein SecB

Chain B:  75% 6% 19%

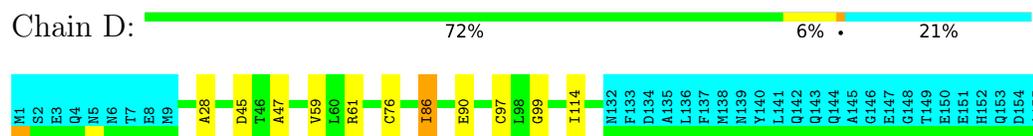


- Molecule 1: Protein-export protein SecB

Chain C:  70% 10% 20%



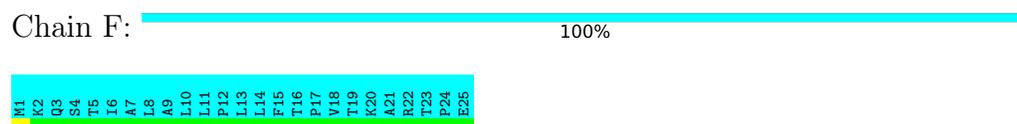
- Molecule 1: Protein-export protein SecB



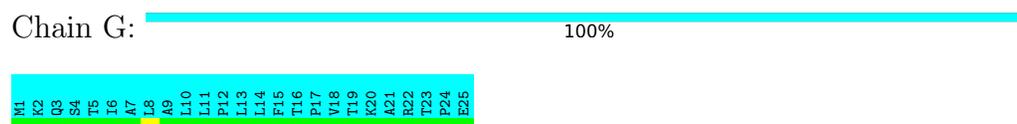
- Molecule 2: Alkaline phosphatase



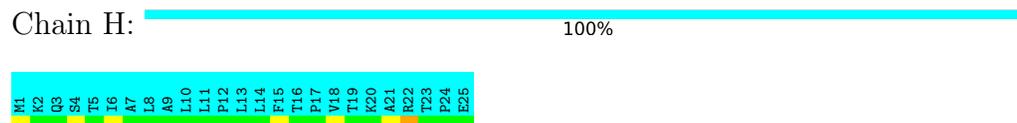
- Molecule 2: Alkaline phosphatase



- Molecule 2: Alkaline phosphatase



- Molecule 2: Alkaline phosphatase



## 5 Refinement protocol and experimental data overview

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

Of the 100 calculated structures, 20 were deposited, based on the following criterion: *target function*.

The following table shows the software used for structure solution, optimisation and refinement.

Software name	Classification	Version
CNS	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	8
Total number of shifts	5090
Number of shifts mapped to atoms	5090
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	13%

## 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	0.83±0.01	0±0/927 ( 0.0± 0.0%)	0.62±0.02	0±0/1266 ( 0.0± 0.0%)
1	B	0.85±0.02	0±0/1004 ( 0.0± 0.0%)	0.63±0.01	0±0/1369 ( 0.0± 0.0%)
1	C	0.84±0.02	0±0/989 ( 0.0± 0.0%)	0.64±0.02	0±0/1349 ( 0.0± 0.0%)
1	D	0.83±0.01	0±0/968 ( 0.0± 0.0%)	0.62±0.01	0±0/1321 ( 0.0± 0.0%)
All	All	0.84	0/77760 ( 0.0%)	0.63	2/106100 ( 0.0%)

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	B	0.0±0.0	0.1±0.2
All	All	0	1

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	101	TYR	CB-CG-CD2	6.52	124.91	121.00	1	1
1	A	101	TYR	CA-CB-CG	5.75	124.31	113.40	1	1

There are no chirality outliers.

All unique planar outliers are listed below.

Mol	Chain	Res	Type	Group	Models (Total)
1	B	10	THR	Peptide	1

## 6.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in each chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes averaged over the ensemble.

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	904	883	881	5±1
1	B	981	955	953	6±2
1	C	966	939	937	7±2
1	D	946	927	925	5±2
2	E	0	0	0	0±0
2	F	0	0	0	0±0
2	G	0	0	0	0±0
2	H	0	0	0	0±0
All	All	75940	74080	73920	407

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

5 of 174 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:B:25:ALA:HB1	1:B:28:ALA:HB2	0.80	1.53	14	7
1:B:13:ILE:HD11	1:B:105:ILE:HD13	0.68	1.66	16	1
1:A:31:VAL:HG21	1:A:73:ALA:HA	0.64	1.67	5	16
1:B:25:ALA:CB	1:B:28:ALA:HB2	0.61	2.24	14	6
1:D:20:ASP:HB3	1:D:79:GLN:HB2	0.60	1.73	19	6

## 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	115/155 (74%)	109±2 (95±1%)	6±2 (5±1%)	0±0 (0±0%)	100	100
1	B	126/155 (81%)	119±2 (94±2%)	7±2 (6±2%)	0±0 (0±0%)	50	82

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	C	124/155 (80%)	115±2 (93±2%)	9±2 (7±2%)	0±0 (0±0%)	54 85
1	D	122/155 (79%)	116±2 (95±1%)	5±2 (4±1%)	0±0 (0±0%)	50 82
2	E	0	-	-	-	-
2	F	0	-	-	-	-
2	G	0	-	-	-	-
2	H	0	-	-	-	-
All	All	9740/14400 (68%)	9171 (94%)	556 (6%)	13 (0%)	54 85

All 4 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	D	28	ALA	6
1	B	9	MET	3
1	B	130	PRO	2
1	C	130	PRO	2

### 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	100/132 (76%)	98±1 (98±1%)	2±1 (2±1%)	59 93
1	B	108/132 (82%)	105±2 (97±2%)	3±2 (3±2%)	43 88
1	C	106/132 (80%)	102±1 (96±1%)	4±1 (4±1%)	36 84
1	D	104/132 (79%)	102±1 (98±1%)	2±1 (2±1%)	57 93
2	E	0	-	-	-
2	F	0	-	-	-
2	G	0	-	-	-
2	H	0	-	-	-
All	All	8360/12320 (68%)	8130 (97%)	230 (3%)	46 90

5 of 70 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	C	34	LYS	20
1	C	117	MET	20
1	B	12	GLN	15
1	D	70	GLU	13
1	D	90	GLU	7

### 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 13% for the well-defined parts and 13% for the entire structure.

### 7.1 Chemical shift list 1

File name: working\_cs.cif

Chemical shift list name: *assigned\_chemical\_shift\_list\_1*

#### 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	1049
Number of shifts mapped to atoms	1049
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

#### 7.1.2 Chemical shift referencing i

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	139	$0.25 \pm 0.13$	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	128	$0.85 \pm 0.17$	Should be checked
$^{13}\text{C}'$	137	$0.29 \pm 0.10$	None needed (< 0.5 ppm)
$^{15}\text{N}$	133	$-1.15 \pm 0.27$	Should be applied

#### 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 13%, i.e. 829 atoms were assigned a chemical shift out of a possible 6525. 0 out of 80 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^1\text{H}$	$^{13}\text{C}$	$^{15}\text{N}$
Backbone	422/2405 (18%)	103/972 (11%)	216/974 (22%)	103/459 (22%)
Sidechain	342/3554 (10%)	189/2328 (8%)	153/1116 (14%)	0/110 (0%)

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	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Aromatic	65/566 (11%)	33/275 (12%)	31/271 (11%)	1/20 (5%)
Overall	829/6525 (13%)	325/3575 (9%)	400/2361 (17%)	104/589 (18%)

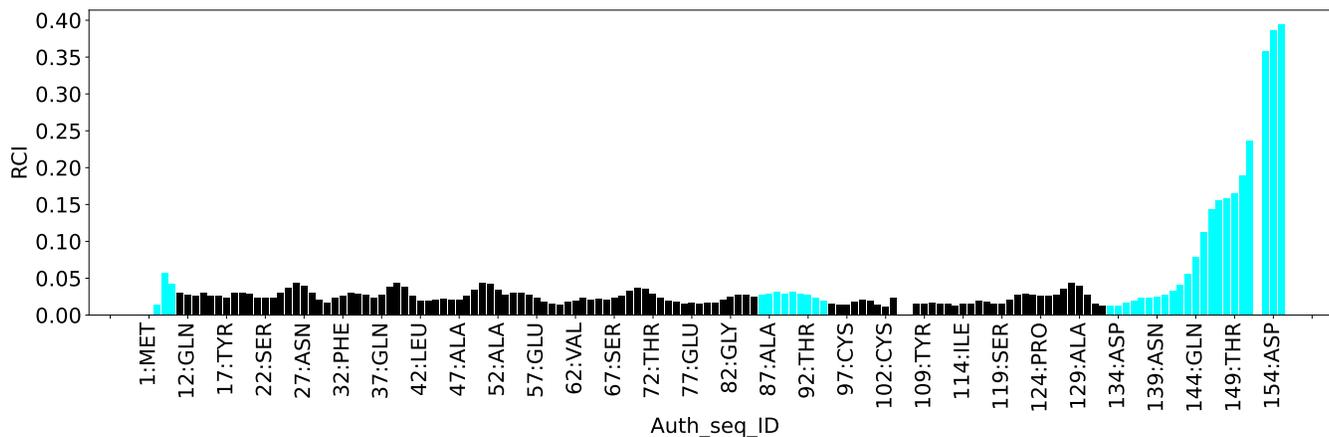
### 7.1.4 Statistically unusual chemical shifts [i](#)

There are no statistically unusual chemical shifts.

### 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:



## 7.2 Chemical shift list 2

File name: working\_cs.cif

Chemical shift list name: *assigned\_chemical\_shift\_list\_2*

### 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	1044
Number of shifts mapped to atoms	1044
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](#)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	140	$0.28 \pm 0.06$	None needed ( $< 0.5$ ppm)
$^{13}\text{C}_\beta$	126	$0.79 \pm 0.20$	Should be checked
$^{13}\text{C}'$	135	$0.26 \pm 0.08$	None needed ( $< 0.5$ ppm)
$^{15}\text{N}$	132	$-1.09 \pm 0.25$	Should be applied

### 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 13%, i.e. 824 atoms were assigned a chemical shift out of a possible 6525. 0 out of 80 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^1\text{H}$	$^{13}\text{C}$	$^{15}\text{N}$
Backbone	419/2405 (17%)	102/972 (10%)	215/974 (22%)	102/459 (22%)
Sidechain	340/3554 (10%)	189/2328 (8%)	151/1116 (14%)	0/110 (0%)
Aromatic	65/566 (11%)	33/275 (12%)	31/271 (11%)	1/20 (5%)
Overall	824/6525 (13%)	324/3575 (9%)	397/2361 (17%)	103/589 (17%)

### 7.2.4 Statistically unusual chemical shifts [i](#)

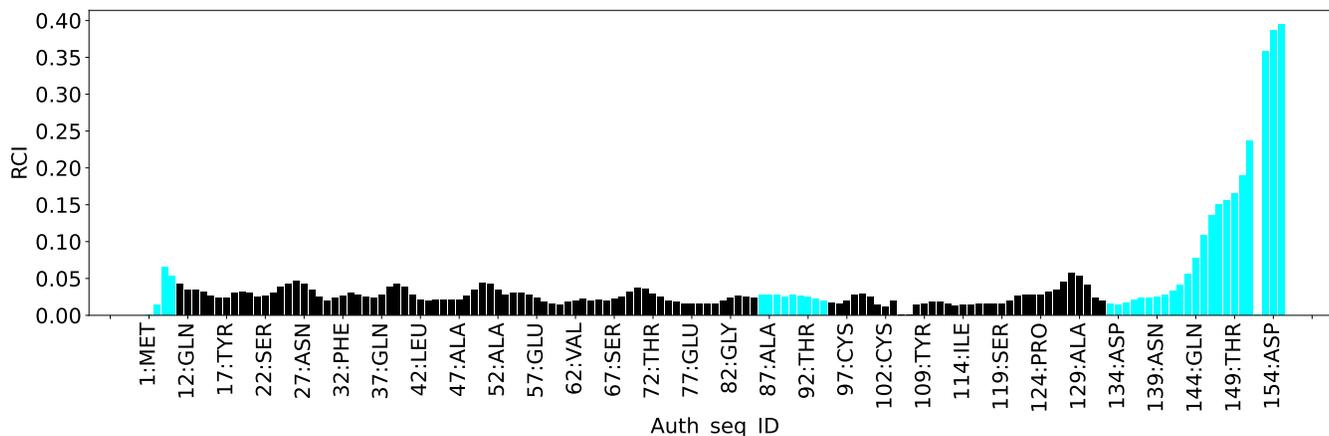
There are no statistically unusual chemical shifts.

### 7.2.5 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:



## 7.3 Chemical shift list 3

File name: working\_cs.cif

Chemical shift list name: *assigned\_chemical\_shift\_list\_3*

### 7.3.1 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	1044
Number of shifts mapped to atoms	1044
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

### 7.3.2 Chemical shift referencing [i](#)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	140	$0.28 \pm 0.08$	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	126	$0.77 \pm 0.14$	Should be checked
$^{13}\text{C}'$	135	$0.26 \pm 0.11$	None needed (< 0.5 ppm)
$^{15}\text{N}$	132	$-1.09 \pm 0.28$	Should be applied

### 7.3.3 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 13%, i.e. 824 atoms were assigned a chemical shift out of a possible 6525. 0 out of 80 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Backbone	419/2405 (17%)	102/972 (10%)	215/974 (22%)	102/459 (22%)
Sidechain	340/3554 (10%)	189/2328 (8%)	151/1116 (14%)	0/110 (0%)
Aromatic	65/566 (11%)	33/275 (12%)	31/271 (11%)	1/20 (5%)
Overall	824/6525 (13%)	324/3575 (9%)	397/2361 (17%)	103/589 (17%)

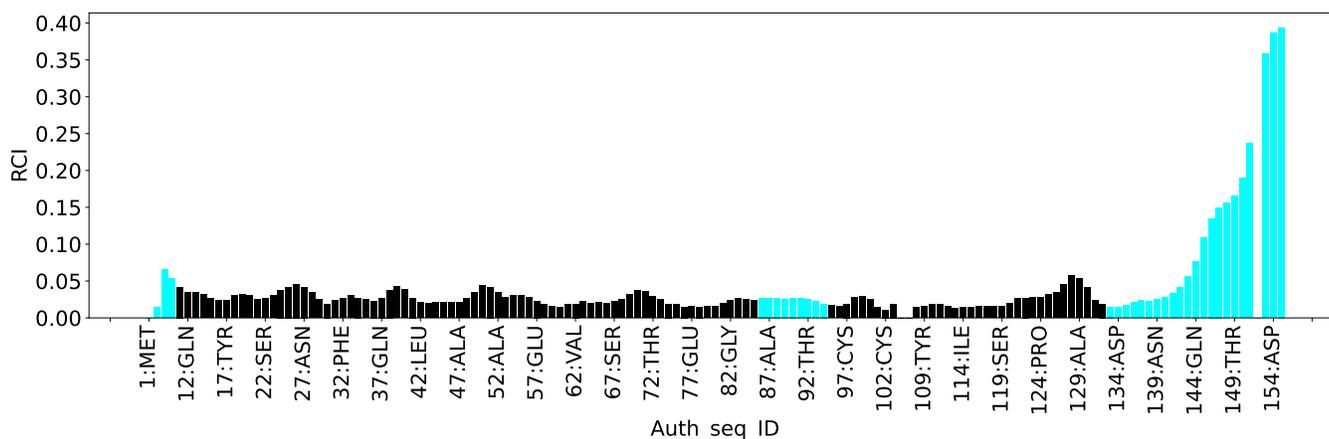
### 7.3.4 Statistically unusual chemical shifts [i](#)

There are no statistically unusual chemical shifts.

### 7.3.5 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:



## 7.4 Chemical shift list 4

File name: working\_cs.cif

Chemical shift list name: *assigned\_chemical\_shift\_list\_4*

#### 7.4.1 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	1049
Number of shifts mapped to atoms	1049
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

#### 7.4.2 Chemical shift referencing [i](#)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	139	$0.25 \pm 0.17$	None needed ( $< 0.5$ ppm)
$^{13}\text{C}_\beta$	128	$0.84 \pm 0.11$	Should be checked
$^{13}\text{C}'$	137	$0.29 \pm 0.17$	None needed ( $< 0.5$ ppm)
$^{15}\text{N}$	133	$-1.15 \pm 0.13$	Should be applied

#### 7.4.3 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 13%, i.e. 829 atoms were assigned a chemical shift out of a possible 6525. 0 out of 80 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^1\text{H}$	$^{13}\text{C}$	$^{15}\text{N}$
Backbone	422/2405 (18%)	103/972 (11%)	216/974 (22%)	103/459 (22%)
Sidechain	342/3554 (10%)	189/2328 (8%)	153/1116 (14%)	0/110 (0%)
Aromatic	65/566 (11%)	33/275 (12%)	31/271 (11%)	1/20 (5%)
Overall	829/6525 (13%)	325/3575 (9%)	400/2361 (17%)	104/589 (18%)

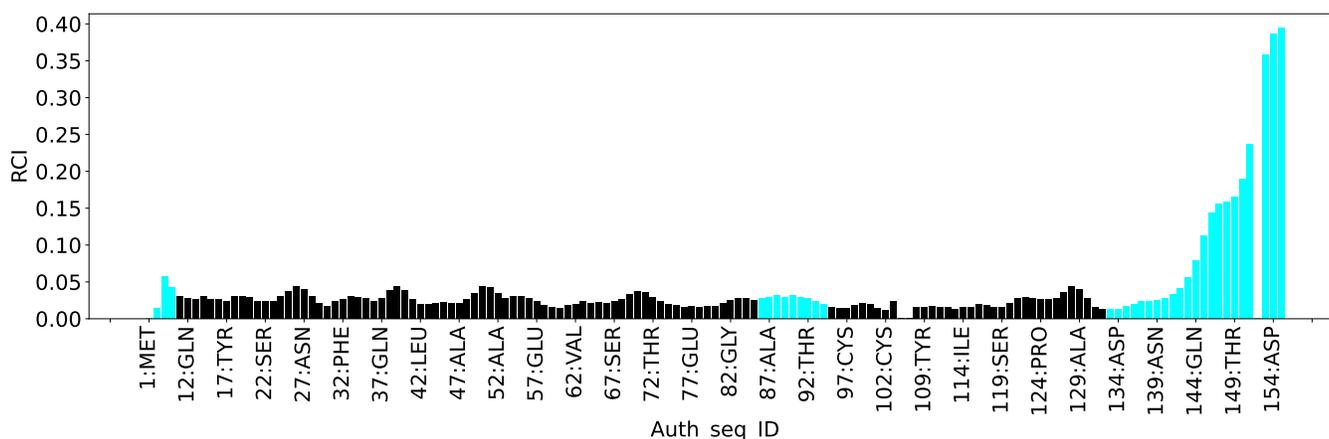
#### 7.4.4 Statistically unusual chemical shifts [i](#)

There are no statistically unusual chemical shifts.

### 7.4.5 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:



## 7.5 Chemical shift list 5

File name: working\_cs.cif

Chemical shift list name: *assigned\_chemical\_shift\_5*

### 7.5.1 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	226
Number of shifts mapped to atoms	226
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

### 7.5.2 Chemical shift referencing [i](#)

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

### 7.5.3 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 0%, i.e. 0 atoms were assigned a chemical shift out of a possible 6525. 0 out of 80 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	<b>Total</b>	<b><sup>1</sup>H</b>	<b><sup>13</sup>C</b>	<b><sup>15</sup>N</b>
Backbone	0/2405 (0%)	0/972 (0%)	0/974 (0%)	0/459 (0%)
Sidechain	0/3554 (0%)	0/2328 (0%)	0/1116 (0%)	0/110 (0%)
Aromatic	0/566 (0%)	0/275 (0%)	0/271 (0%)	0/20 (0%)
Overall	0/6525 (0%)	0/3575 (0%)	0/2361 (0%)	0/589 (0%)

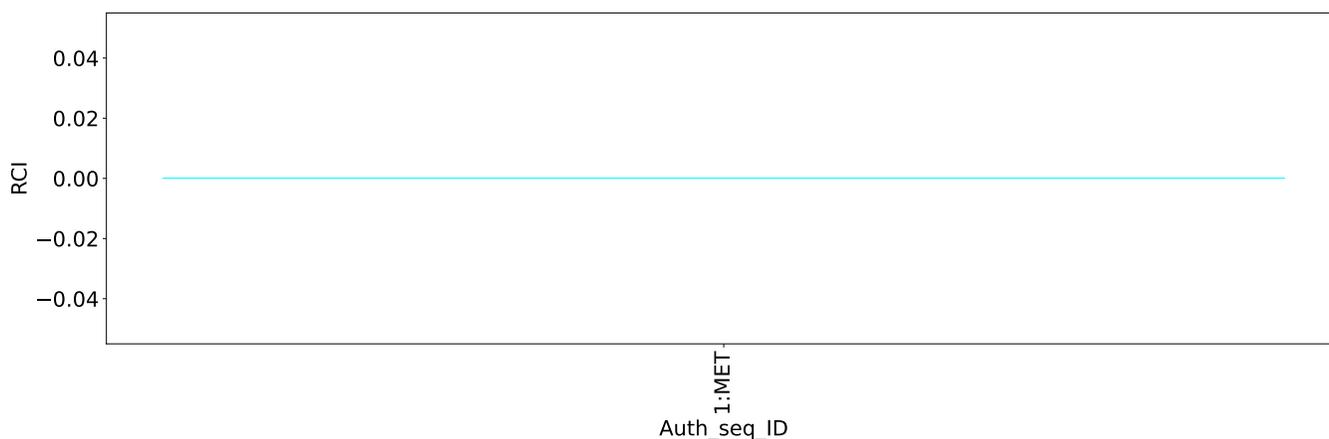
### 7.5.4 Statistically unusual chemical shifts [i](#)

There are no statistically unusual chemical shifts.

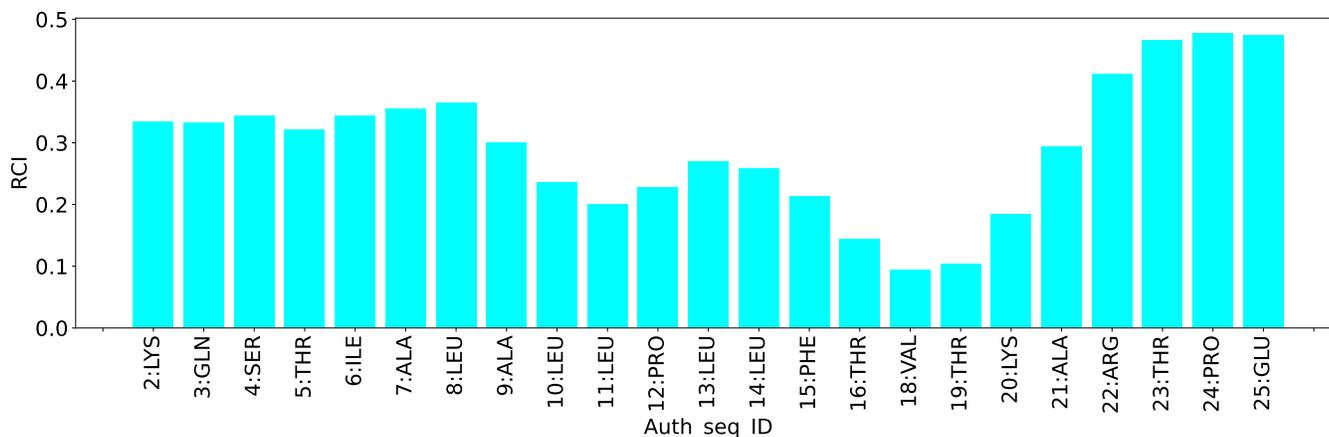
### 7.5.5 Random Coil Index (RCI) plots [i](#)

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:



Random coil index (RCI) for chain E:



## 7.6 Chemical shift list 6

File name: working\_cs.cif

Chemical shift list name: *assigned\_chemical\_shift\_6*

### 7.6.1 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	226
Number of shifts mapped to atoms	226
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

### 7.6.2 Chemical shift referencing [i](#)

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

### 7.6.3 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 0%, i.e. 0 atoms were assigned a chemical shift out of a possible 6525. 0 out of 80 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Backbone	0/2405 (0%)	0/972 (0%)	0/974 (0%)	0/459 (0%)

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	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Sidechain	0/3554 (0%)	0/2328 (0%)	0/1116 (0%)	0/110 (0%)
Aromatic	0/566 (0%)	0/275 (0%)	0/271 (0%)	0/20 (0%)
Overall	0/6525 (0%)	0/3575 (0%)	0/2361 (0%)	0/589 (0%)

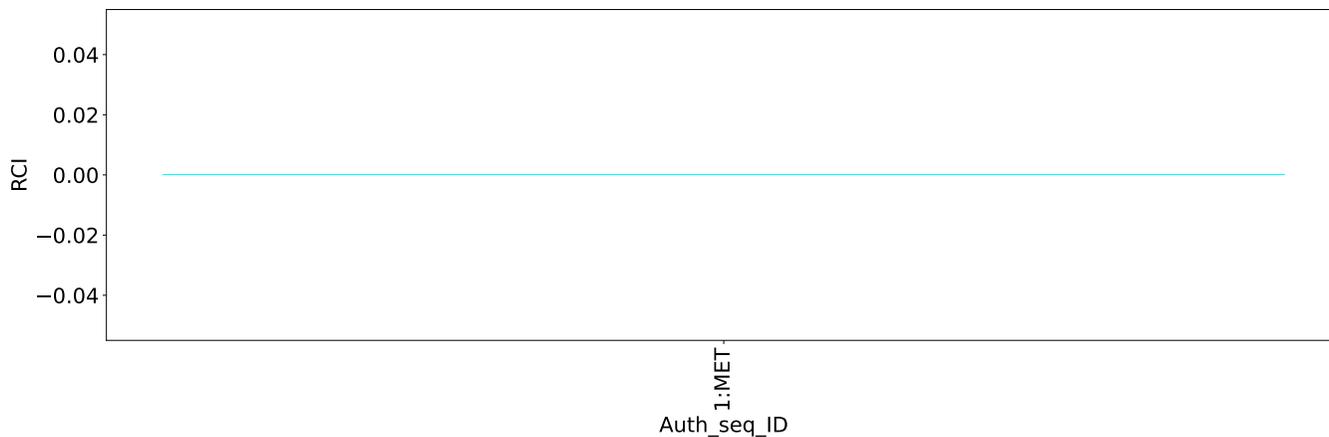
#### 7.6.4 Statistically unusual chemical shifts [i](#)

There are no statistically unusual chemical shifts.

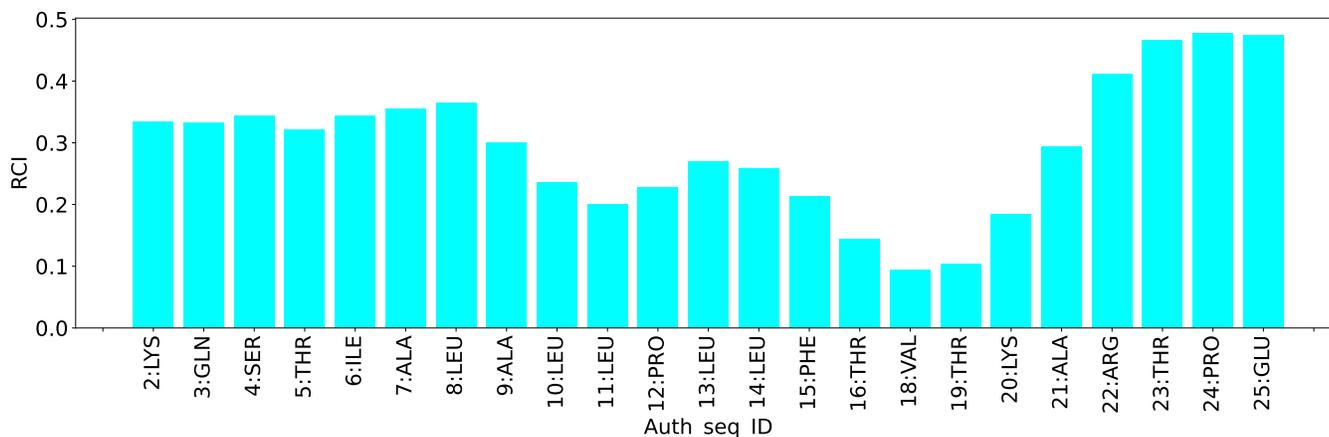
#### 7.6.5 Random Coil Index (RCI) plots [i](#)

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:



Random coil index (RCI) for chain E:



## 7.7 Chemical shift list 7

File name: working\_cs.cif

Chemical shift list name: *assigned\_chemical\_shift\_7*

### 7.7.1 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	226
Number of shifts mapped to atoms	226
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

### 7.7.2 Chemical shift referencing [i](#)

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

### 7.7.3 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 0%, i.e. 0 atoms were assigned a chemical shift out of a possible 6525. 0 out of 80 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Backbone	0/2405 (0%)	0/972 (0%)	0/974 (0%)	0/459 (0%)

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	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Sidechain	0/3554 (0%)	0/2328 (0%)	0/1116 (0%)	0/110 (0%)
Aromatic	0/566 (0%)	0/275 (0%)	0/271 (0%)	0/20 (0%)
Overall	0/6525 (0%)	0/3575 (0%)	0/2361 (0%)	0/589 (0%)

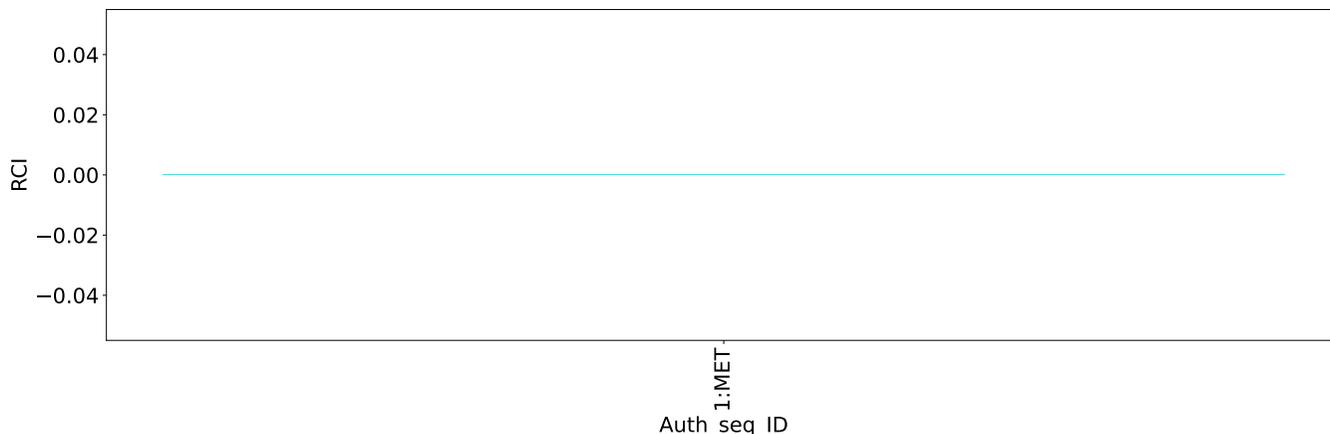
#### 7.7.4 Statistically unusual chemical shifts [i](#)

There are no statistically unusual chemical shifts.

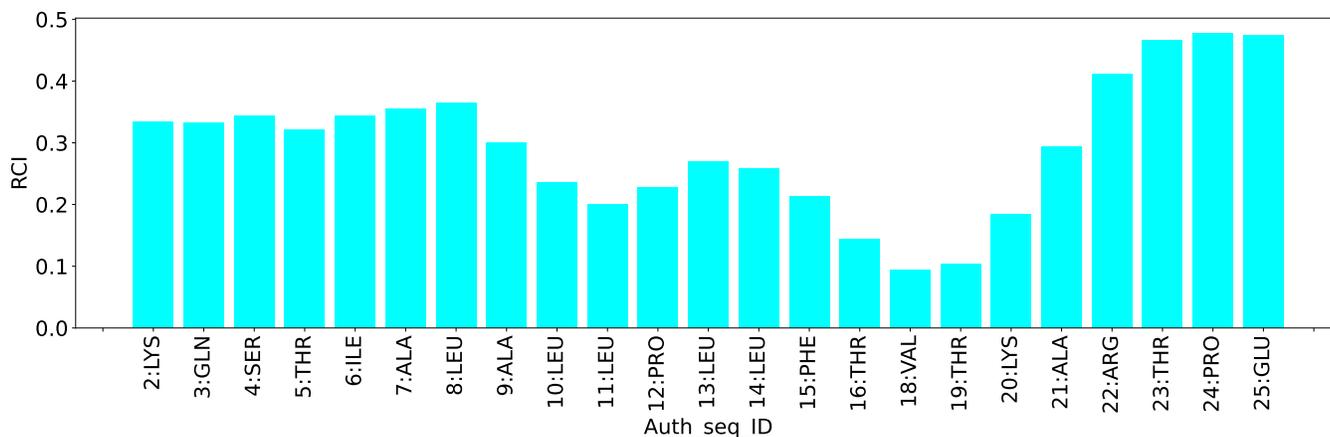
#### 7.7.5 Random Coil Index (RCI) plots [i](#)

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:



Random coil index (RCI) for chain E:



## 7.8 Chemical shift list 8

File name: working\_cs.cif

Chemical shift list name: *assigned\_chemical\_shift\_8*

### 7.8.1 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	226
Number of shifts mapped to atoms	226
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

### 7.8.2 Chemical shift referencing [i](#)

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

### 7.8.3 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 0%, i.e. 0 atoms were assigned a chemical shift out of a possible 6525. 0 out of 80 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Backbone	0/2405 (0%)	0/972 (0%)	0/974 (0%)	0/459 (0%)

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	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Sidechain	0/3554 (0%)	0/2328 (0%)	0/1116 (0%)	0/110 (0%)
Aromatic	0/566 (0%)	0/275 (0%)	0/271 (0%)	0/20 (0%)
Overall	0/6525 (0%)	0/3575 (0%)	0/2361 (0%)	0/589 (0%)

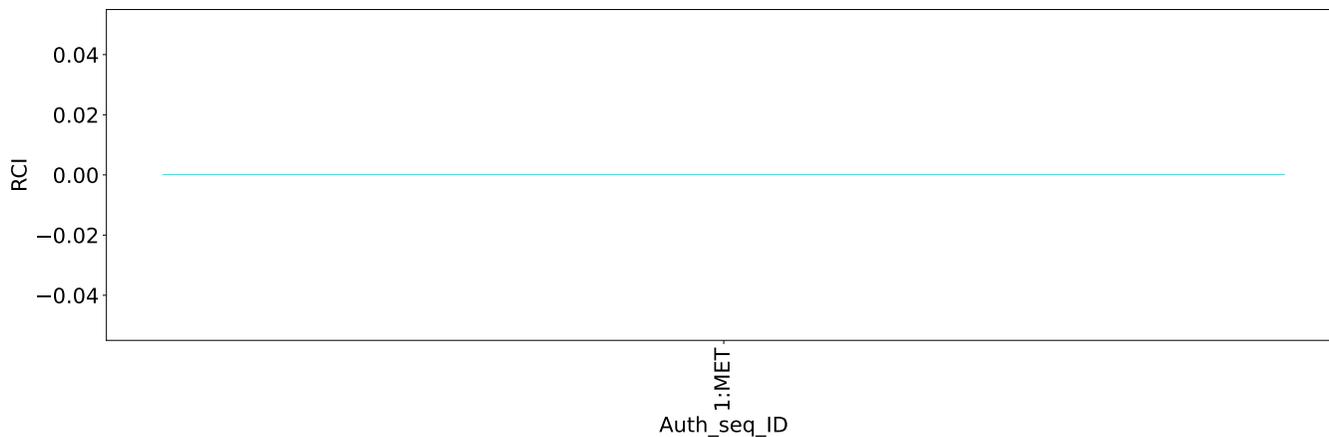
#### 7.8.4 Statistically unusual chemical shifts [i](#)

There are no statistically unusual chemical shifts.

#### 7.8.5 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:



Random coil index (RCI) for chain E:

