



wwPDB NMR Structure Validation Summary Report ⓘ

Mar 8, 2026 – 10:58 AM UTC

PDB ID : 2N1T / pdb_00002n1t
BMRB ID : 6235
Title : Dynamic binding mode of a synaptotagmin-1-SNARE complex in solution
Authors : Brewer, K.; Bacaj, T.; Cavalli, A.; Camilloni, C.; Swarbrick, J.; Liu, J.; Zhou, A.; Zhou, P.; Barlow, N.; Xu, J.; Seven, A.; Prinslow, E.; Voleti, R.; Haussinger, D.; Bonvin, A.; Tomchick, D.; Vendruscolo, M.; Graham, B.; Sudhof, T.; Rizo, J.
Deposited on : 2015-04-21

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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

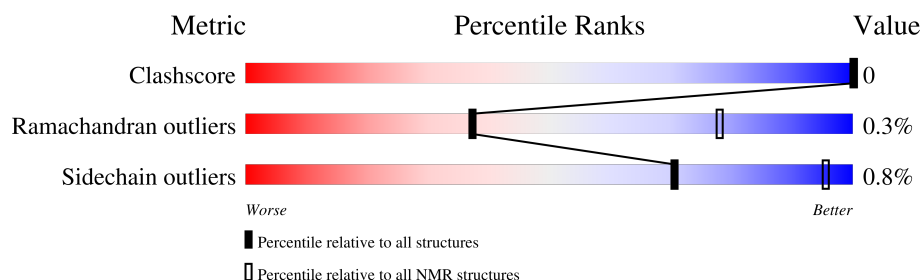
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 12%.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	NMR archive (#Entries)
Clashscore	229148	14424
Ramachandran outliers	224038	12848
Sidechain outliers	223484	12823

The table below summarises the geometric issues observed across the polymeric chains and their fit to the experimental data. The red, orange, yellow and green segments indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A cyan segment indicates the fraction of residues that are not part of the well-defined cores, and a grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	69	84% 16%
2	B	72	86% 14%
3	C	77	83% 17%
4	D	74	88% • 11%
5	E	156	94% 6%

2 Ensemble composition and analysis

This entry contains 5 models. Model 5 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *all these conformers contribute to this dynamics ensemble*.

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:27-A:84, B:195-B:256, C:18-C:81, D:132-D:137, D:142-D:201 (250)	0.95	5
2	E:273-E:418 (146)	1.66	2

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	4, 5
2	1, 3
Single-model clusters	2

3 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 7196 atoms, of which 3605 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Vesicle-associated membrane protein 2.

Mol	Chain	Residues	Atoms						Trace
1	A	69	Total	C	H	N	O	S	0
			1134	347	569	106	111	1	

- Molecule 2 is a protein called Syntaxin-1A.

Mol	Chain	Residues	Atoms						Trace
2	B	72	Total	C	H	N	O	S	0
			1165	362	578	100	120	5	

- Molecule 3 is a protein called Synaptosomal-associated protein 25.

Mol	Chain	Residues	Atoms						Trace
3	C	77	Total	C	H	N	O	S	0
			1242	371	617	115	133	6	

- Molecule 4 is a protein called Synaptosomal-associated protein 25.

Mol	Chain	Residues	Atoms						Trace
4	D	74	Total	C	H	N	O	S	0
			1163	346	576	115	121	5	

- Molecule 5 is a protein called Synaptotagmin-1.

Mol	Chain	Residues	Atoms						Trace
5	E	156	Total	C	H	N	O	S	0
			2492	787	1265	210	225	5	

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	263	SER	-	expression tag	UNP P21579
E	264	GLY	-	expression tag	UNP P21579
E	265	GLY	-	expression tag	UNP P21579
E	266	GLY	-	expression tag	UNP P21579
E	267	GLY	-	expression tag	UNP P21579
E	268	GLY	-	expression tag	UNP P21579

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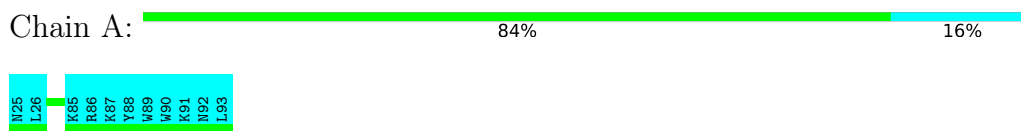
Chain	Residue	Modelled	Actual	Comment	Reference
E	269	ILE	-	expression tag	UNP P21579
E	270	LEU	-	expression tag	UNP P21579

4 Residue-property plots [i](#)

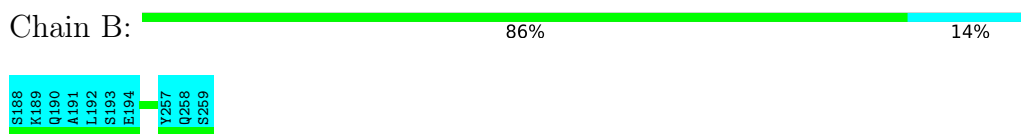
4.1 Average score per residue in the NMR ensemble

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.

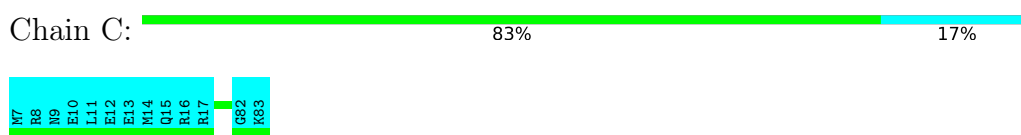
- Molecule 1: Vesicle-associated membrane protein 2



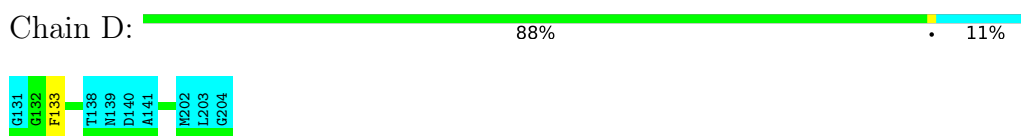
- Molecule 2: Syntaxin-1A



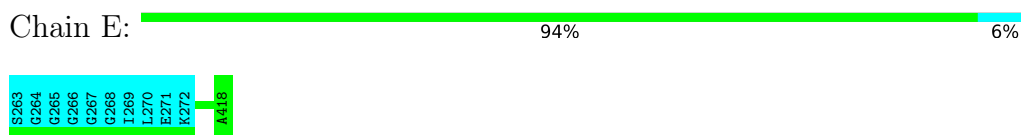
- Molecule 3: Synaptosomal-associated protein 25



- Molecule 4: Synaptosomal-associated protein 25



- Molecule 5: Synaptotagmin-1

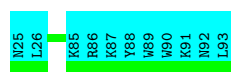


4.2 Residue scores for the representative (medoid) model from the NMR ensemble

The representative model is number 5. Colouring as in section 4.1 above.

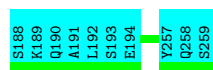
- Molecule 1: Vesicle-associated membrane protein 2

Chain A:  84% 16%



- Molecule 2: Syntaxin-1A

Chain B:  86% 14%



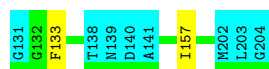
- Molecule 3: Synaptosomal-associated protein 25

Chain C:  83% 17%

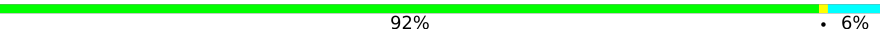


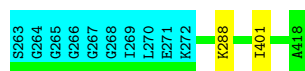
- Molecule 4: Synaptosomal-associated protein 25

Chain D:  86% 11%



- Molecule 5: Synaptotagmin-1

Chain E:  92% 6%



5 Refinement protocol and experimental data overview

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

Of the 10000 calculated structures, 5 were deposited, based on the following criterion: *Contribution to fit PCS data*.

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

Software name	Classification	Version
NAMD	refinement	2.7
GROMACS	refinement	
PLUMED2	refinement	
ALMOST	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	4
Total number of shifts	702
Number of shifts mapped to atoms	702
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	12%

6 Model quality

6.1 Standard geometry

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	0.68±0.10	0±0/455 (0.0± 0.0%)	1.26±0.17	0±0/613 (0.0± 0.0%)
2	B	0.75±0.08	0±0/513 (0.0± 0.0%)	1.31±0.13	0±0/688 (0.0± 0.0%)
3	C	0.69±0.10	0±0/511 (0.0± 0.0%)	1.27±0.19	0±1/683 (0.1± 0.1%)
4	D	0.72±0.09	0±0/536 (0.0± 0.0%)	1.26±0.15	0±0/715 (0.0± 0.0%)
5	E	0.75±0.05	0±0/1190 (0.0± 0.0%)	1.19±0.08	0±1/1607 (0.0± 0.0%)
All	All	0.73	0/16025 (0.0%)	1.25	4/21530 (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
4	D	0.0±0.0	0.6±1.2
5	E	0.0±0.0	0.4±0.5
All	All	0	5

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
3	C	42	ALA	CA-C-N	5.58	126.30	119.99	1	1
3	C	42	ALA	C-N-CA	5.58	126.30	119.99	1	1
5	E	400	PRO	CA-C-N	5.33	127.75	120.35	1	1
5	E	400	PRO	C-N-CA	5.33	127.75	120.35	1	1

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)
4	D	136	ARG	Sidechain	1
4	D	176	ARG	Sidechain	1
4	D	191	ARG	Sidechain	1
5	E	399	ARG	Sidechain	1
5	E	288	LYS	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
All	All	15860	15900	15900	-

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 -.

There are no clashes.

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	58/69 (84%)	57±0 (99±1%)	1±0 (1±1%)	0±0 (0±0%)	100	100
2	B	62/72 (86%)	62±0 (100±0%)	0±0 (0±0%)	0±0 (0±0%)	100	100
3	C	64/77 (83%)	64±0 (100±0%)	0±0 (0±0%)	0±0 (0±0%)	100	100
4	D	66/74 (89%)	64±0 (98±1%)	1±1 (2±1%)	1±0 (1±1%)	16	66
5	E	145/156 (93%)	135±2 (93±1%)	9±2 (6±1%)	1±0 (0±0%)	31	76
All	All	1975/2240 (88%)	1914 (97%)	55 (3%)	6 (0%)	37	78

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)
4	D	133	PHE	2
5	E	333	ASN	2
5	E	381	ASN	1
4	D	137	VAL	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	50/61 (82%)	50±0 (99±1%)	0±0 (1±1%)	70 95
2	B	57/66 (86%)	57±1 (99±1%)	0±1 (1±1%)	73 96
3	C	57/69 (83%)	57±1 (99±1%)	0±1 (1±1%)	73 96
4	D	58/63 (92%)	57±1 (98±2%)	1±1 (2±2%)	52 92
5	E	129/134 (96%)	128±1 (100±1%)	1±1 (0±1%)	78 96
All	All	1755/1965 (89%)	1741 (99%)	14 (1%)	70 95

5 of 13 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)
4	D	133	PHE	2
2	B	214	ASP	1
2	B	250	ASP	1
3	C	23	ASP	1
3	C	81	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](#)

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](#)

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

The completeness of assignment taking into account all chemical shift lists is 12% for the well-defined parts and 11% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *nmr_parameters_1*

7.1.1 Bookkeeping

The following table shows the results of parsing the chemical shift list and reports the number of nuclei with statistically unusual chemical shifts.

Total number of shifts	165
Number of shifts mapped to atoms	165
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

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	55	-0.67 ± 0.16	Should be checked
$^{13}\text{C}_\beta$	0	—	None (insufficient data)
$^{13}\text{C}'$	0	—	None (insufficient data)
^{15}N	55	-0.46 ± 0.27	None needed (< 0.5 ppm)

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 3%, i.e. 147 atoms were assigned a chemical shift out of a possible 5533. 0 out of 67 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	147/1986 (7%)	49/804 (6%)	49/792 (6%)	49/390 (13%)
Sidechain	0/3315 (0%)	0/2132 (0%)	0/1030 (0%)	0/153 (0%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	0/232 (0%)	0/116 (0%)	0/106 (0%)	0/10 (0%)
Overall	147/5533 (3%)	49/3052 (2%)	49/1928 (3%)	49/553 (9%)

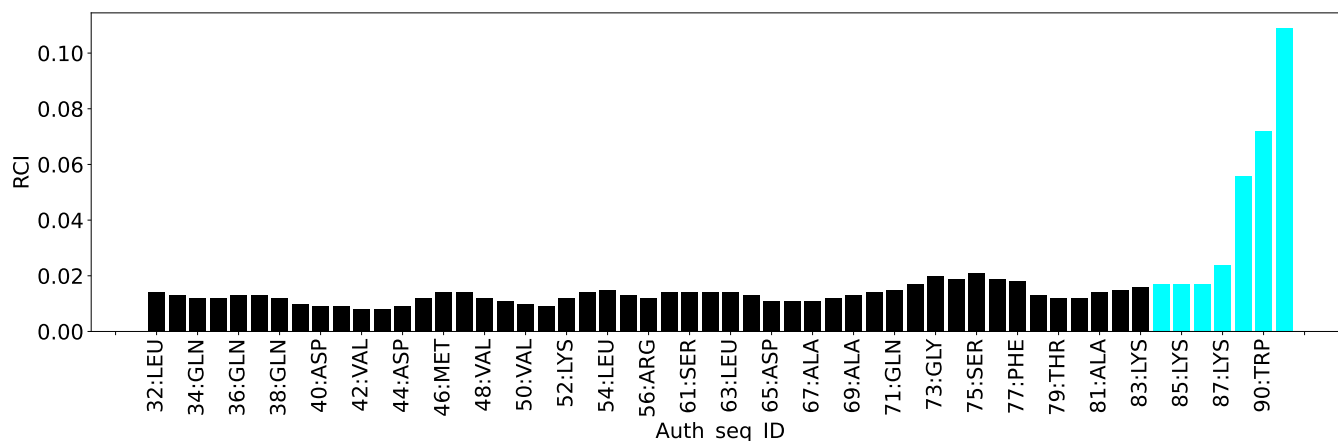
7.1.4 Statistically unusual chemical shifts [i](#)

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: *nmr_parameters_1_dup*

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	152
Number of shifts mapped to atoms	152
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
$^{13}\text{C}_\alpha$	52	-0.85 ± 0.19	Should be checked
$^{13}\text{C}_\beta$	0	—	None (insufficient data)
$^{13}\text{C}'$	0	—	None (insufficient data)
^{15}N	50	-1.28 ± 0.27	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 3%, i.e. 152 atoms were assigned a chemical shift out of a possible 5533. 0 out of 67 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	152/1986 (8%)	50/804 (6%)	52/792 (7%)	50/390 (13%)
Sidechain	0/3315 (0%)	0/2132 (0%)	0/1030 (0%)	0/153 (0%)
Aromatic	0/232 (0%)	0/116 (0%)	0/106 (0%)	0/10 (0%)
Overall	152/5533 (3%)	50/3052 (2%)	52/1928 (3%)	50/553 (9%)

7.2.4 Statistically unusual chemical shifts [i](#)

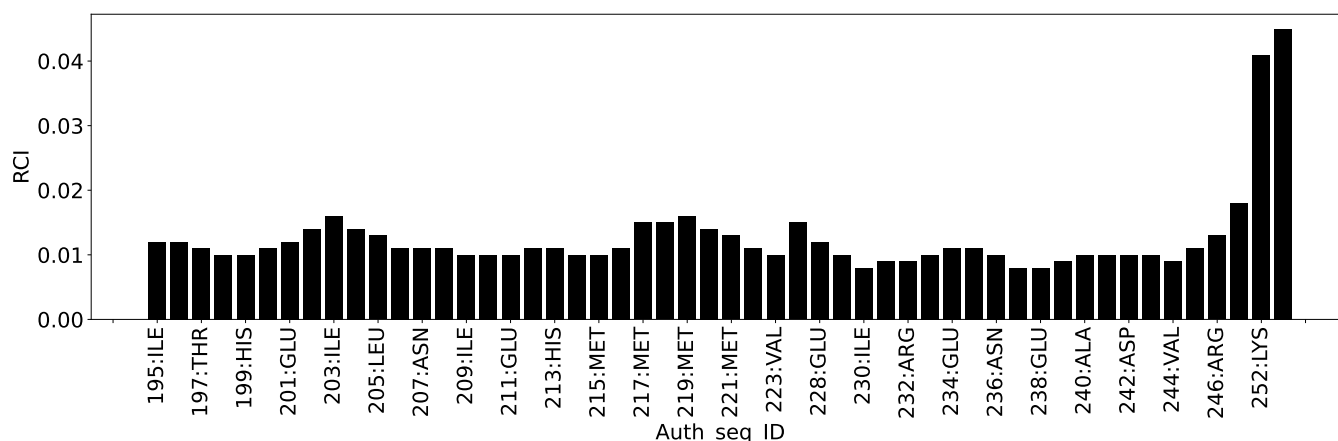
There are no statistically unusual chemical shifts.

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 B:



7.3 Chemical shift list 3

File name: working_cs.cif

Chemical shift list name: *nmr_parameters_1_dup_dup*

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	211
Number of shifts mapped to atoms	211
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
$^{13}\text{C}_\alpha$	71	-0.93 ± 0.08	Should be checked
$^{13}\text{C}_\beta$	0	—	None (insufficient data)
$^{13}\text{C}'$	0	—	None (insufficient data)
^{15}N	70	-0.23 ± 0.41	None needed (< 0.5 ppm)

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 3%, i.e. 192 atoms were assigned a chemical shift out of a possible 5533. 0 out of 67 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	192/1986 (10%)	64/804 (8%)	64/792 (8%)	64/390 (16%)
Sidechain	0/3315 (0%)	0/2132 (0%)	0/1030 (0%)	0/153 (0%)
Aromatic	0/232 (0%)	0/116 (0%)	0/106 (0%)	0/10 (0%)
Overall	192/5533 (3%)	64/3052 (2%)	64/1928 (3%)	64/553 (12%)

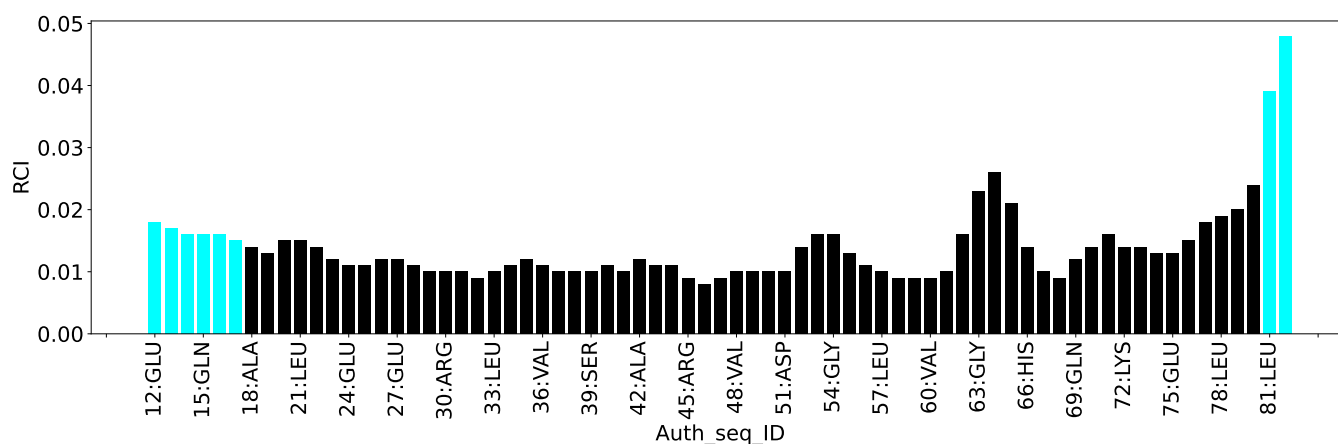
7.3.4 Statistically unusual chemical shifts [i](#)

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 C:



7.4 Chemical shift list 4

File name: working_cs.cif

Chemical shift list name: *nmr_parameters_1_dup_dup_dup*

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	174
Number of shifts mapped to atoms	174
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
$^{13}\text{C}_\alpha$	58	-0.97 ± 0.11	Should be checked
$^{13}\text{C}_\beta$	0	—	None (insufficient data)
$^{13}\text{C}'$	0	—	None (insufficient data)
^{15}N	58	-0.20 ± 0.23	None needed (< 0.5 ppm)

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 3%, i.e. 168 atoms were assigned a chemical shift out of a possible 5533. 0 out of 67 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	168/1986 (8%)	56/804 (7%)	56/792 (7%)	56/390 (14%)
Sidechain	0/3315 (0%)	0/2132 (0%)	0/1030 (0%)	0/153 (0%)
Aromatic	0/232 (0%)	0/116 (0%)	0/106 (0%)	0/10 (0%)
Overall	168/5533 (3%)	56/3052 (2%)	56/1928 (3%)	56/553 (10%)

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 D:

