wwPDB NMR Structure Validation Summary Report (i)

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PDB ID	:	2MQS
BMRB ID	:	25048
Title	:	Transient Collagen Triple Helix Binding to a Key Metalloproteinase in Invasion and Development: Spin Labels to Structure
Authors	:	Zhao, Y.; Marcink, T.; Van Doren, S.R.
Deposited on	:	2014-06-26

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:

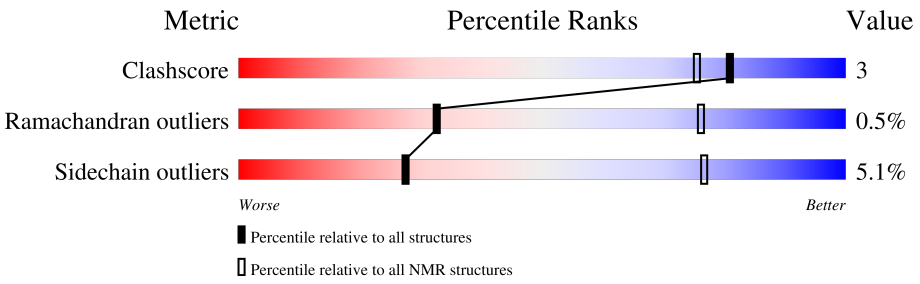
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
BMRB Restraints Analysis	:	v1.2
Ideal geometry (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 26%.

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	196	90% 9% •
2	B	36	75% • 22%
2	C	36	78% 22%
3	D	33	76% • 21%

2 Ensemble composition and analysis (i)

This entry contains 15 models. Model 15 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:316-A:511, B:0-B:1, B:3-B:4, B:6-B:7, B:9-B:22, B:24-B:25, B:27-B:28, B:30-B:31, B:33-B:34, C:100-C:101, C:103-C:104, C:106-C:107, C:109-C:122, C:124-C:125, C:127-C:128, C:130-C:131, C:133-C:134, D:200-D:201, D:203-D:204, D:206-D:207, D:209-D:222, D:224-D:225, D:227-D:228, D:230-D:231 (278)	0.47	15

Ill-defined regions of proteins are excluded from the global statistics.

Ligands and non-protein polymers are included in the analysis.

NmrClust was unable to cluster the ensemble.

Error message: No clusters in NmrClust output

3 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 2788 atoms, of which 473 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Matrix metalloproteinase-14.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	196	1999	1067	362	277	284	9	0

- Molecule 2 is a protein called THP_L_and_M_chain.

Mol	Chain	Residues	Atoms					Trace
			Total	C	H	N	O	
2	B	36	271	145	39	41	46	0
2	C	36	269	145	37	41	46	0

- Molecule 3 is a protein called THP_T_chain.

Mol	Chain	Residues	Atoms					Trace
			Total	C	H	N	O	
3	D	33	249	133	35	38	43	0

4 Residue-property plots (i)

4.1 Average score per residue in the NMR ensemble

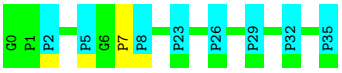
These plots are provided for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-coded according to the number of geometric quality criteria for 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: Matrix metalloproteinase-14

Chain A:

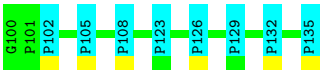
• Molecule 2: THP_L_and_M_chain

Chain B:



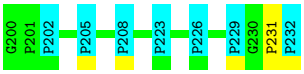
• Molecule 2: THP_L_and_M_chain

Chain C:



• Molecule 3: THP_T_chain

Chain D:

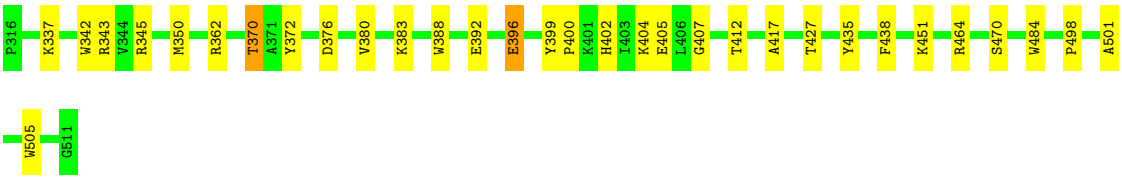


4.2 Residue scores for the representative (medoid) model from the NMR ensemble

The representative model is number 15. Colouring as in section 4.1 above.

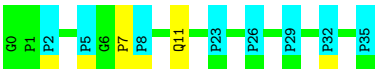
• Molecule 1: Matrix metalloproteinase-14

Chain A: 84% 15%



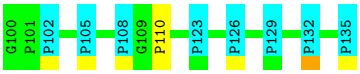
• Molecule 2: THP_L_and_M_chain

Chain B: 72% 6% 22%



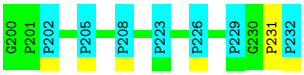
• Molecule 2: THP_L_and_M_chain

Chain C: 75% 22%



• Molecule 3: THP_T_chain

Chain D: 76% 21%



5 Refinement protocol and experimental data overview (i)

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

Of the 200 calculated structures, 15 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
HADDOCK	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	1
Total number of shifts	956
Number of shifts mapped to atoms	836
Number of unparsed shifts	0
Number of shifts with mapping errors	120
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	26%

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: HYP

There are no covalent bond-length or bond-angle outliers.

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no planarity outliers.

6.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	1637	362	1561	10±3
2	C	168	29	165	0±0
2	B	168	31	168	1±1
3	D	157	28	155	1±1
All	All	31950	6750	30735	160

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:370:THR:HG21	1:A:417:ALA:HA	0.73	1.59	6	12
1:A:481:ASN:HD21	1:A:502:LEU:HG	0.71	1.45	1	1
1:A:370:THR:HB	1:A:382:PHE:HB2	0.70	1.62	11	1
1:A:421:TRP:HB2	1:A:428:TYR:HE2	0.67	1.50	6	2
2:B:11:GLN:HG3	2:C:110:PRO:HG2	0.65	1.65	15	3

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	194/196 (99%)	178±2 (92±1%)	14±2 (7±1%)	1±1 (1±0%)	26	73
2	B	27/36 (75%)	27±0 (99±1%)	0±0 (1±1%)	0±0 (0±0%)	100	100
2	C	27/36 (75%)	27±0 (100±1%)	0±0 (0±1%)	0±0 (0±0%)	100	100
3	D	25/33 (76%)	24±1 (98±2%)	1±1 (2±2%)	0±0 (0±0%)	100	100
All	All	4095/4515 (91%)	3843 (94%)	231 (6%)	21 (1%)	32	76

5 of 8 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	392	GLU	6
1	A	367	SER	5
1	A	362	ARG	3
1	A	442	LEU	2
1	A	322	ASN	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	169/169 (100%)	158±2 (94±1%)	11±2 (6±1%)	21	70
2	B	15/15 (100%)	15±0 (98±3%)	0±0 (2±3%)	61	94
2	C	15/15 (100%)	15±0 (100±2%)	0±0 (0±2%)	91	98
3	D	14/14 (100%)	14±0 (100±0%)	0±0 (0±0%)	100	100
All	All	3195/3195 (100%)	3031 (95%)	164 (5%)	27	77

5 of 39 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	412	THR	14
1	A	370	THR	13
1	A	376	ASP	13
1	A	470	SER	9
1	A	504	ASP	9

6.3.3 RNA (i)

There are no RNA molecules in this entry.

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

23 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	HYP	C	126	2	6,8,9	0.83±0.03	0±0 (0±0%)
2	HYP	C	105	2	6,8,9	0.78±0.03	0±0 (0±0%)
3	HYP	D	226	3	6,8,9	0.83±0.02	0±0 (0±0%)
2	HYP	C	132	2	6,8,9	0.84±0.03	0±0 (0±0%)
3	HYP	D	223	3	6,8,9	0.85±0.02	0±0 (0±0%)
2	HYP	C	129	2	6,8,9	0.85±0.02	0±0 (0±0%)
2	HYP	B	29	2	6,8,9	0.85±0.02	0±0 (0±0%)
2	HYP	B	8	2	6,8,9	0.80±0.02	0±0 (0±0%)
2	HYP	B	35	2	6,8,9	0.99±0.03	0±0 (0±0%)
2	HYP	B	5	2	6,8,9	0.84±0.03	0±0 (0±0%)
3	HYP	D	202	3	6,8,9	0.79±0.03	0±0 (0±0%)
3	HYP	D	205	3	6,8,9	0.82±0.04	0±0 (0±0%)
2	HYP	B	2	2	6,8,9	0.80±0.04	0±0 (0±0%)
3	HYP	D	208	3	6,8,9	0.80±0.03	0±0 (0±0%)
2	HYP	C	108	2	6,8,9	0.81±0.04	0±0 (0±0%)
3	HYP	D	229	3	6,8,9	0.84±0.02	0±0 (0±0%)
2	HYP	C	123	2	6,8,9	0.86±0.03	0±0 (0±0%)
2	HYP	C	102	2	6,8,9	0.84±0.03	0±0 (0±0%)

Mol	Type	Chain	Res	Link	Bond lengths		
					Counts	RMSZ	#Z>2
2	HYP	B	32	2	6,8,9	0.84±0.02	0±0 (0±0%)
2	HYP	C	135	2	6,8,9	0.75±0.05	0±0 (0±0%)
2	HYP	B	23	2	6,8,9	0.84±0.03	0±0 (0±0%)
3	HYP	D	232	3	9,9,9	0.91±0.04	0±0 (0±0%)
2	HYP	B	26	2	6,8,9	0.84±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	HYP	C	126	2	5,10,12	1.24±0.14	1±0 (14±8%)
2	HYP	C	105	2	5,10,12	1.55±0.21	1±0 (21±4%)
3	HYP	D	226	3	5,10,12	1.22±0.19	0±0 (9±9%)
2	HYP	C	132	2	5,10,12	1.19±0.19	0±0 (9±9%)
3	HYP	D	223	3	5,10,12	1.16±0.08	0±0 (8±9%)
2	HYP	C	129	2	5,10,12	1.12±0.11	0±0 (6±9%)
2	HYP	B	29	2	5,10,12	1.14±0.13	0±0 (4±8%)
2	HYP	B	8	2	5,10,12	1.15±0.22	0±0 (8±9%)
2	HYP	B	35	2	5,10,12	1.22±0.17	0±0 (6±9%)
2	HYP	B	5	2	5,10,12	1.20±0.15	1±0 (13±9%)
3	HYP	D	202	3	5,10,12	1.18±0.18	0±0 (6±9%)
3	HYP	D	205	3	5,10,12	1.13±0.10	0±0 (2±6%)
2	HYP	B	2	2	5,10,12	1.39±0.23	1±0 (18±8%)
3	HYP	D	208	3	5,10,12	1.34±0.16	1±0 (16±8%)
2	HYP	C	108	2	5,10,12	1.28±0.25	1±0 (13±9%)
3	HYP	D	229	3	5,10,12	1.15±0.09	1±0 (10±9%)
2	HYP	C	123	2	5,10,12	0.98±0.10	0±0 (1±4%)
2	HYP	C	102	2	5,10,12	1.19±0.16	0±0 (8±9%)
2	HYP	B	32	2	5,10,12	1.18±0.16	0±0 (6±9%)
2	HYP	C	135	2	5,10,12	1.42±0.19	1±0 (14±8%)
2	HYP	B	23	2	5,10,12	1.13±0.19	0±0 (5±8%)
3	HYP	D	232	3	10,12,12	1.26±0.17	1±0 (6±4%)

Mol	Type	Chain	Res	Link	Bond angles		
					Counts	RMSZ	#Z>2
2	HYP	B	26	2	5,10,12	1.17±0.18	0±0 (6±9%)

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	HYP	C	126	2	-	0±0,0,11,13	0±0,1,1,1
2	HYP	B	35	2	-	0±0,0,11,13	0±0,1,1,1
2	HYP	B	8	2	-	0±0,0,11,13	0±0,1,1,1
2	HYP	C	123	2	-	0±0,0,11,13	0±0,1,1,1
2	HYP	B	23	2	-	0±0,0,11,13	0±0,1,1,1
2	HYP	B	29	2	-	0±0,0,11,13	0±0,1,1,1
2	HYP	B	2	2	-	0±0,0,11,13	0±0,1,1,1
3	HYP	D	229	3	-	0±0,0,11,13	0±0,1,1,1
2	HYP	C	129	2	-	0±0,0,11,13	0±0,1,1,1
3	HYP	D	208	3	-	0±0,0,11,13	0±0,1,1,1
2	HYP	C	102	2	-	0±0,0,11,13	0±0,1,1,1
3	HYP	D	202	3	-	0±0,0,11,13	0±0,1,1,1
2	HYP	C	132	2	-	0±0,0,11,13	0±0,1,1,1
2	HYP	B	5	2	-	0±0,0,11,13	0±0,1,1,1
3	HYP	D	232	3	-	0±0,4,13,13	0±0,1,1,1
2	HYP	B	26	2	-	0±0,0,11,13	0±0,1,1,1
3	HYP	D	223	3	-	0±0,0,11,13	0±0,1,1,1
2	HYP	C	108	2	-	0±0,0,11,13	0±0,1,1,1
2	HYP	C	135	2	-	0±0,0,11,13	0±0,1,1,1
3	HYP	D	205	3	-	0±0,0,11,13	0±0,1,1,1
3	HYP	D	226	3	-	0±0,0,11,13	0±0,1,1,1
2	HYP	B	32	2	-	0±0,0,11,13	0±0,1,1,1
2	HYP	C	105	2	-	0±0,0,11,13	0±0,1,1,1

There are no bond-length outliers.

5 of 25 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	C	108	HYP	CB-CG-CD	3.89	108.03	103.27	15	10
3	D	232	HYP	CB-CG-CD	3.83	107.96	103.27	3	10
2	B	2	HYP	CB-CG-CD	3.79	107.91	103.27	8	13
2	B	8	HYP	CB-CG-CD	3.59	107.66	103.27	15	6

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})	Models	
								Worst	Total
2	C	105	HYP	CB-CG-CD	3.49	107.55	103.27	8	15

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 26% for the well-defined parts and 26% 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	956
Number of shifts mapped to atoms	836
Number of unparsed shifts	0
Number of shifts with mapping errors	120
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

The following assigned chemical shifts were not mapped to the molecules present in the coordinate file.

- No matching atom found in the structure. First 5 (of 120) occurrences are reported below.

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	318	ILE	HD11	-0.26	0.04	1
1	A	318	ILE	HD12	-0.26	0.04	1
1	A	318	ILE	HD13	-0.26	0.04	1
1	A	326	VAL	HG11	0.77	0.04	1
1	A	326	VAL	HG12	0.77	0.04	1
1	A	326	VAL	HG13	0.77	0.04	1
1	A	326	VAL	HG21	0.36	0.04	1
1	A	326	VAL	HG22	0.36	0.04	1
1	A	326	VAL	HG23	0.36	0.04	1
1	A	329	LEU	HD11	-0.33	0.04	1
1	A	329	LEU	HD12	-0.33	0.04	1
1	A	329	LEU	HD13	-0.33	0.04	1
1	A	329	LEU	HD21	0.19	0.04	1
1	A	329	LEU	HD22	0.19	0.04	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	329	LEU	HD23	0.19	0.04	1
1	A	335	VAL	HG11	-0.14	0.04	1
1	A	335	VAL	HG12	-0.14	0.04	1
1	A	335	VAL	HG13	-0.14	0.04	1
1	A	335	VAL	HG21	0.49	0.04	1
1	A	335	VAL	HG22	0.49	0.04	1
1	A	335	VAL	HG23	0.49	0.04	1
1	A	344	VAL	HG11	0.58	0.04	1
1	A	344	VAL	HG12	0.58	0.04	1
1	A	344	VAL	HG13	0.58	0.04	1
1	A	344	VAL	HG21	0.41	0.04	1
1	A	344	VAL	HG22	0.41	0.04	1
1	A	344	VAL	HG23	0.41	0.04	1
1	A	349	VAL	HG11	1.29	0.04	1
1	A	349	VAL	HG12	1.29	0.04	1
1	A	349	VAL	HG13	1.29	0.04	1
1	A	349	VAL	HG21	0.96	0.04	1
1	A	349	VAL	HG22	0.96	0.04	1
1	A	349	VAL	HG23	0.96	0.04	1
1	A	357	ILE	HD11	1.23	0.04	1
1	A	357	ILE	HD12	1.23	0.04	1
1	A	357	ILE	HD13	1.23	0.04	1
1	A	364	LEU	HD21	0.94	0.04	1
1	A	364	LEU	HD11	0.94	0.04	1
1	A	364	LEU	HD12	0.94	0.04	1
1	A	364	LEU	HD13	0.94	0.04	1
1	A	364	LEU	HD22	0.94	0.04	1
1	A	364	LEU	HD23	0.94	0.04	1
1	A	368	ILE	HD11	-0.06	0.04	1
1	A	368	ILE	HD12	-0.06	0.04	1
1	A	368	ILE	HD13	-0.06	0.04	1
1	A	380	VAL	HG11	0.61	0.04	1
1	A	380	VAL	HG12	0.61	0.04	1
1	A	380	VAL	HG13	0.61	0.04	1
1	A	380	VAL	HG21	0.65	0.04	1
1	A	380	VAL	HG22	0.65	0.04	1
1	A	380	VAL	HG23	0.65	0.04	1
1	A	389	VAL	HG11	0.56	0.04	1
1	A	389	VAL	HG12	0.56	0.04	1
1	A	389	VAL	HG13	0.56	0.04	1
1	A	389	VAL	HG21	0.61	0.04	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	389	VAL	HG22	0.61	0.04	1
1	A	389	VAL	HG23	0.61	0.04	1
1	A	395	LEU	HD11	0.47	0.04	1
1	A	395	LEU	HD12	0.47	0.04	1
1	A	395	LEU	HD13	0.47	0.04	1
1	A	395	LEU	HD21	0.49	0.04	1
1	A	395	LEU	HD22	0.49	0.04	1
1	A	395	LEU	HD23	0.49	0.04	1
1	A	403	ILE	HD11	0.57	0.04	1
1	A	403	ILE	HD12	0.57	0.04	1
1	A	403	ILE	HD13	0.57	0.04	1
1	A	406	LEU	HD11	1.24	0.04	1
1	A	406	LEU	HD12	1.24	0.04	1
1	A	406	LEU	HD13	1.24	0.04	1
1	A	410	LEU	HD11	-0.09	0.04	1
1	A	410	LEU	HD12	-0.09	0.04	1
1	A	410	LEU	HD13	-0.09	0.04	1
1	A	410	LEU	HD21	0.05	0.04	1
1	A	410	LEU	HD22	0.05	0.04	1
1	A	410	LEU	HD23	0.05	0.04	1
1	A	415	ILE	HD11	-0.26	0.04	1
1	A	415	ILE	HD12	-0.26	0.04	1
1	A	415	ILE	HD13	-0.26	0.04	1
1	A	419	LEU	HD11	1.07	0.04	1
1	A	419	LEU	HD12	1.07	0.04	1
1	A	419	LEU	HD13	1.07	0.04	1
1	A	442	LEU	HD11	0.92	0.04	1
1	A	442	LEU	HD12	0.92	0.04	1
1	A	442	LEU	HD13	0.92	0.04	1
1	A	442	LEU	HD21	0.84	0.04	1
1	A	442	LEU	HD22	0.84	0.04	1
1	A	442	LEU	HD23	0.84	0.04	1
1	A	453	ILE	HD11	0.76	0.04	1
1	A	453	ILE	HD12	0.76	0.04	1
1	A	453	ILE	HD13	0.76	0.04	1
1	A	455	VAL	HG11	1.24	0.04	1
1	A	455	VAL	HG12	1.24	0.04	1
1	A	455	VAL	HG13	1.24	0.04	1
1	A	455	VAL	HG21	0.78	0.04	1
1	A	455	VAL	HG22	0.78	0.04	1
1	A	455	VAL	HG23	0.78	0.04	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	459	ILE	HD11	-0.25	0.04	1
1	A	459	ILE	HD12	-0.25	0.04	1
1	A	459	ILE	HD13	-0.25	0.04	1
1	A	473	VAL	HG11	0.09	0.04	1
1	A	473	VAL	HG12	0.09	0.04	1
1	A	473	VAL	HG13	0.09	0.04	1
1	A	473	VAL	HG21	0.75	0.04	1
1	A	473	VAL	HG22	0.75	0.04	1
1	A	473	VAL	HG23	0.75	0.04	1
1	A	491	LEU	HD11	0.74	0.04	1
1	A	491	LEU	HD12	0.74	0.04	1
1	A	491	LEU	HD13	0.74	0.04	1
1	A	493	VAL	HG11	1.41	0.04	1
1	A	493	VAL	HG12	1.41	0.04	1
1	A	493	VAL	HG13	1.41	0.04	1
1	A	493	VAL	HG21	1.43	0.04	1
1	A	493	VAL	HG22	1.43	0.04	1
1	A	493	VAL	HG23	1.43	0.04	1
1	A	502	LEU	HD21	0.93	0.04	1
1	A	502	LEU	HD11	0.93	0.04	1
1	A	502	LEU	HD12	0.93	0.04	1
1	A	502	LEU	HD13	0.93	0.04	1
1	A	502	LEU	HD22	0.93	0.04	1
1	A	502	LEU	HD23	0.93	0.04	1

7.1.2 Chemical shift referencing (i)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	165	0.88 ± 0.12	Should be checked
$^{13}C_{\beta}$	143	1.34 ± 0.17	Should be checked
$^{13}C'$	156	3.14 ± 0.14	Should be applied
^{15}N	164	0.23 ± 0.36	None needed (< 0.5 ppm)

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 26%, i.e. 956 atoms were assigned a chemical shift out of a possible 3629. 0 out of 28 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	649/1370 (47%)	164/573 (29%)	321/556 (58%)	164/241 (68%)
Sidechain	307/1880 (16%)	123/1215 (10%)	181/581 (31%)	3/84 (4%)
Aromatic	0/379 (0%)	0/185 (0%)	0/184 (0%)	0/10 (0%)
Overall	956/3629 (26%)	287/1973 (15%)	502/1321 (38%)	167/335 (50%)

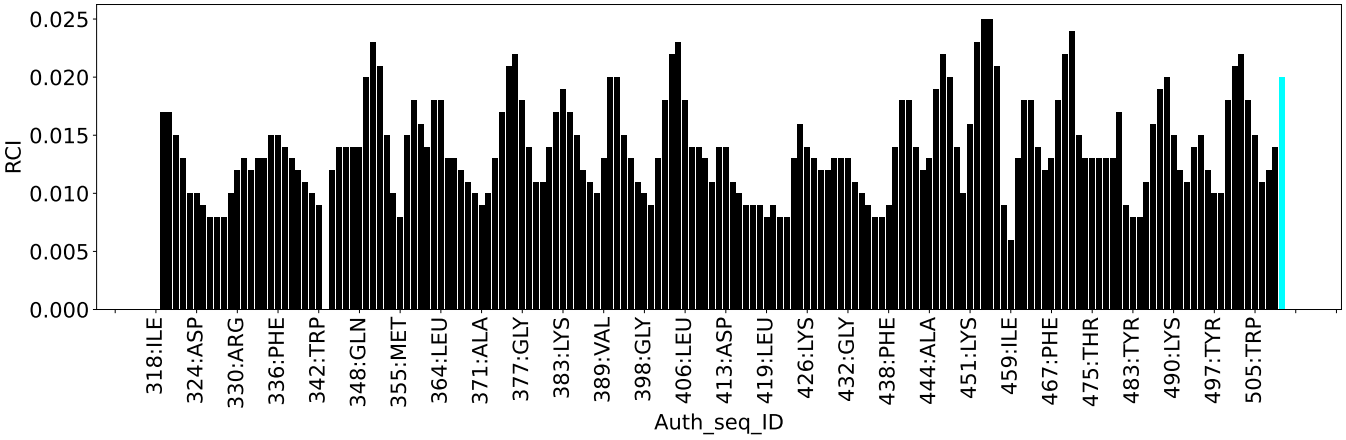
7.1.4 Statistically unusual chemical shifts (i)

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:



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	73
Intra-residue (|i-j|=0)	0
Sequential (|i-j|=1)	0
Medium range (|i-j|>1 and |i-j|<5)	0
Long range (|i-j|≥5)	0
Inter-chain	73
Hydrogen bond restraints	0
Disulfide bond restraints	0
Total dihedral-angle restraints	0
Number of unmapped restraints	25
Number of restraints per residue	0.2
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 (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)	0.2	0.13
0.2-0.5 (Medium)	None	None
>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)

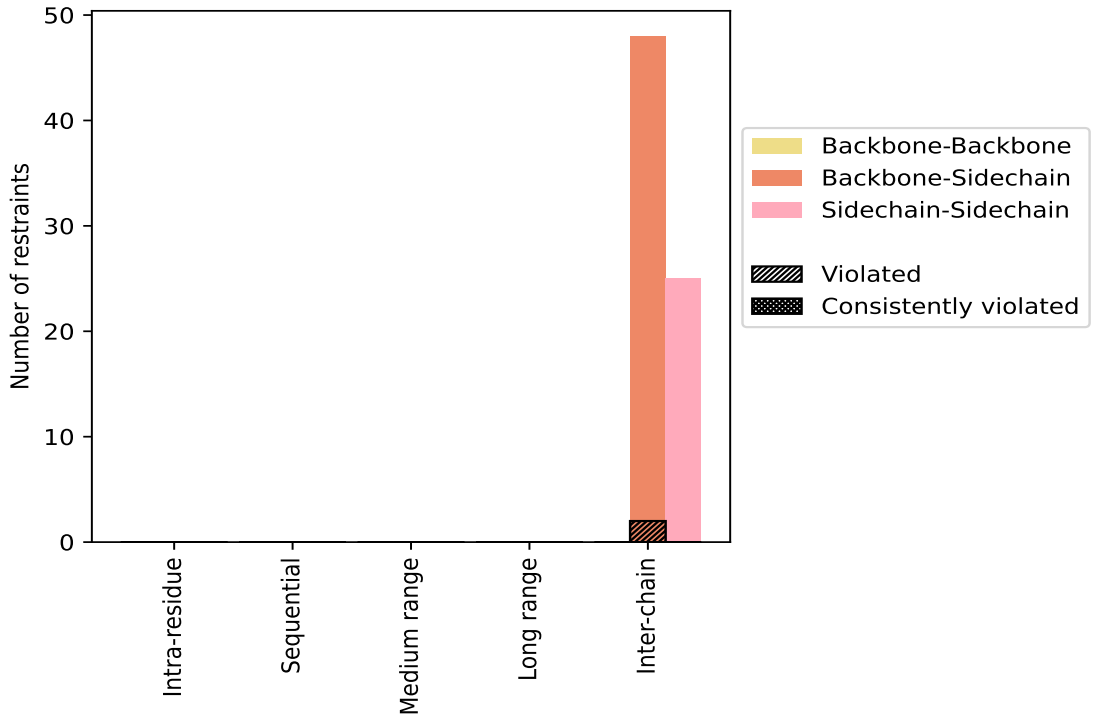
9.1 Summary of distance violations (i)

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)	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)	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
Medium range (|i-j|>1 & |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
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	73	100.0	2	2.7	2.7	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	48	65.8	2	4.2	2.7	0	0.0	0.0
Sidechain-Sidechain	25	34.2	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	73	100.0	2	2.7	2.7	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	48	65.8	2	4.2	2.7	0	0.0	0.0
Sidechain-Sidechain	25	34.2	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 (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	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	1	1	0.13	0.13	0.0	0.13
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	0	0	0	1	1	0.11	0.11	0.0	0.11
10	0	0	0	0	0	0	0.0	0.0	0.0	0.0
11	0	0	0	0	1	1	0.13	0.13	0.0	0.13

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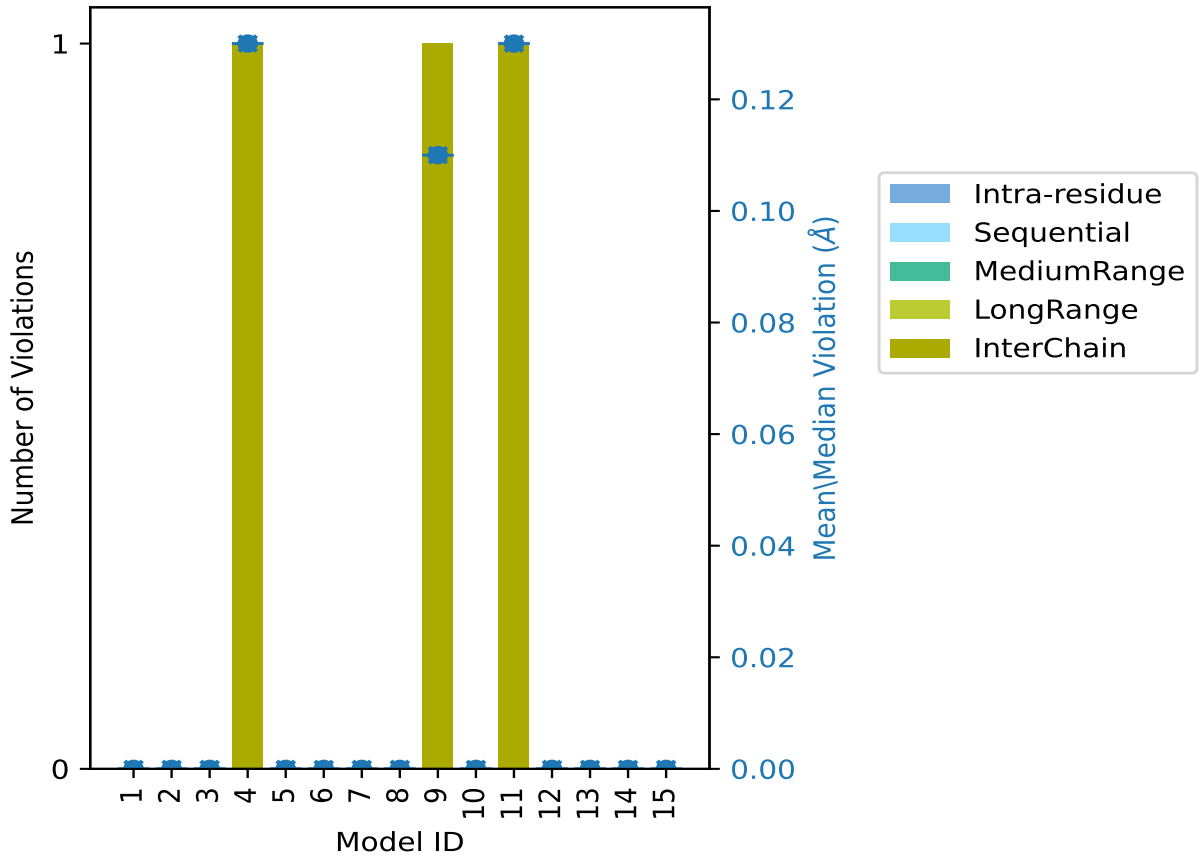
Model ID	Number of violations						Mean (Å)	Max (Å)	SD[6] (Å)	Median (Å)
	IR[1]	SQ[2]	MR[3]	LR[4]	IC[5]	Total				
12	0	0	0	0	0	0	0.0	0.0	0.0	0.0
13	0	0	0	0	0	0	0.0	0.0	0.0	0.0
14	0	0	0	0	0	0	0.0	0.0	0.0	0.0
15	0	0	0	0	0	0	0.0	0.0	0.0	0.0

[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)

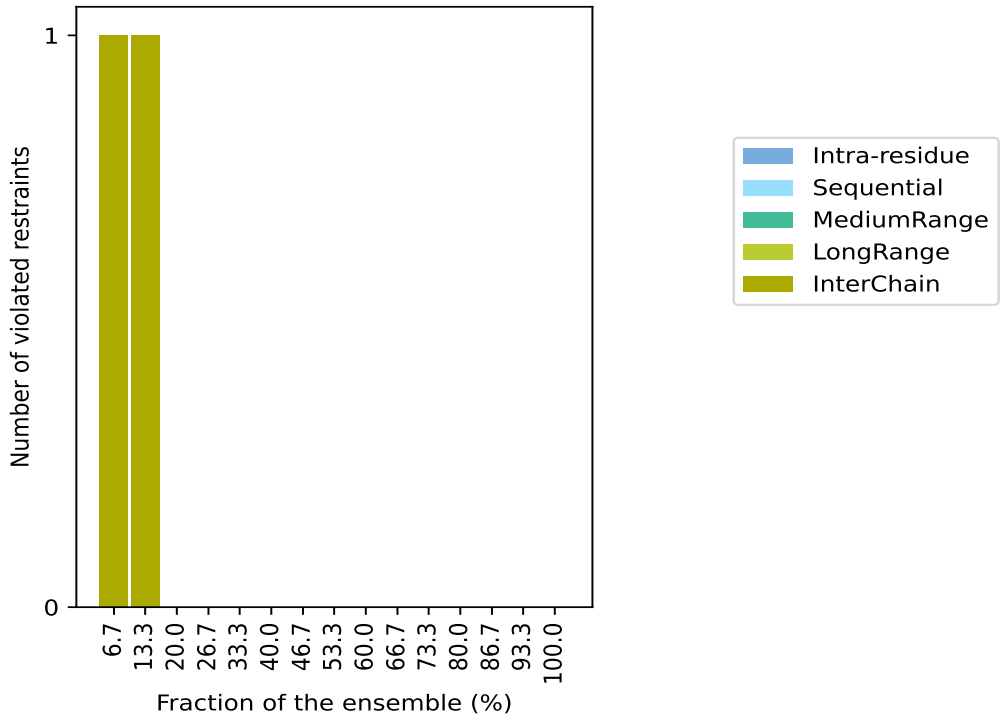
Violation analysis may find that some restraints are violated in few models and some are violated in most of models. The following table provides this information as number of violated restraints

for a given fraction of the ensemble. In total, 71(IR:0, SQ:0, MR:0, LR:0, IC:71) 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	0	0	0	1	1	1	6.7
0	0	0	0	1	1	2	13.3
0	0	0	0	0	0	3	20.0
0	0	0	0	0	0	4	26.7
0	0	0	0	0	0	5	33.3
0	0	0	0	0	0	6	40.0
0	0	0	0	0	0	7	46.7
0	0	0	0	0	0	8	53.3
0	0	0	0	0	0	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	0	0	12	80.0
0	0	0	0	0	0	13	86.7
0	0	0	0	0	0	14	93.3
0	0	0	0	0	0	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

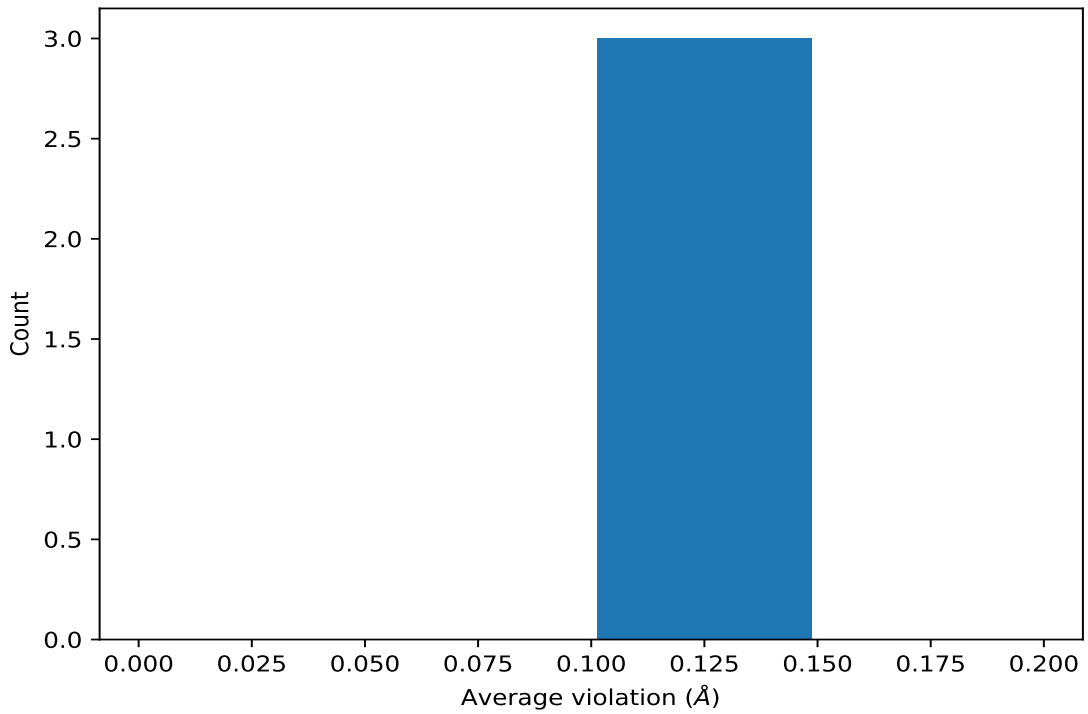
9.3.1 Bar graph : Distance violation statistics for the ensemble (i)



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.

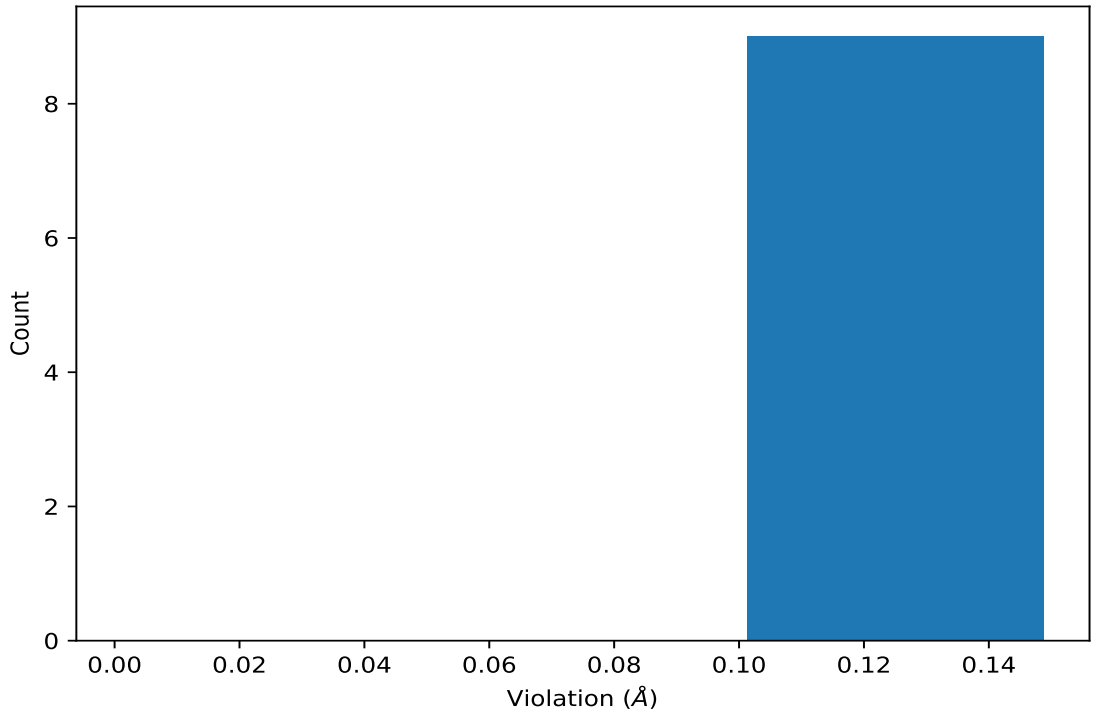
Key	Atom-1	Atom-2	Models[1]	Mean (Å)	SD[1] (Å)	Median (Å)
(1,13)	1:A:379:PHE:H	2:B:16:GLN:CD	2	0.13	0.0	0.13
(1,13)	1:A:379:PHE:H	2:C:116:GLN:CD	2	0.13	0.0	0.13
(1,13)	1:A:379:PHE:H	3:D:216:GLN:CD	2	0.13	0.0	0.13

[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 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)
(1,13)	1:A:379:PHE:H	2:B:16:GLN:CD	4	0.13
(1,13)	1:A:379:PHE:H	2:C:116:GLN:CD	4	0.13
(1,13)	1:A:379:PHE:H	3:D:216:GLN:CD	4	0.13
(1,13)	1:A:379:PHE:H	2:B:16:GLN:CD	11	0.13
(1,13)	1:A:379:PHE:H	2:C:116:GLN:CD	11	0.13
(1,13)	1:A:379:PHE:H	3:D:216:GLN:CD	11	0.13
(1,25)	1:A:482:LYS:H	2:B:16:GLN:CD	9	0.11
(1,25)	1:A:482:LYS:H	2:C:116:GLN:CD	9	0.11
(1,25)	1:A:482:LYS:H	3:D:216:GLN:CD	9	0.11

10 Dihedral-angle violation analysis (i)

No dihedral-angle restraints found