wwPDB NMR Structure Validation Summary Report (i)

Jun 4, 2023 – 11:44 AM EDT

PDB ID	:	2LAJ
BMRB ID	:	17529
Title	:	Third WW domain of human Nedd4L in complex with doubly phosphorylated human smad3 derived peptide
Authors	:	Macias, M.J.; Aragon, E.; Goerner, N.; Zaromytidou, A.; Xi, Q.; Escobedo, A.; Massague, J.
Deposited on	:	2011-03-16

This is a wwPDB NMR Structure Validation Summary 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:

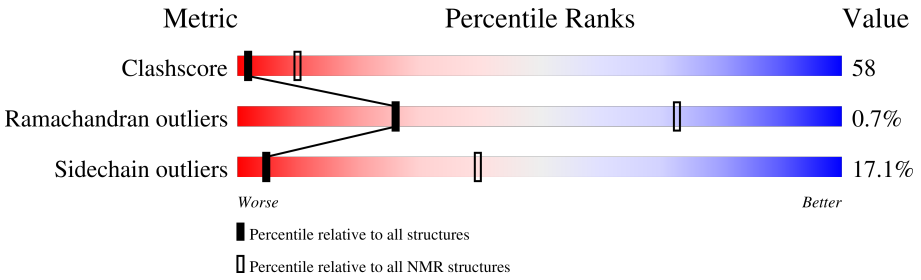
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
BMRB Restraints Analysis	:	v1.2
Ideal geometry (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 39%.

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	44	20% 48% 5% • 16% 9%
2	B	10	40% 60%

2 Ensemble composition and analysis (i)

This entry contains 15 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: *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:478-A:510, B:205-B:207, B:209-B:209 (37)	0.30	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 2 clusters and 5 single-model clusters were found.

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

3 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 803 atoms, of which 385 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called E3 ubiquitin-protein ligase NEDD4-like.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	40	666	224	323	60	58	1	0

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	472	GLY	-	expression tag	UNP Q96PU5
A	473	ALA	-	expression tag	UNP Q96PU5
A	474	MET	-	expression tag	UNP Q96PU5
A	475	GLU	-	expression tag	UNP Q96PU5
A	496	TYR	ILE	engineered mutation	UNP Q96PU5

- Molecule 2 is a protein called Mothers against decapentaplegic homolog 3.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	P	
2	B	10	137	40	62	12	21	2	0

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: E3 ubiquitin-protein ligase NEDD4-like

Chain A:

- Molecule 2: Mothers against decapentaplegic homolog 3

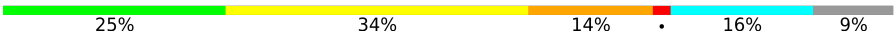
Chain B:

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: E3 ubiquitin-protein ligase NEDD4-like

Chain A:



- Molecule 2: Mothers against decapentaplegic homolog 3

Chain B:

5 Refinement protocol and experimental data overview (i)

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

Of the 300 calculated structures, 15 were deposited, based on the following criterion: *structures with acceptable covalent geometry*.

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

Software name	Classification	Version
CNS	structure solution	1.3
CNS	refinement	1.3

The following table shows chemical shift validation statistics as aggregates over all chemical shift files. Detailed validation can be found in section 7 of this report.

Chemical shift file(s)	working_cs.cif
Number of chemical shift lists	1
Total number of shifts	264
Number of shifts mapped to atoms	264
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	39%

6 Model quality (i)

6.1 Standard geometry (i)

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

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	0.79±0.01	0±0/297 (0.1± 0.1%)	1.06±0.03	3±1/408 (0.7± 0.2%)
2	B	0.33±0.03	0±0/31 (0.0± 0.0%)	0.50±0.08	0±0/41 (0.0± 0.0%)
All	All	0.76	3/4920 (0.1%)	1.03	43/6735 (0.6%)

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	2.0±0.0
All	All	0	30

All unique bond outliers are listed below.

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
1	A	483	TRP	NE1-CE2	-5.09	1.30	1.37	15	3

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
1	A	478	PHE	CB-CG-CD2	-8.66	114.74	120.80	8	14
1	A	478	PHE	CB-CA-C	-8.33	93.74	110.40	1	15
1	A	494	PHE	CB-CG-CD1	6.28	125.19	120.80	12	3
1	A	494	PHE	CB-CG-CD2	-5.97	116.62	120.80	12	3
1	A	478	PHE	CB-CG-CD1	5.76	124.84	120.80	11	8

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	478	PHE	Peptide	15
1	A	482	GLY	Peptide	15

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	283	264	263	34±4
2	B	30	31	31	4±1
All	All	4695	4425	4410	527

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 58.

5 of 108 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:483:TRP:CH2	1:A:497:ASP:HB2	0.84	2.07	14	15
1:A:492:ARG:HD2	1:A:505:TRP:CH2	0.83	2.08	3	7
1:A:488:ALA:HB2	1:A:494:PHE:CZ	0.81	2.11	12	14
1:A:479:LEU:HD21	1:A:483:TRP:CB	0.80	2.05	2	1
1:A:505:TRP:CZ2	2:B:209:PRO:HD2	0.80	2.11	14	13

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	33/44 (75%)	30±0 (89±2%)	3±1 (10±2%)	0±1 (1±2%)	24 71

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
2	B	4/10 (40%)	3±0 (63±12%)	1±0 (37±12%)	0±0 (0±0%)	100 100
All	All	555/810 (69%)	481 (87%)	70 (13%)	4 (1%)	26 73

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	489	PRO	3
1	A	499	ASN	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	30/39 (77%)	25±1 (83±5%)	5±1 (17±5%)	5 39
2	B	4/6 (67%)	3±0 (85±12%)	1±0 (15±12%)	6 44
All	All	510/675 (76%)	423 (83%)	87 (17%)	5 40

5 of 18 unique residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	478	PHE	15
1	A	494	PHE	15
1	A	498	HIS	11
2	B	206	ASN	8
1	A	503	THR	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)

2 non-standard protein/DNA/RNA residues are 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	SEP	B	208	2	8,9,10	1.24±0.04	1±1 (10±8%)
2	SEP	B	204	2	8,9,10	1.26±0.03	2±0 (22±5%)

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	SEP	B	208	2	8,12,14	1.37±0.15	1±0 (12±4%)
2	SEP	B	204	2	8,12,14	1.36±0.11	2±0 (21±5%)

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	SEP	B	208	2	-	0±0,5,8,10	-
2	SEP	B	204	2	-	0±0,5,8,10	-

All unique bond 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(Å)	Ideal(Å)	Models	
								Worst	Total
2	B	208	SEP	P-O3P	2.34	1.45	1.54	9	8
2	B	204	SEP	P-O2P	2.28	1.46	1.54	1	13
2	B	204	SEP	P-O3P	2.20	1.46	1.54	2	14
2	B	208	SEP	P-O2P	2.08	1.46	1.54	13	4

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	208	SEP	OG-CB-CA	3.70	111.74	108.14	11	14
2	B	204	SEP	OG-CB-CA	3.66	111.71	108.14	10	15
2	B	204	SEP	P-OG-CB	2.29	124.59	118.30	9	11
2	B	208	SEP	P-OG-CB	2.00	123.81	118.30	6	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 (i)

The completeness of assignment taking into account all chemical shift lists is 39% for the well-defined parts and 38% 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 (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	264
Number of shifts mapped to atoms	264
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	6

7.1.2 Chemical shift referencing (i)

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

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 39%, i.e. 206 atoms were assigned a chemical shift out of a possible 528. 0 out of 3 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	**^{1}H**	**^{13}C**	**^{15}N**
Backbone	67/173 (39%)	67/69 (97%)	0/74 (0%)	0/30 (0%)
Sidechain	114/284 (40%)	114/183 (62%)	0/88 (0%)	0/13 (0%)
Aromatic	25/71 (35%)	25/35 (71%)	0/32 (0%)	0/4 (0%)
Overall	206/528 (39%)	206/287 (72%)	0/194 (0%)	0/47 (0%)

7.1.4 Statistically unusual chemical shifts (i)

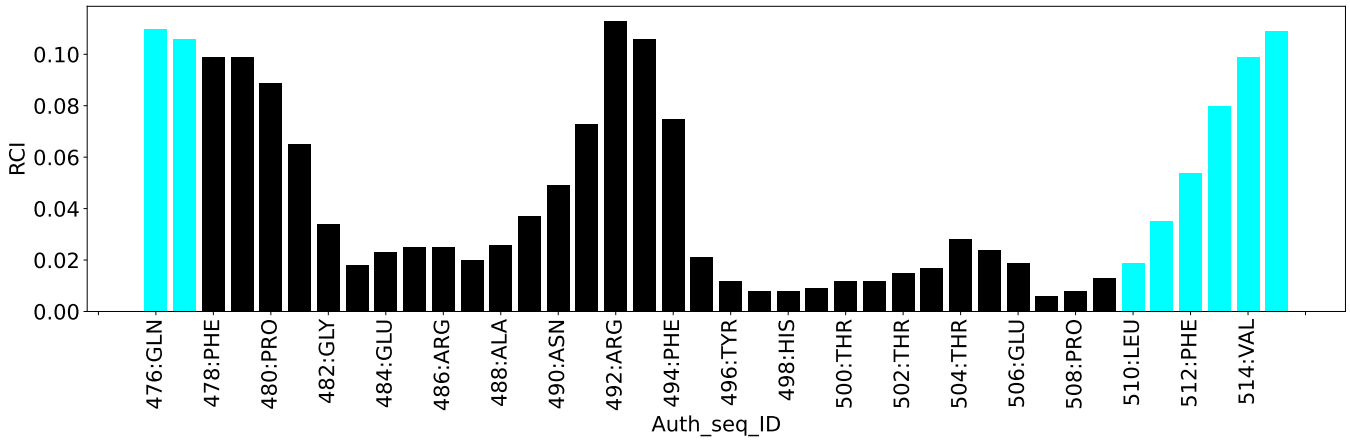
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, *ppm*	Expected range, *ppm*	Z-score
1	A	497	ASP	HB3	-0.36	1.32 – 4.00	-11.3
1	A	486	ARG	HD2	1.10	1.97 – 4.26	-8.8
1	A	486	ARG	HB3	-0.51	0.43 – 3.11	-8.5
1	A	486	ARG	HD3	1.00	1.81 – 4.39	-8.2
1	A	507	ASP	HA	2.17	3.04 – 6.12	-7.8
1	A	508	PRO	HG3	0.17	0.33 – 3.48	-5.5

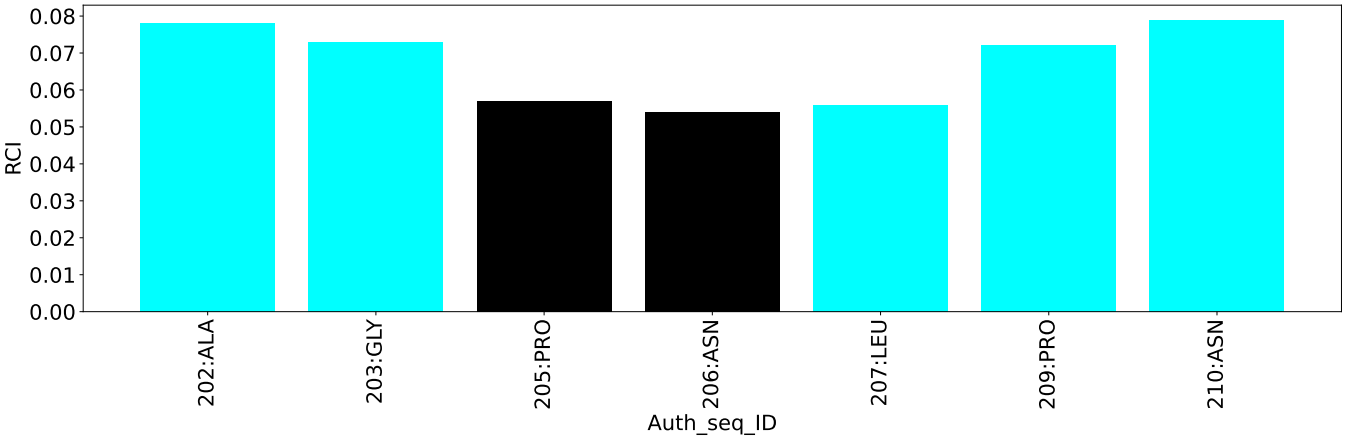
7.1.5 Random Coil Index (RCI) plots (i)

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:



Random coil index (RCI) for chain B:


0.08
0.07
0.06
0.05
0.04
0.03
0.02
0.01
0.00
RCI
202:ALA
203:GLY
205:PRO
206:ASN
207:LEU
209:PRO
210:ASN
Auth_seq_ID

8 NMR restraints analysis (i)

8.1 Conformationally restricting restraints (i)

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	461
Intra-residue (|i-j|=0)	0
Sequential (|i-j|=1)	174
Medium range (|i-j|>1 and |i-j|<5)	53
Long range (|i-j|≥5)	155
Inter-chain	61
Hydrogen bond restraints	18
Disulfide bond restraints	0
Total dihedral-angle restraints	0
Number of unmapped restraints	12
Number of restraints per residue	8.5
Number of long range restraints per residue[1]	3.2

[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 (i)

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 (i)

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)	3.7	0.2
0.2-0.5 (Medium)	0.5	0.5
>0.5 (Large)	2.5	1.12

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)

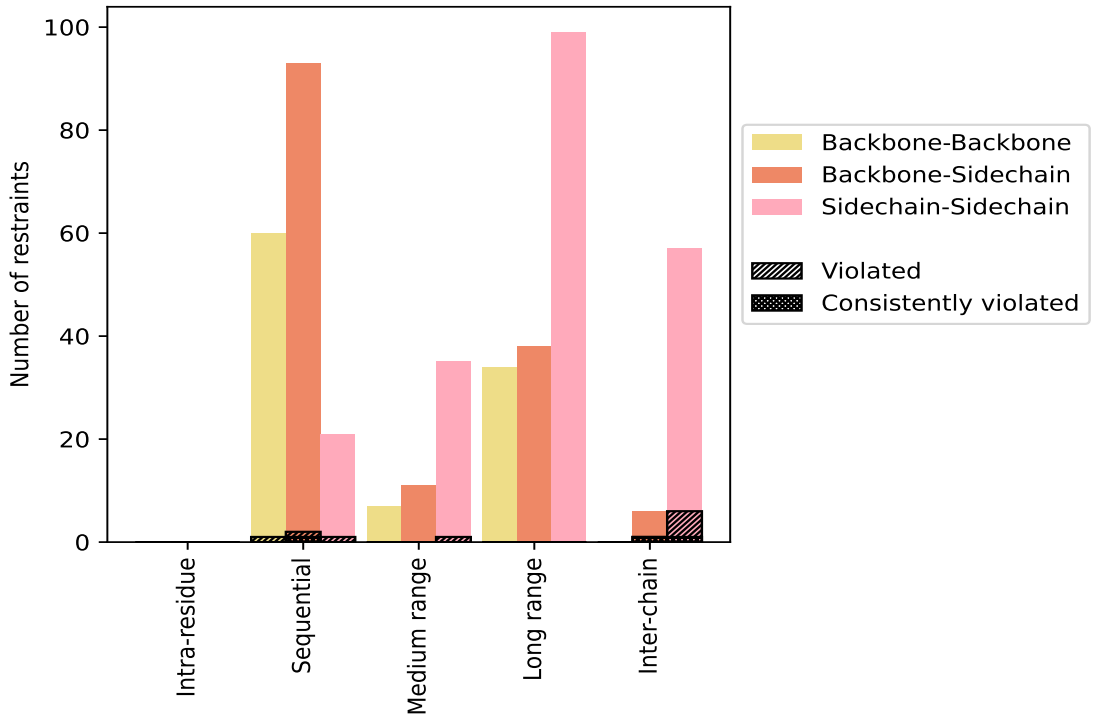
9.1 Summary of distance violations (i)

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)	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
Sequential (|i-j|=1)	174	37.7	4	2.3	0.9	1	0.6	0.2
Backbone-Backbone	60	13.0	1	1.7	0.2	0	0.0	0.0
Backbone-Sidechain	93	20.2	2	2.2	0.4	1	1.1	0.2
Sidechain-Sidechain	21	4.6	1	4.8	0.2	0	0.0	0.0
Medium range (|i-j|>1 & |i-j|<5)	53	11.5	1	1.9	0.2	0	0.0	0.0
Backbone-Backbone	7	1.5	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	11	2.4	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	35	7.6	1	2.9	0.2	0	0.0	0.0
Long range (|i-j|≥5)	155	33.6	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	18	3.9	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	38	8.2	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	99	21.5	0	0.0	0.0	0	0.0	0.0
Inter-chain	61	13.2	7	11.5	1.5	2	3.3	0.4
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	4	0.9	1	25.0	0.2	1	25.0	0.2
Sidechain-Sidechain	57	12.4	6	10.5	1.3	1	1.8	0.2
Hydrogen bond	18	3.9	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	461	100.0	12	2.6	2.6	3	0.7	0.7
Backbone-Backbone	101	21.9	1	1.0	0.2	0	0.0	0.0
Backbone-Sidechain	148	32.1	3	2.0	0.7	2	1.4	0.4
Sidechain-Sidechain	212	46.0	8	3.8	1.7	1	0.5	0.2

[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 (i)



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 (i)

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	2	0	0	5	7	0.4	0.91	0.29	0.36
2	0	3	1	0	3	7	0.24	0.57	0.19	0.12
3	0	2	1	0	3	6	0.32	0.95	0.32	0.12
4	0	1	0	0	5	6	0.44	0.85	0.29	0.4
5	0	1	0	0	5	6	0.46	1.11	0.36	0.36
6	0	1	0	0	5	6	0.55	1.12	0.38	0.48
7	0	2	1	0	5	8	0.35	0.93	0.27	0.26
8	0	2	0	0	3	5	0.33	0.78	0.27	0.13
9	0	2	0	0	4	6	0.34	0.95	0.31	0.16
10	0	2	1	0	5	8	0.29	1.02	0.31	0.12
11	0	2	0	0	7	9	0.37	1.08	0.32	0.13

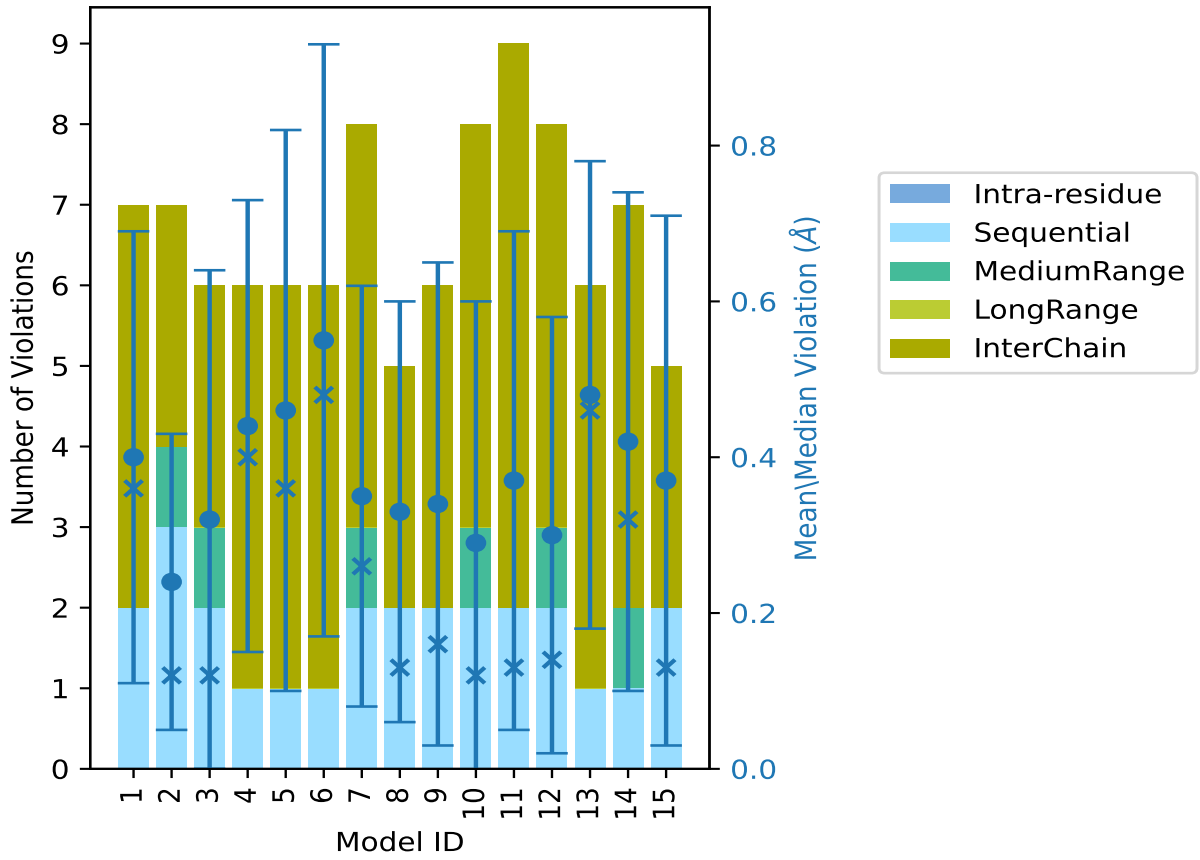
Continued on next page...

Continued from previous page...

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				
12	0	2	1	0	5	8	0.3	0.81	0.28	0.14
13	0	1	0	0	5	6	0.48	0.99	0.3	0.46
14	0	1	1	0	5	7	0.42	0.89	0.32	0.32
15	0	2	0	0	3	5	0.37	0.98	0.34	0.13

[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 (i)



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 (i)

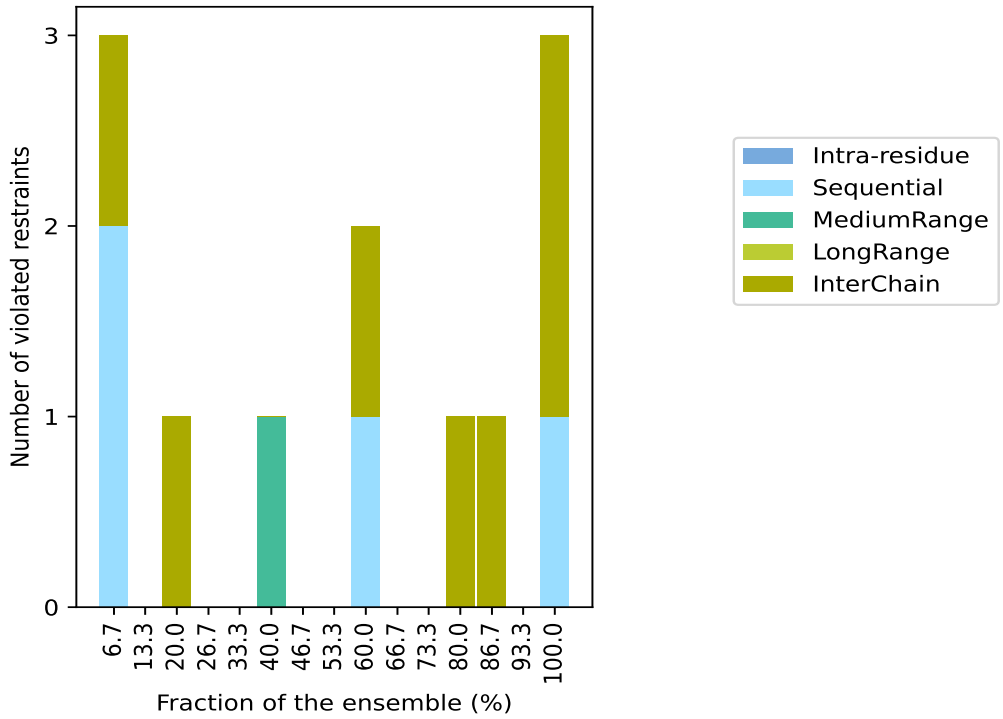
Violation analysis may find that some restraints are violated in few models and some are violated in most of models. The following table provides this information as number of violated restraints

for a given fraction of the ensemble. In total, 431(IR:0, SQ:170, MR:52, LR:155, IC:54) 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	2	0	0	1	3	1	6.7
0	0	0	0	0	0	2	13.3
0	0	0	0	1	1	3	20.0
0	0	0	0	0	0	4	26.7
0	0	0	0	0	0	5	33.3
0	0	1	0	0	1	6	40.0
0	0	0	0	0	0	7	46.7
0	0	0	0	0	0	8	53.3
0	1	0	0	1	2	9	60.0
0	0	0	0	0	0	10	66.7
0	0	0	0	0	0	11	73.3
0	0	0	0	1	1	12	80.0
0	0	0	0	1	1	13	86.7
0	0	0	0	0	0	14	93.3
0	1	0	0	2	3	15	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

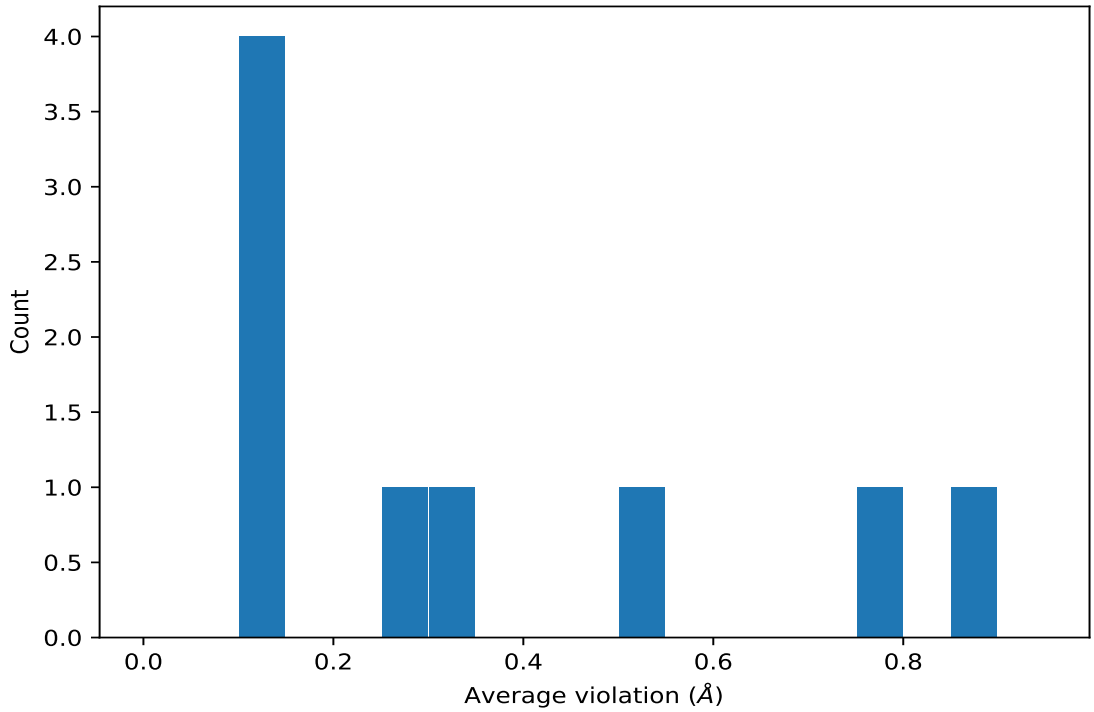
9.3.1 Bar graph : Distance violation statistics for the ensemble (i)



9.4 Most violated distance restraints in the ensemble (i)

9.4.1 Histogram : Distribution of mean distance violations (i)

The following histogram shows the distribution of the average value of the violation. The average is calculated for each restraint that is violated in more than one model over all the violated models in the ensemble



9.4.2 Table: Most violated distance restraints (i)

The following table provides the mean and the standard deviation of the violation for each restraint sorted by number of violated models and the mean 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.

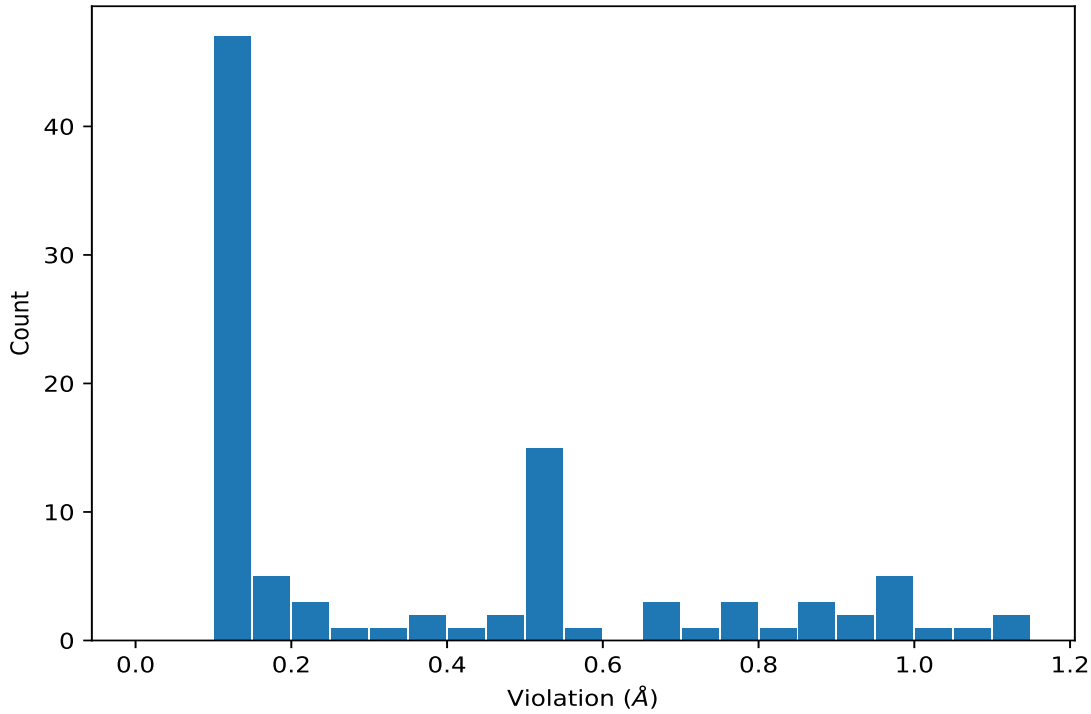
Key	Atom-1	Atom-2	Models[1]	Mean (Å)	SD[1] (Å)	Median (Å)
(2,1)	1:A:491:GLY:H	2:B:208:SEP:O1P	15	0.5	0.08	0.52
(1,189)	1:A:512:PHE:HA	1:A:513:PRO:HD3	15	0.13	0.01	0.13
(1,47)	1:A:498:HIS:HD1	2:B:205:PRO:HD3	15	0.12	0.01	0.11
(1,8)	1:A:505:TRP:HD1	2:B:209:PRO:HB3	13	0.88	0.19	0.95
(1,6)	1:A:505:TRP:HD1	2:B:209:PRO:HG3	12	0.76	0.23	0.83
(1,12)	1:A:505:TRP:HE3	2:B:209:PRO:HG2	9	0.29	0.11	0.32
(1,183)	1:A:510:LEU:HA	1:A:509:ARG:H	9	0.11	0.0	0.11
(1,333)	1:A:480:PRO:HB3	1:A:483:TRP:HD1	6	0.11	0.01	0.11
(1,55)	1:A:492:ARG:HH11	2:B:211:PRO:HG3	3	0.3	0.14	0.2

[1]Number of violated models, [2]Standard deviation

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.



9.5.2 Table : All distance violations (i)

The following table provides the 10 worst performing restraints, sorted by the violation 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)
(1,8)	1:A:505:TRP:HD1	2:B:209:PRO:HB3	6	1.12
(1,8)	1:A:505:TRP:HD1	2:B:209:PRO:HB3	5	1.11
(1,8)	1:A:505:TRP:HD1	2:B:209:PRO:HB3	11	1.08
(1,8)	1:A:505:TRP:HD1	2:B:209:PRO:HB3	10	1.02
(1,6)	1:A:505:TRP:HD1	2:B:209:PRO:HG3	13	0.99
(1,8)	1:A:505:TRP:HD1	2:B:209:PRO:HB3	15	0.98
(1,6)	1:A:505:TRP:HD1	2:B:209:PRO:HG3	6	0.96
(1,8)	1:A:505:TRP:HD1	2:B:209:PRO:HB3	3	0.95
(1,8)	1:A:505:TRP:HD1	2:B:209:PRO:HB3	9	0.95
(1,6)	1:A:505:TRP:HD1	2:B:209:PRO:HG3	7	0.93

10 Dihedral-angle violation analysis (i)

No dihedral-angle restraints found