Full wwPDB NMR Structure Validation Report (i)

Jun 5, 2023 – 03:15 AM EDT

PDB ID	:	2LYW
BMRB ID	:	21029
Title	:	Intermolecular interactions between neurotensin and the third extracellular loop of human neurotensin 1 receptor
Authors	:	Monti, J.; Da Costa, G.
Deposited on	:	2012-09-20

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:

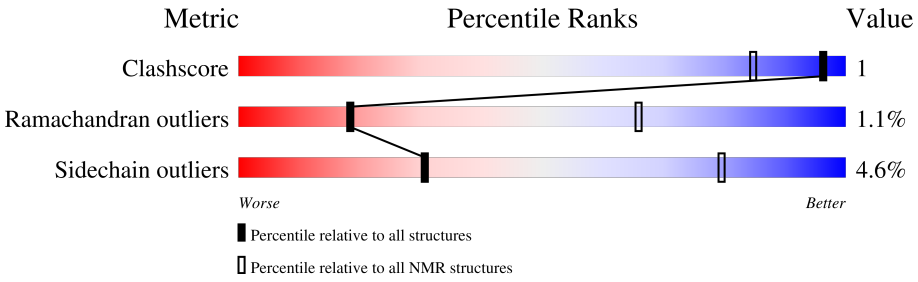
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
BMRB Restraints Analysis	:	v1.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.33

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 50%.

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	24	71% 12% 17%
2	B	13	46% 8% 8% 38%

2 Ensemble composition and analysis (i)

This entry contains 10 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: *closest to the average*.

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:2-A:21, B:6-B:13 (28)	3.45	5

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 3 clusters. No single-model clusters were found.

Cluster number	Models
1	1, 2, 4, 5, 8, 10
2	3, 9
3	6, 7

3 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 674 atoms, of which 328 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Neurotensin receptor type 1.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	24	433	153	206	34	39	1	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	7	SER	CYS	engineered mutation	UNP P30989

- Molecule 2 is a protein called Neurotensin.

Mol	Chain	Residues	Atoms					Trace
			Total	C	H	N	O	
2	B	13	241	78	122	21	20	0

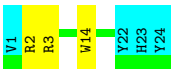
4 Residue-property plots

4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outliers are shown as green connectors. Residues which are classified as ill-defined in the NMR ensemble, are shown in cyan with an underline colour-coded according to the previous scheme. Residues which were present in the experimental sample, but not modelled in the final structure are shown in grey.

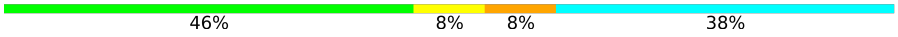
• Molecule 1: Neurotensin receptor type 1

Chain A:



• Molecule 2: Neurotensin

Chain B:



4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

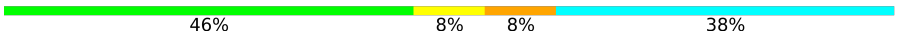
4.2.1 Score per residue for model 1

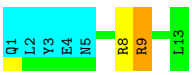
• Molecule 1: Neurotensin receptor type 1

Chain A:

• Molecule 2: Neurotensin

Chain B:





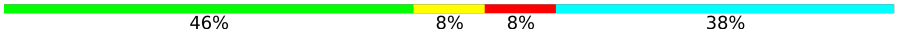
4.2.2 Score per residue for model 2

• Molecule 1: Neurotensin receptor type 1

Chain A:

• Molecule 2: Neurotensin

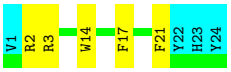
Chain B:



4.2.3 Score per residue for model 3

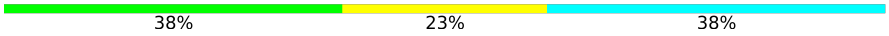
• Molecule 1: Neurotensin receptor type 1

Chain A:



• Molecule 2: Neurotensin

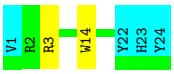
Chain B:



4.2.4 Score per residue for model 4

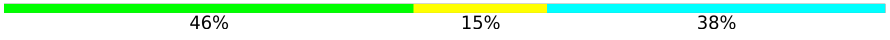
• Molecule 1: Neurotensin receptor type 1

Chain A:



• Molecule 2: Neurotensin

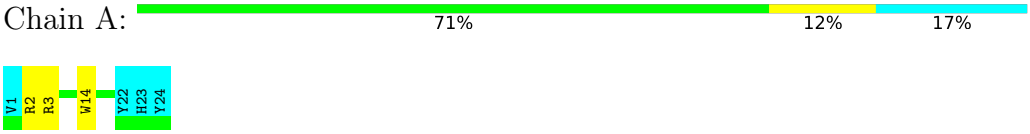
Chain B:



4.2.5 Score per residue for model 5 (medoid)

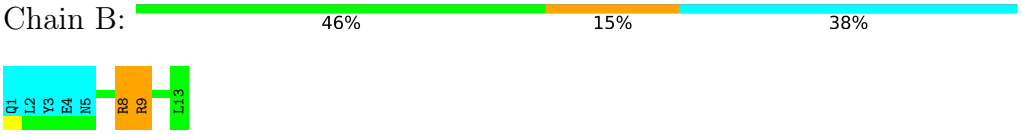
• Molecule 1: Neurotensin receptor type 1

Chain A:



• Molecule 2: Neurotensin

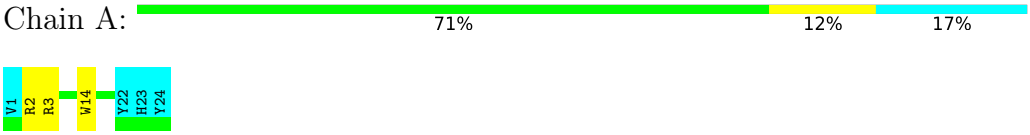
Chain B:



4.2.6 Score per residue for model 6

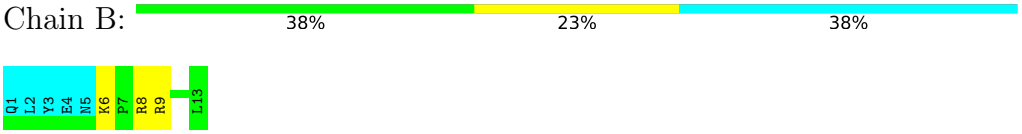
• Molecule 1: Neurotensin receptor type 1

Chain A:



• Molecule 2: Neurotensin

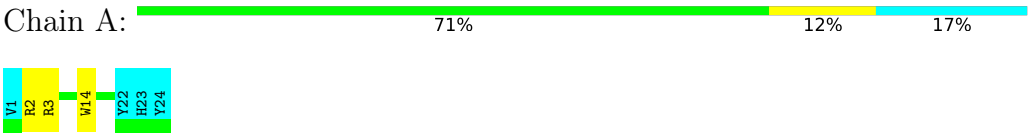
Chain B:



4.2.7 Score per residue for model 7

• Molecule 1: Neurotensin receptor type 1

Chain A:



• Molecule 2: Neurotensin

Chain B:

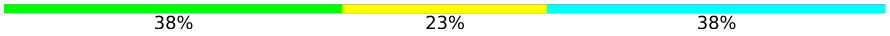
4.2.8 Score per residue for model 8

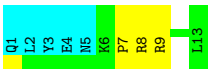
• Molecule 1: Neurotensin receptor type 1

Chain A:

• Molecule 2: Neurotensin

Chain B:

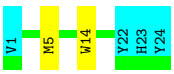




4.2.9 Score per residue for model 9

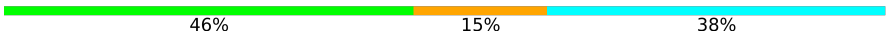
• Molecule 1: Neurotensin receptor type 1

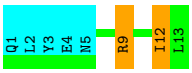
Chain A:



• Molecule 2: Neurotensin

Chain B:

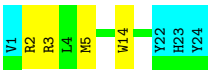




4.2.10 Score per residue for model 10

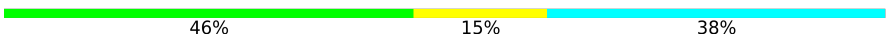
• Molecule 1: Neurotensin receptor type 1

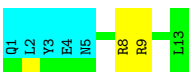
Chain A:



• Molecule 2: Neurotensin

Chain B:





5 Refinement protocol and experimental data overview

The models were refined using the following method: *DGSA-distance geometry simulated annealing.*

Of the 100 calculated structures, 10 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
Insight II	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	293
Number of shifts mapped to atoms	293
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	50%

6 Model quality

6.1 Standard geometry

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

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	0.97±0.17	0±0/193 (0.0± 0.0%)	1.26±0.17	3±1/262 (1.2± 0.4%)
2	B	0.92±0.14	0±0/76 (0.0± 0.0%)	1.51±0.21	2±1/100 (2.2± 0.7%)
All	All	0.97	0/2690 (0.0%)	1.35	54/3620 (1.5%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	Chirality	Planarity
1	A	0.0±0.0	0.2±0.4
2	B	0.0±0.0	0.1±0.3
All	All	0	3

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(^{o})	Ideal(^{o})	Models	
								Worst	Total
2	B	8	ARG	NE-CZ-NH1	8.76	124.68	120.30	5	8
1	A	2	ARG	NE-CZ-NH1	8.52	124.56	120.30	3	8
2	B	9	ARG	NE-CZ-NH1	8.15	124.38	120.30	10	10
1	A	3	ARG	NE-CZ-NH1	7.95	124.28	120.30	3	9
2	B	8	ARG	NE-CZ-NH2	-6.47	117.06	120.30	5	2
1	A	14	TRP	CD1-NE1-CE2	-5.84	103.74	109.00	4	10
2	B	9	ARG	NE-CZ-NH2	-5.79	117.40	120.30	3	2
1	A	21	PHE	CB-CG-CD2	-5.64	116.85	120.80	3	1
1	A	3	ARG	NE-CZ-NH2	-5.34	117.63	120.30	1	3
1	A	2	ARG	NE-CZ-NH2	-5.32	117.64	120.30	6	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)
1	A	2	ARG	Sidechain	2
2	B	9	ARG	Sidechain	1

6.2 Too-close contacts

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	185	169	169	0±1
2	B	74	84	84	0±1
All	All	2590	2530	2530	4

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 1.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:17:PHE:HA	2:B:7:PRO:HG3	0.64	1.69	8	1
1:A:17:PHE:HA	2:B:7:PRO:CG	0.64	2.23	8	1
1:A:17:PHE:HA	2:B:7:PRO:CB	0.60	2.27	8	1
2:B:12:ILE:HD13	2:B:12:ILE:H	0.42	1.75	9	1

6.3 Torsion angles

6.3.1 Protein backbone

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	20/24 (83%)	16±2 (80±9%)	4±1 (18±7%)	0±0 (2±2%)	14	59

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
2	B	7/13 (54%)	6±1 (81±11%)	1±1 (19±11%)	0±0 (0±0%)	100 100
All	All	270/370 (73%)	217 (80%)	50 (19%)	3 (1%)	18 66

All 2 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	17	PHE	2
1	A	12	GLU	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	20/24 (83%)	20±0 (98±2%)	0±0 (2±2%)	57 93
2	B	8/12 (67%)	7±1 (89±9%)	1±1 (11±9%)	9 53
All	All	280/360 (78%)	267 (95%)	13 (5%)	31 79

All 7 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)
2	B	9	ARG	5
2	B	6	LYS	2
1	A	5	MET	2
1	A	12	GLU	1
2	B	8	ARG	1
1	A	9	ILE	1
2	B	12	ILE	1

6.3.3 RNA (i)

There are no RNA molecules in this entry.

6.4 Non-standard residues in protein, DNA, RNA chains (i)

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

In the following table, the Counts columns list the number of bonds for which Mogul statistics could be retrieved, the number of bonds that are observed in the model and the number of bonds that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length is the number of standard deviations the observed value is removed from the expected value. A bond length with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond lengths.

Mol	Type	Chain	Res	Link	Bond lengths		
					Counts	RMSZ	#Z>2
2	PCA	B	1	2	7,8,9	0.61±0.02	0±0 (0±0%)

In the following table, the Counts columns list the number of angles for which Mogul statistics could be retrieved, the number of angles that are observed in the model and the number of angles that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond angle is the number of standard deviations the observed value is removed from the expected value. A bond angle with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond angles.

Mol	Type	Chain	Res	Link	Bond angles		
					Counts	RMSZ	#Z>2
2	PCA	B	1	2	9,10,12	1.04±0.18	0±1 (5±7%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	PCA	B	1	2	-	0±0,0,11,13	0±0,1,1,1

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(^{o})	Ideal(^{o})	Models	
								Worst	Total
2	B	1	PCA	CB-CA-C	3.02	116.85	112.70	1	4
2	B	1	PCA	O-C-CA	2.44	118.38	124.78	8	1

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6.5 Carbohydrates (i)

There are no monosaccharides in this entry.

6.6 Ligand geometry (i)

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 50% for the well-defined parts and 50% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *assigned_chem_shift_list_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	109
Number of shifts mapped to atoms	109
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

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

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 16%, i.e. 72 atoms were assigned a chemical shift out of a possible 448. 0 out of 3 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	14/134 (10%)	14/53 (26%)	0/56 (0%)	0/25 (0%)
Sidechain	54/245 (22%)	54/158 (34%)	0/73 (0%)	0/14 (0%)
Aromatic	4/69 (6%)	4/33 (12%)	0/35 (0%)	0/1 (0%)
Overall	72/448 (16%)	72/244 (30%)	0/164 (0%)	0/40 (0%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 18%, i.e. 103 atoms were assigned a chemical shift out of a possible 572. 0 out of 5 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	22/174 (13%)	22/69 (32%)	0/72 (0%)	0/33 (0%)
Sidechain	73/294 (25%)	73/190 (38%)	0/89 (0%)	0/15 (0%)
Aromatic	8/104 (8%)	8/49 (16%)	0/52 (0%)	0/3 (0%)
Overall	103/572 (18%)	103/308 (33%)	0/213 (0%)	0/51 (0%)

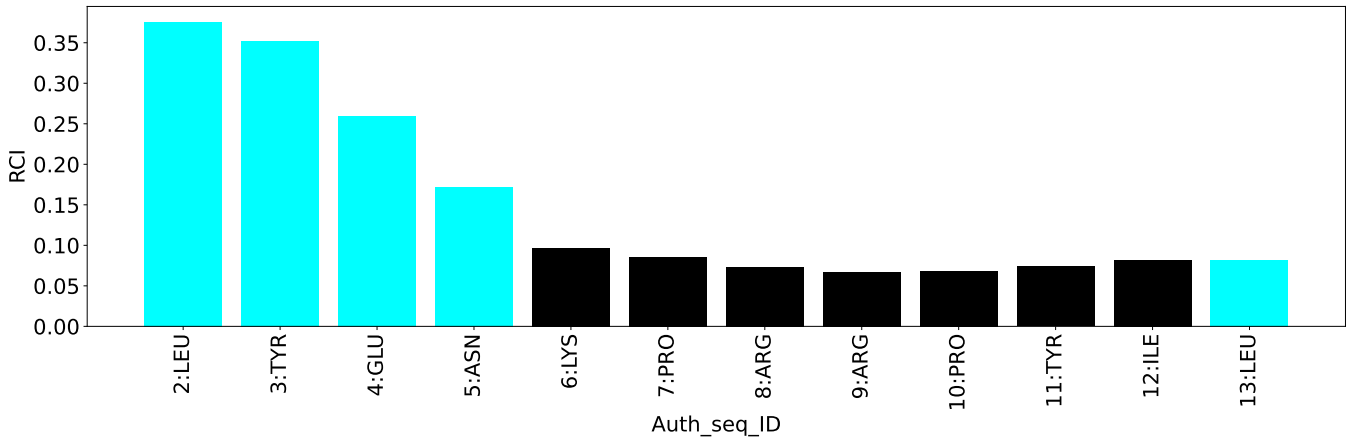
7.1.4 Statistically unusual chemical shifts (i)

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 B:



7.2 Chemical shift list 2

File name: working_cs.cif

Chemical shift list name: *assigned_chem_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	184
Number of shifts mapped to atoms	184
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 34%, i.e. 154 atoms were assigned a chemical shift out of a possible 448. 0 out of 3 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	37/134 (28%)	37/53 (70%)	0/56 (0%)	0/25 (0%)
Sidechain	88/245 (36%)	88/158 (56%)	0/73 (0%)	0/14 (0%)
Aromatic	29/69 (42%)	29/33 (88%)	0/35 (0%)	0/1 (0%)
Overall	154/448 (34%)	154/244 (63%)	0/164 (0%)	0/40 (0%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 32%, i.e. 184 atoms were assigned a chemical shift out of a possible 572. 0 out of 5 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	44/174 (25%)	44/69 (64%)	0/72 (0%)	0/33 (0%)
Sidechain	101/294 (34%)	101/190 (53%)	0/89 (0%)	0/15 (0%)
Aromatic	39/104 (38%)	39/49 (80%)	0/52 (0%)	0/3 (0%)
Overall	184/572 (32%)	184/308 (60%)	0/213 (0%)	0/51 (0%)

7.2.4 Statistically unusual chemical shifts (i)

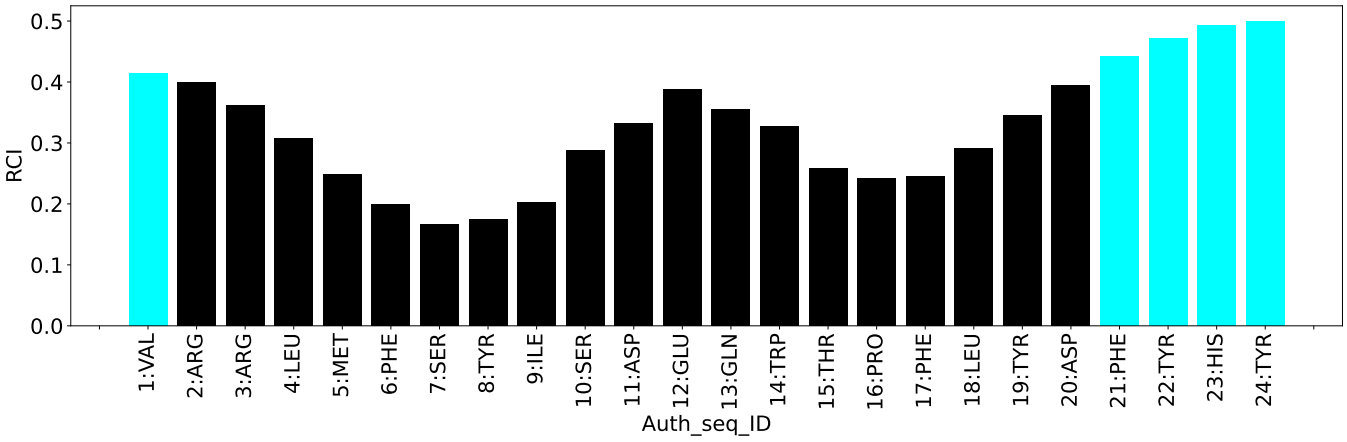
There are no statistically unusual chemical shifts.

7.2.5 Random Coil Index (RCI) plots (i)

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:



8 NMR restraints analysis

8.1 Conformationally restricting restraints

The following table provides the summary of experimentally observed NMR restraints in different categories. Restraints are classified into different categories based on the sequence separation of the atoms involved.

Description	Value
Total distance restraints	376
Intra-residue (|i-j|=0)	247
Sequential (|i-j|=1)	108
Medium range (|i-j|>1 and |i-j|<5)	15
Long range (|i-j|≥5)	0
Inter-chain	6
Hydrogen bond restraints	0
Disulfide bond restraints	0
Total dihedral-angle restraints	0
Number of unmapped restraints	0
Number of restraints per residue	10.2
Number of long range restraints per residue[1]	0.0

[1]Long range hydrogen bonds and disulfide bonds are counted as long range restraints while calculating the number of long range restraints per residue

8.2 Residual restraint violations

This section provides the overview of the restraint violations analysis. The violations are binned as small, medium and large violations based on its absolute value. Average number of violations per model is calculated by dividing the total number of violations in each bin by the size of the ensemble.

8.2.1 Average number of distance violations per model

Distance violations less than 0.1 Å are not included in the calculation.

Bins (Å)	Average number of violations per model	Max (Å)
0.1-0.2 (Small)	0.1	0.17
0.2-0.5 (Medium)	0.1	0.21
>0.5 (Large)	None	None

8.2.2 Average number of dihedral-angle violations per model (i)

Dihedral-angle violations less than 1° are not included in the calculation.There are no dihedral-angle violations

9 Distance violation analysis (i)

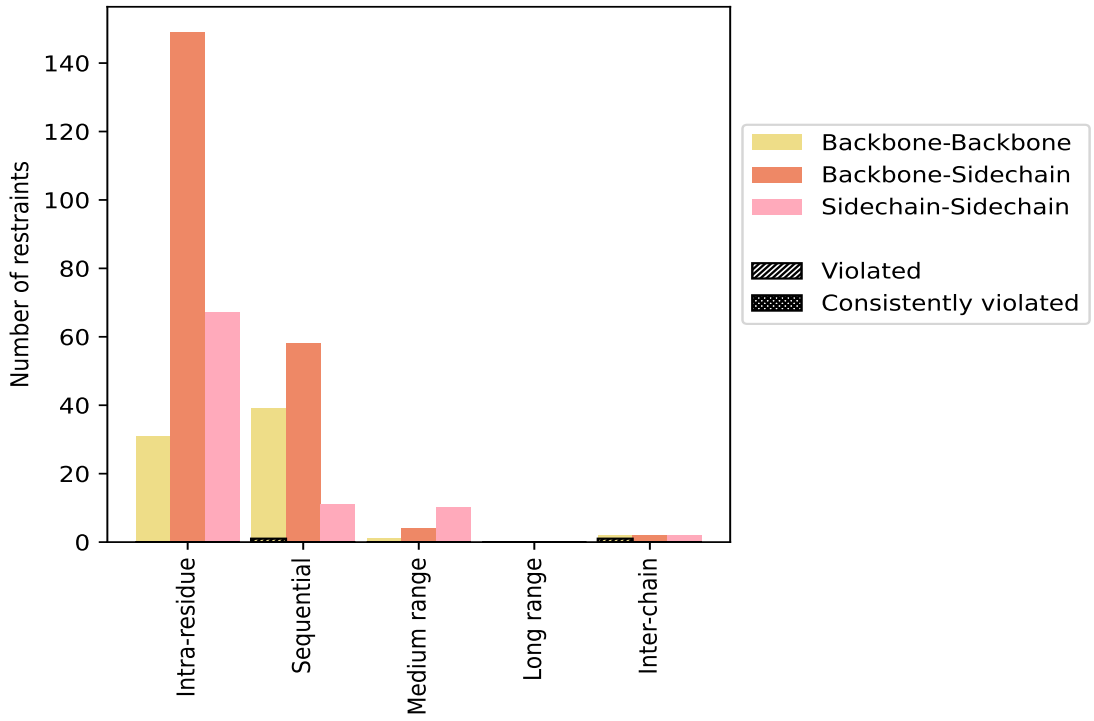
9.1 Summary of distance violations (i)

The following table shows the summary of distance violations in different restraint categories based on the sequence separation of the atoms involved. Each category is further sub-divided into three sub-categories based on the atoms involved. Violations less than 0.1 Å are not included in the statistics.

Restraints type	Count	%[1]	Violated[3]			Consistently Violated[4]		
			Count	%[2]	%[1]	Count	%[2]	%[1]
Intra-residue (|i-j|=0)	247	65.7	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	31	8.2	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	149	39.6	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	67	17.8	0	0.0	0.0	0	0.0	0.0
Sequential (|i-j|=1)	108	28.7	1	0.9	0.3	0	0.0	0.0
Backbone-Backbone	39	10.4	1	2.6	0.3	0	0.0	0.0
Backbone-Sidechain	58	15.4	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	11	2.9	0	0.0	0.0	0	0.0	0.0
Medium range (|i-j|>1 & |i-j|<5)	15	4.0	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	1	0.3	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	4	1.1	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	10	2.7	0	0.0	0.0	0	0.0	0.0
Long range (|i-j|≥5)	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Inter-chain	6	1.6	1	16.7	0.3	0	0.0	0.0
Backbone-Backbone	2	0.5	1	50.0	0.3	0	0.0	0.0
Backbone-Sidechain	2	0.5	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	2	0.5	0	0.0	0.0	0	0.0	0.0
Hydrogen bond	0	0.0	0	0.0	0.0	0	0.0	0.0
Disulfide bond	0	0.0	0	0.0	0.0	0	0.0	0.0
Total	376	100.0	2	0.5	0.5	0	0.0	0.0
Backbone-Backbone	73	19.4	2	2.7	0.5	0	0.0	0.0
Backbone-Sidechain	213	56.6	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	90	23.9	0	0.0	0.0	0	0.0	0.0

[1] percentage calculated with respect to the total number of distance restraints, [2] percentage calculated with respect to the number of restraints in a particular restraint category, [3] violated in at least one model, [4] violated in all the models

9.1.1 Bar chart : Distribution of distance restraints and violations



Violated and consistently violated restraints are shown using different hatch patterns in their respective categories. The hydrogen bonds and disulfied bonds are counted in their appropriate category on the x-axis

9.2 Distance violation statistics for each model

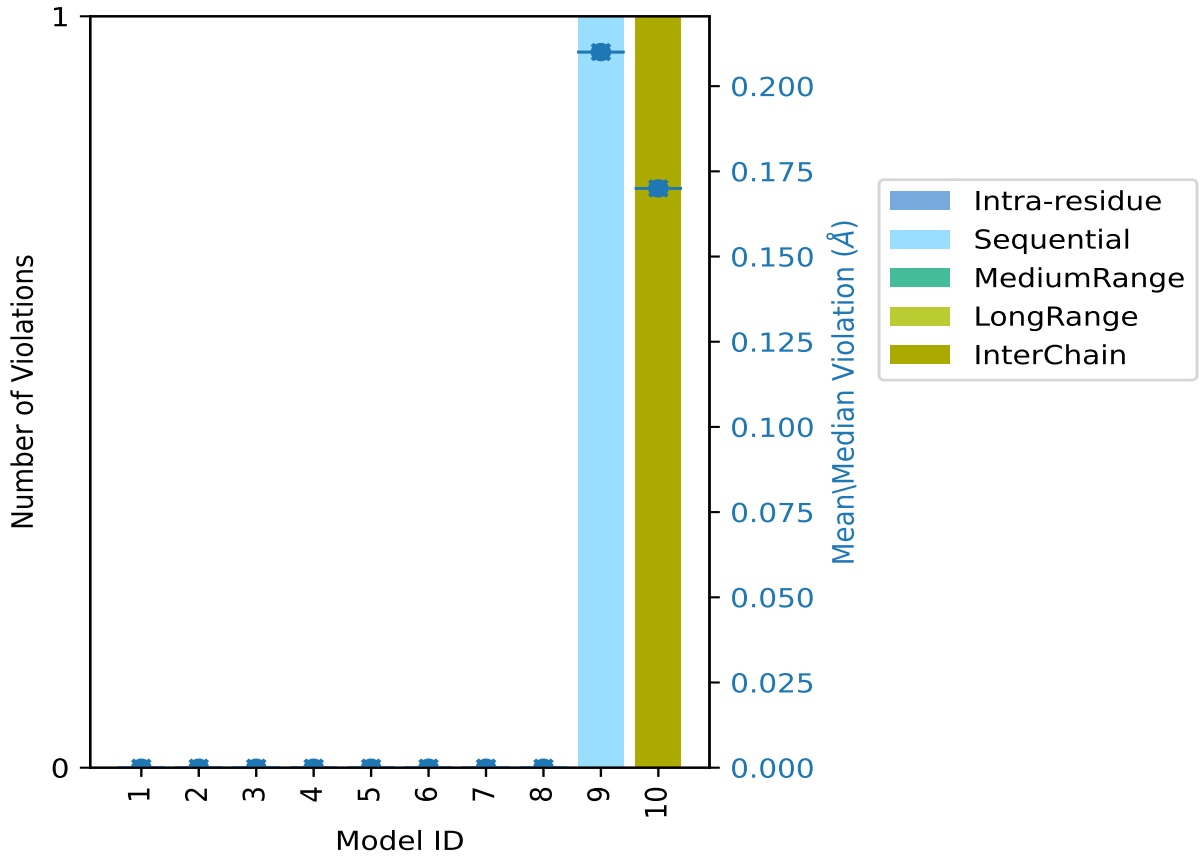
The following table provides the distance violation statistics for each model in the ensemble. Violations less than 0.1 Å are not included in the statistics.

Model ID	Number of violations						Mean (Å)	Max (Å)	SD[6] (Å)	Median (Å)
	IR[1]	SQ[2]	MR[3]	LR[4]	IC[5]	Total				
1	0	0	0	0	0	0	0.0	0.0	0.0	0.0
2	0	0	0	0	0	0	0.0	0.0	0.0	0.0
3	0	0	0	0	0	0	0.0	0.0	0.0	0.0
4	0	0	0	0	0	0	0.0	0.0	0.0	0.0
5	0	0	0	0	0	0	0.0	0.0	0.0	0.0
6	0	0	0	0	0	0	0.0	0.0	0.0	0.0
7	0	0	0	0	0	0	0.0	0.0	0.0	0.0
8	0	0	0	0	0	0	0.0	0.0	0.0	0.0
9	0	1	0	0	0	1	0.21	0.21	0.0	0.21
10	0	0	0	0	1	1	0.17	0.17	0.0	0.17

[1]Intra-residue restraints, [2]Sequential restraints, [3]Medium range restraints, [4]Long range restraints,

[5]Inter-chain restraints, [6]Standard deviation

9.2.1 Bar graph : Distance Violation statistics for each model



The mean(dot),median(x) and the standard deviation are shown in blue with respect to the y axis on the right

9.3 Distance violation statistics for the ensemble

Violation analysis may find that some restraints are violated in few models and some are violated in most of models. The following table provides this information as number of violated restraints for a given fraction of the ensemble. In total, 374(IR:247, SQ:107, MR:15, LR:0, IC:5) restraints are not violated in the ensemble.

Number of violated restraints						Fraction of the ensemble	
IR[1]	SQ[2]	MR[3]	LR[4]	IC[5]	Total	Count[6]	%
0	1	0	0	1	2	1	10.0
0	0	0	0	0	0	2	20.0
0	0	0	0	0	0	3	30.0
0	0	0	0	0	0	4	40.0

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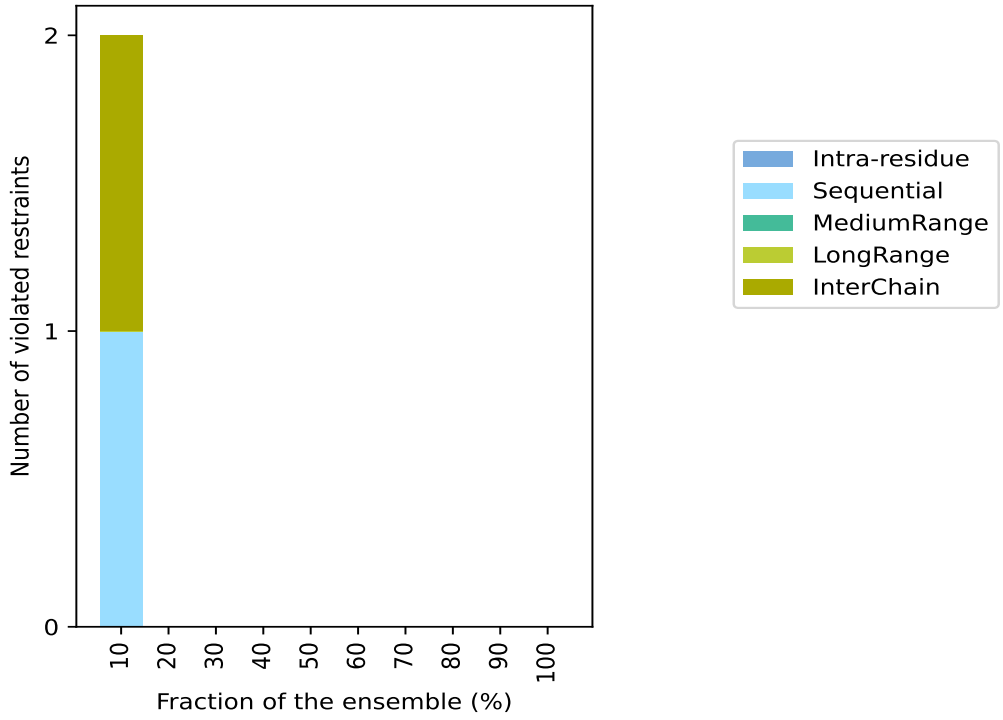
Number of violated restraints						Fraction of the ensemble	
IR[1]	SQ[2]	MR[3]	LR[4]	IC[5]	Total	Count[6]	%
0	0	0	0	0	0	5	50.0
0	0	0	0	0	0	6	60.0
0	0	0	0	0	0	7	70.0
0	0	0	0	0	0	8	80.0
0	0	0	0	0	0	9	90.0
0	0	0	0	0	0	10	100.0

[1]Intra-residue restraints, [2]Sequential restraints, [3]Medium range restraints, [4]Long range restraints, [5]Inter-chain restraints, [6] Number of models with violations

9.3.1 Bar graph : Distance violation statistics for the ensemble



9.4 Most violated distance restraints in the ensemble

No violations found

9.5 All violated distance restraints (i)

9.5.1 Histogram : Distribution of distance violations (i)

The following histogram shows the distribution of the absolute value of the violation for all violated restraints in the ensemble.
Data insufficient to plot histogram

9.5.2 Table : All distance violations (i)

The following table lists the absolute value of the violation for each restraint in the ensemble sorted by its value. The Key (restraint list ID, restraint ID) is the unique identifier for a given restraint. Rows with same key represent combinatorial or ambiguous restraints and are counted as a single restraint.

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,265)	1:A:10:SER:HA	1:A:11:ASP:H	9	0.21
(2,99)	1:A:3:ARG:H	2:B:12:ILE:H	10	0.17

10 Dihedral-angle violation analysis (i)

Dihedral angle analysis failed due to data error in the dihedral angle restraints, possibly missing target value