wwPDB NMR Structure Validation Summary Report

Dec 24, 2024 – 05:58 PM EST

PDB ID	:	2LTQ
BMRB ID	:	18493
Title	:	High resolution structure of DsbB C41S by joint calculation with solid-state NMR and X-ray data
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Deposited on	:	2012-05-30

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:

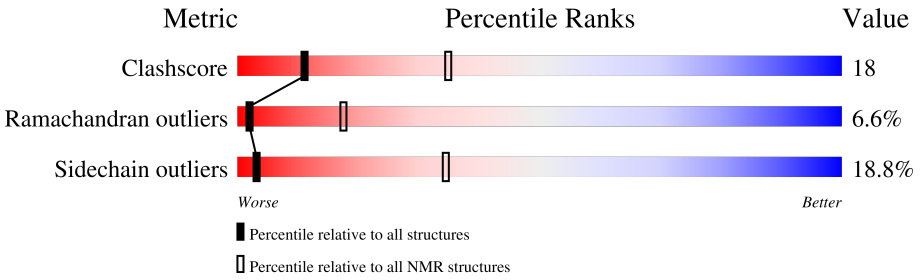
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
BMRB Restraints Analysis	:	v1.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.40

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
SOLID-STATE NMR

The overall completeness of chemical shifts assignment is 2%.

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	210492	14027
Ramachandran outliers	207382	12486
Sidechain outliers	206894	12463

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	176	9% 14% • 61% 16%
1	D	176	9% 8% • 67% 16%
2	B	239	50% 32% 9% 9%
2	E	239	55% 27% 8% • 9%
3	C	221	52% 34% 11% •
3	F	221	52% 36% 8% • •

2 Ensemble composition and analysis (i)

This entry contains 10 models. Model 4 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:15-A:29, A:53-A:55, A:73-A:93, A:151-A:152, B:21-B:132, B:134-B:239, C:1-C:100, C:105-C:119, C:121-C:221, D:53-D:62, D:72-D:91, E:21-E:132, E:134-E:239, F:1-F:119, F:121-F:215 (937)	0.13	4

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 1 clusters. No single-model clusters were found.

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

3 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 17810 atoms, of which 8819 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Disulfide bond formation protein B.

Mol	Chain	Residues	Atoms						Trace
1	A	148	Total	C	H	N	O	S	0
			2387	794	1212	183	189	9	
1	D	148	Total	C	H	N	O	S	0
			2387	794	1212	183	189	9	

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	8	ALA	CYS	engineered mutation	UNP P0A6M2
A	41	SER	CYS	engineered mutation	UNP P0A6M2
A	49	VAL	CYS	engineered mutation	UNP P0A6M2
D	8	ALA	CYS	engineered mutation	UNP P0A6M2
D	41	SER	CYS	engineered mutation	UNP P0A6M2
D	49	VAL	CYS	engineered mutation	UNP P0A6M2

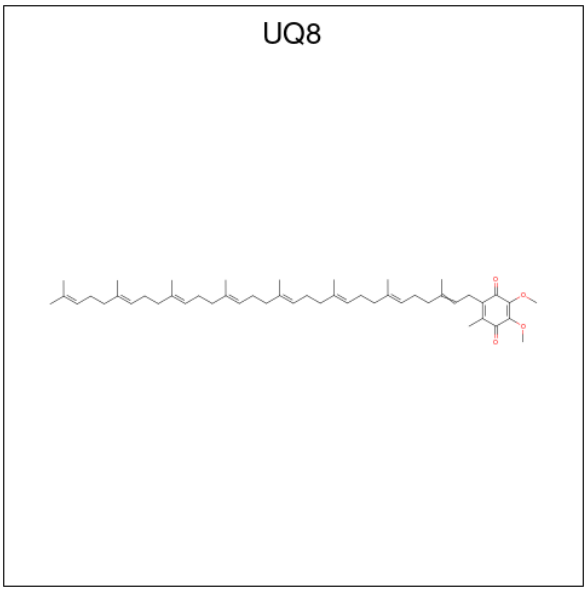
- Molecule 2 is a protein called Fab fragment light chain.

Mol	Chain	Residues	Atoms						Trace
2	B	218	Total	C	H	N	O	S	0
			3319	1052	1629	283	347	8	
2	E	218	Total	C	H	N	O	S	0
			3319	1052	1629	283	347	8	

- Molecule 3 is a protein called Fab fragment heavy chain.

Mol	Chain	Residues	Atoms						Trace
3	C	216	Total	C	H	N	O	S	0
			3189	1017	1574	264	325	9	
3	F	214	Total	C	H	N	O	S	0
			3173	1015	1563	262	324	9	

- Molecule 4 is Ubiquinone-8 (three-letter code: UQ8) (formula: $C_{49}H_{74}O_4$).



Mol	Chain	Residues	Atoms		
4	A	1	Total	C	O
			18	14	4
4	D	1	Total	C	O
			18	14	4

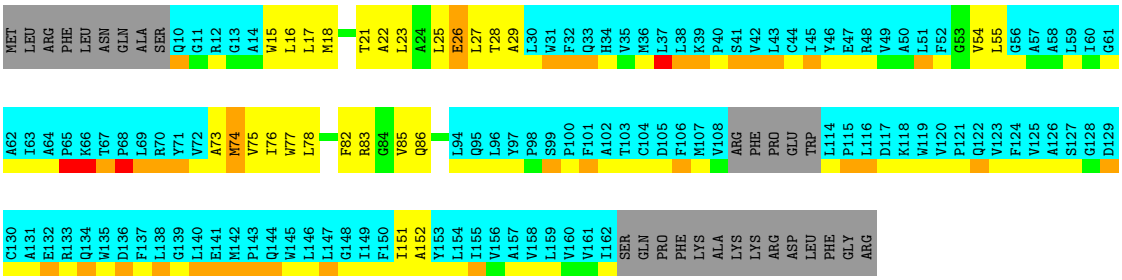
4 Residue-property plots

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.

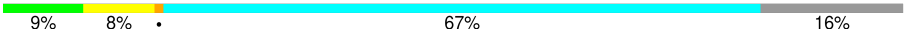
• Molecule 1: Disulfide bond formation protein B

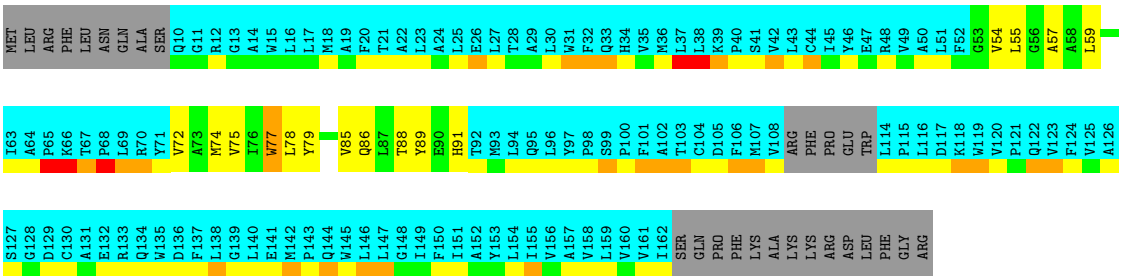
Chain A:



• Molecule 1: Disulfide bond formation protein B

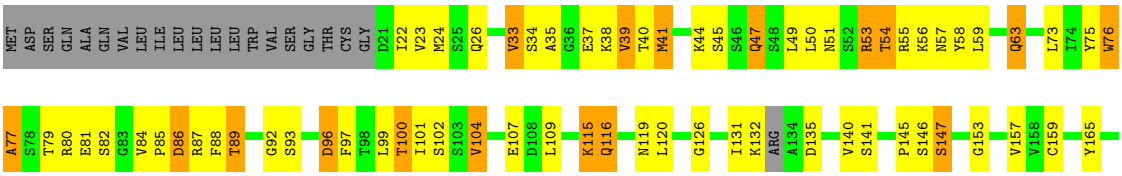
Chain D:



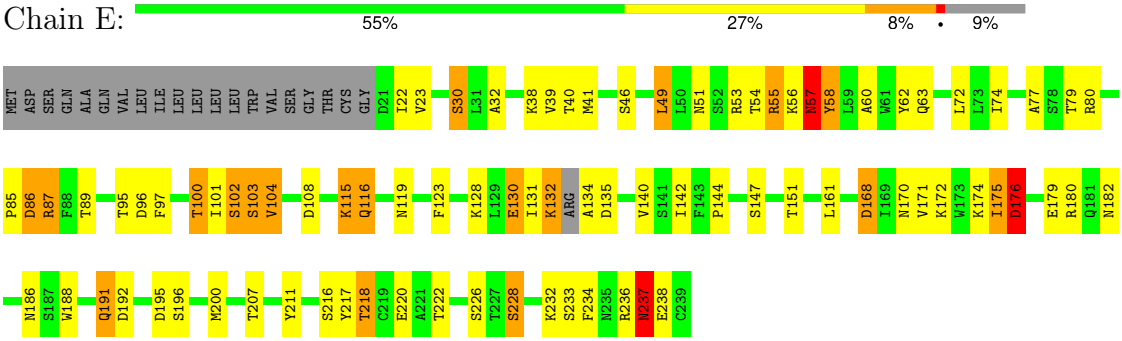


• Molecule 2: Fab fragment light chain

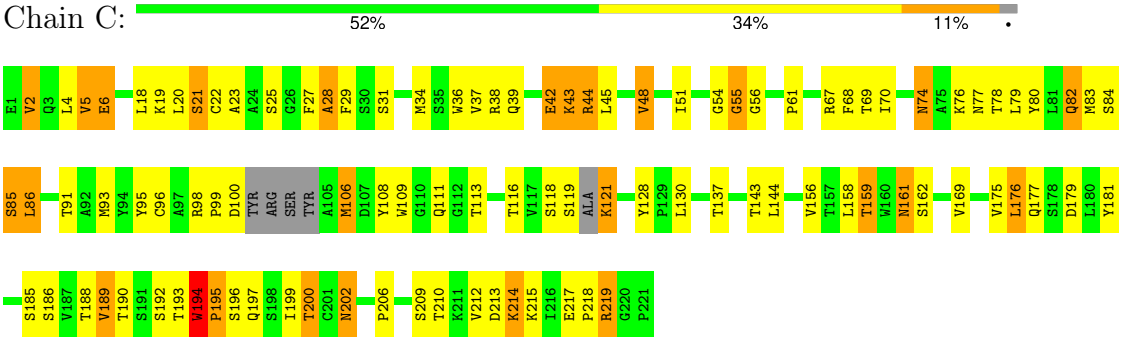
Chain B:



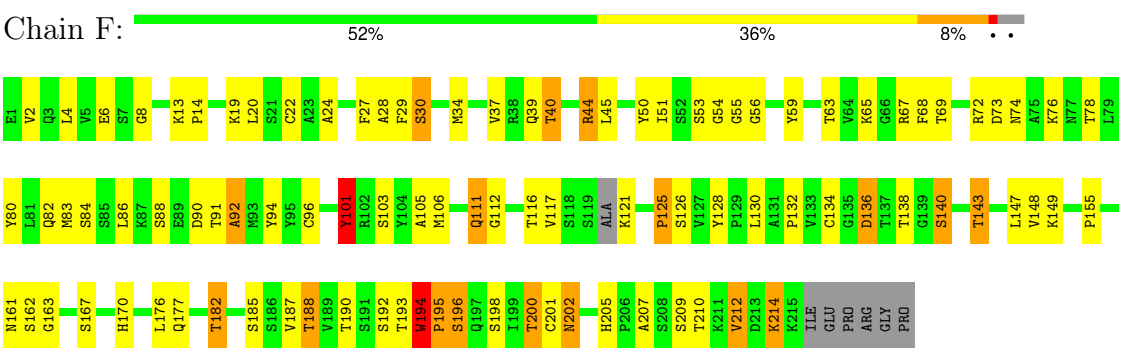
• Molecule 2: Fab fragment light chain



• Molecule 3: Fab fragment heavy chain



• Molecule 3: Fab fragment heavy chain

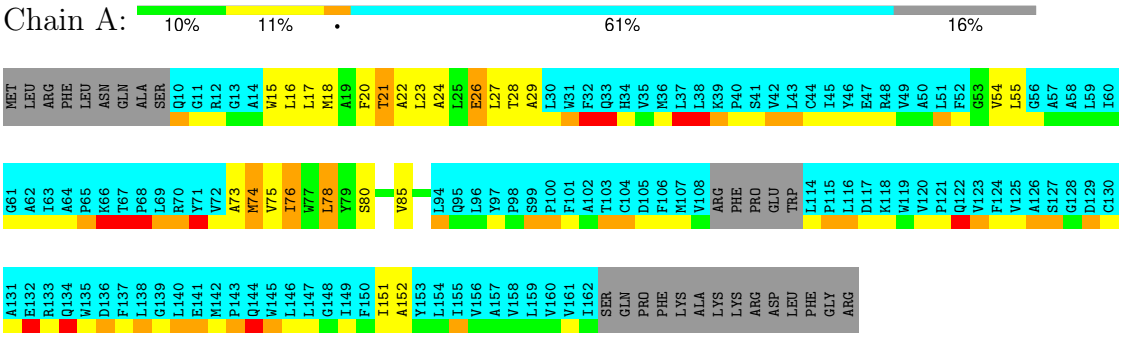


4.2 Residue scores for the representative (medoid) model from the NMR ensemble

The representative model is number 4. Colouring as in section 4.1 above.

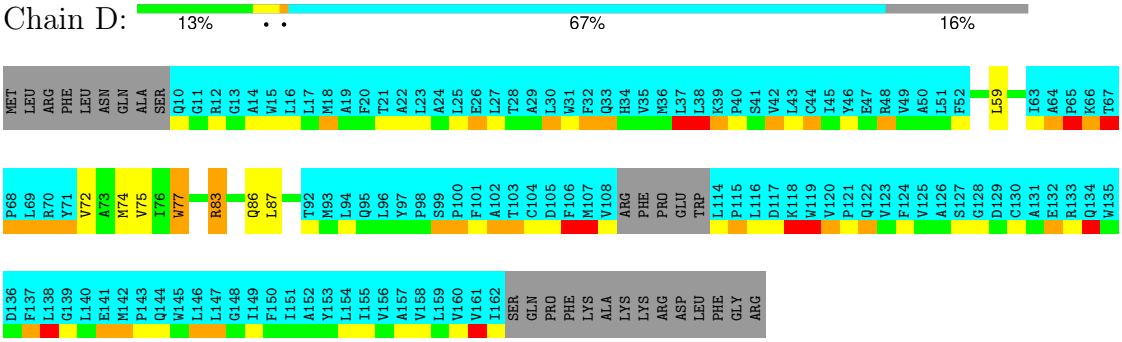
• Molecule 1: Disulfide bond formation protein B

Chain A:



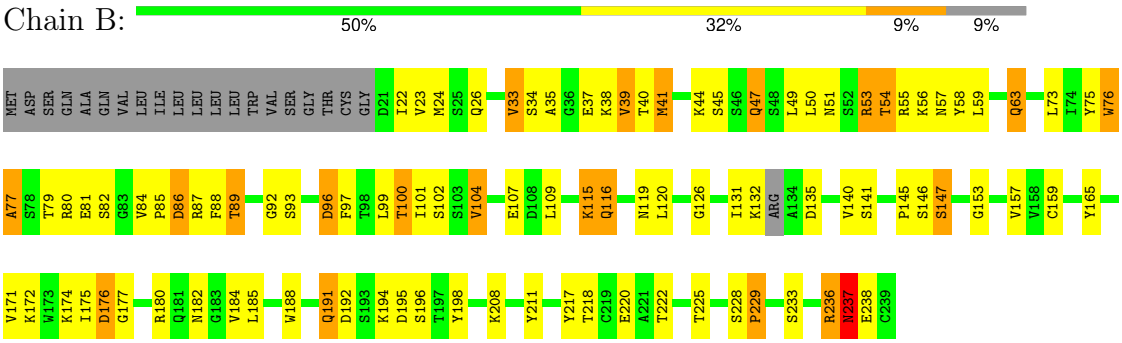
• Molecule 1: Disulfide bond formation protein B

Chain D:



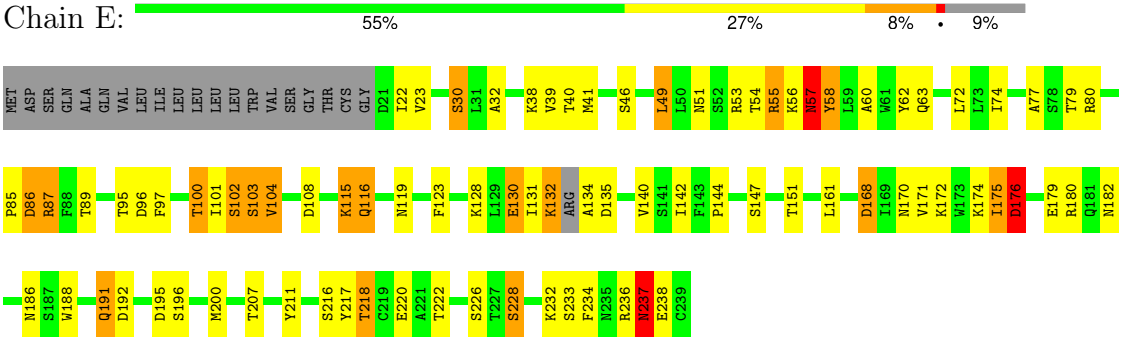
• Molecule 2: Fab fragment light chain

Chain B:



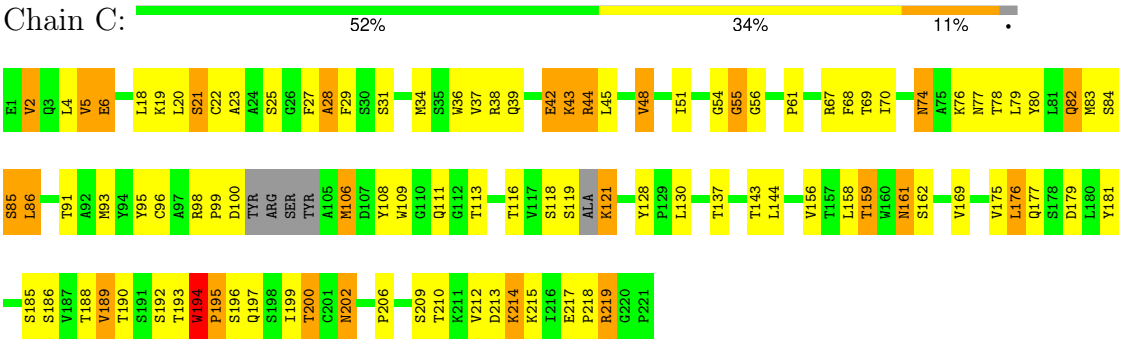
• Molecule 2: Fab fragment light chain

Chain E:



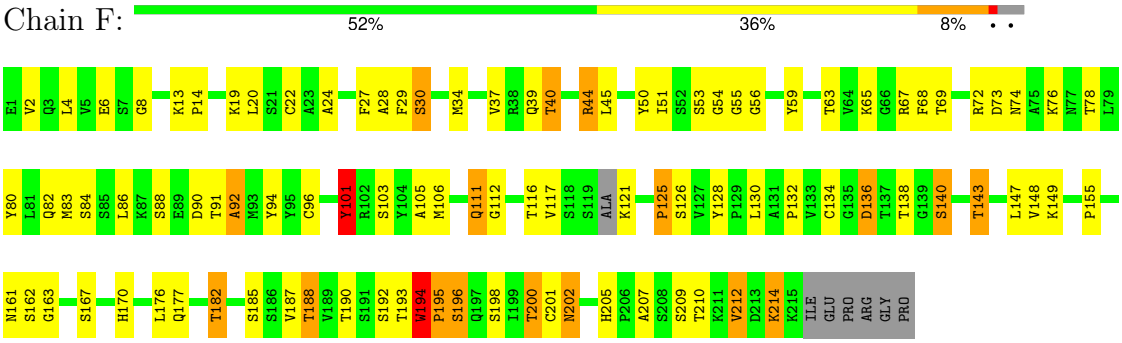
• Molecule 3: Fab fragment heavy chain

Chain C:



• Molecule 3: Fab fragment heavy chain

Chain F:



5 Refinement protocol and experimental data overview

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

Of the 200 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
X-PLOR NIH	refinement	
X-PLOR NIH	structure solution	

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	744
Number of shifts mapped to atoms	671
Number of unparsed shifts	0
Number of shifts with mapping errors	73
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	2%

Note: This is a solid-state NMR structure, where hydrogen atoms are typically not assigned a chemical shift value, which may lead to lower completeness of assignment measure.

6 Model quality

6.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: UQ8

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

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
2	E	0.0±0.0	1.0±0.0
3	C	0.0±0.0	1.0±0.0
3	F	0.0±0.0	1.0±0.0
All	All	0	30

There are no bond-length outliers.

There are no bond-angle outliers.

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)
3	C	194	TRP	Peptide	10
2	E	57	ASN	Peptide	10
3	F	194	TRP	Peptide	10

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	324	335	334	18±5
1	D	226	232	231	9±4
2	B	1690	1629	1625	66±1
2	E	1690	1629	1625	45±1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes
3	C	1615	1574	1570	66±1
3	F	1610	1563	1560	54±1
4	A	18	0	15	0±0
4	D	18	0	15	0±0
All	All	71910	69620	69750	2534

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 18.

5 of 421 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:115:LYS:HB2	2:B:115:LYS:NZ	1.21	1.48	6	10
2:B:44:LYS:NZ	2:B:96:ASP:OD1	1.08	1.85	6	10
2:B:26:GLN:NE2	2:B:126:GLY:H	1.07	1.46	5	10
2:B:40:THR:HG22	2:B:100:THR:HB	1.05	1.23	1	10
2:B:115:LYS:CB	2:B:115:LYS:HZ3	1.03	1.66	6	4

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	41/176 (23%)	38±1 (93±3%)	2±2 (5±4%)	1±1 (2±1%)	8	47
1	D	30/176 (17%)	29±1 (96±3%)	1±1 (4±3%)	0±0 (0±0%)	100	100
2	B	214/239 (90%)	171±0 (80±0%)	28±0 (13±0%)	15±0 (7±0%)	2	16
2	E	214/239 (90%)	177±0 (83±0%)	26±0 (12±0%)	11±0 (5±0%)	3	23
3	C	210/221 (95%)	165±0 (79±0%)	32±0 (15±0%)	13±0 (6±0%)	2	19
3	F	210/221 (95%)	160±0 (76±0%)	29±0 (14±0%)	21±0 (10±0%)	1	9
All	All	9190/12720 (72%)	7397 (80%)	1184 (13%)	609 (7%)	2	17

5 of 62 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
2	B	35	ALA	10
2	B	54	THR	10
2	B	76	TRP	10
2	B	77	ALA	10
2	B	82	SER	10

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	32/147 (22%)	24±1 (76±4%)	8±1 (24±4%)	2	25
1	D	21/147 (14%)	16±2 (75±9%)	5±2 (25±9%)	2	23
2	B	194/212 (92%)	163±0 (84±0%)	31±0 (16±0%)	4	40
2	E	194/212 (92%)	157±0 (81±0%)	37±0 (19±0%)	3	34
3	C	184/188 (98%)	145±0 (79±0%)	39±0 (21±0%)	2	30
3	F	183/188 (97%)	151±0 (83±0%)	32±0 (17±0%)	3	37
All	All	8080/10940 (74%)	6562 (81%)	1518 (19%)	3	34

5 of 183 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	23	VAL	10
2	B	33	VAL	10
2	B	39	VAL	10
2	B	41	MET	10
2	B	47	GLN	10

6.3.3 RNA (i)

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

6.6 Ligand geometry (i)

2 ligands 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
4	UQ8	A	201	-	18,18,53	2.24±0.01	2±0 (11±0%)
4	UQ8	D	201	-	18,18,53	2.18±0.00	2±0 (11±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
4	UQ8	A	201	-	24,25,67	1.24±0.00	3±0 (12±0%)
4	UQ8	D	201	-	24,25,67	1.18±0.00	2±0 (8±0%)

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
4	UQ8	A	201	-	-	0±0,9,33,75	0±0,1,1,1
4	UQ8	D	201	-	-	0±0,9,33,75	0±0,1,1,1

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
4	A	201	UQ8	C6-C1	8.41	1.50	1.35	7	10
4	D	201	UQ8	C6-C1	8.12	1.49	1.35	1	10
4	D	201	UQ8	C4-C3	3.60	1.49	1.36	6	10
4	A	201	UQ8	C4-C3	3.44	1.48	1.36	9	10

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
4	D	201	UQ8	C7-C6-C1	2.82	120.06	124.89	1	10
4	A	201	UQ8	C7-C6-C1	2.56	120.51	124.89	9	10
4	A	201	UQ8	C10-C9-C11	2.28	119.83	114.59	6	10
4	A	201	UQ8	C1M-C1-C6	2.18	120.87	124.45	1	10
4	D	201	UQ8	C1M-C1-C6	2.12	120.97	124.45	10	10

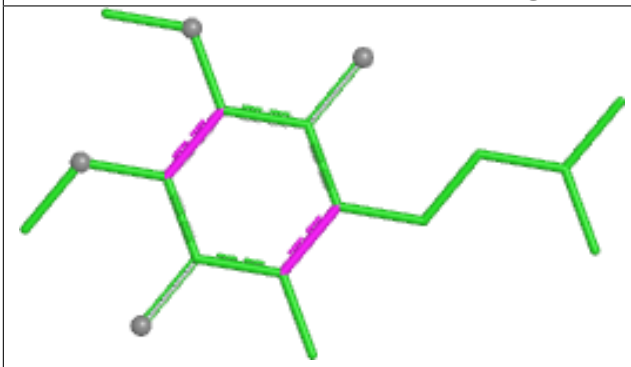
There are no chirality outliers.

There are no torsion outliers.

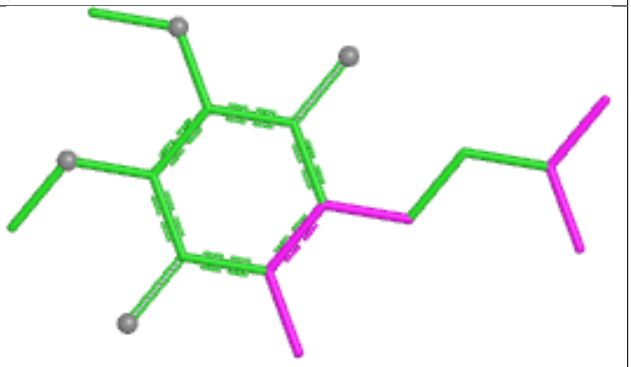
There are no ring outliers.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

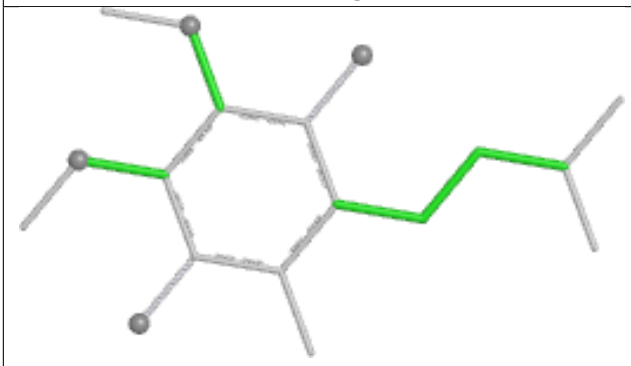
Ligand UQ8 A 201



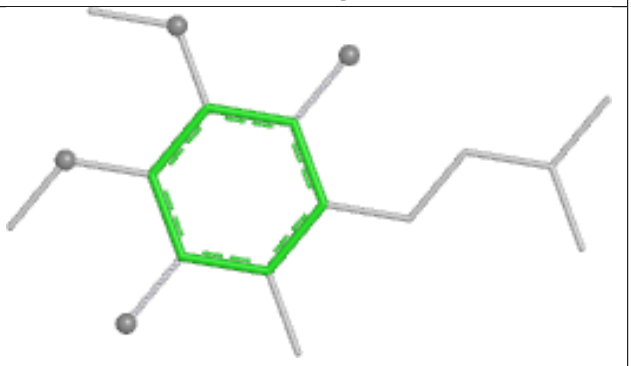
Bond lengths



Bond angles

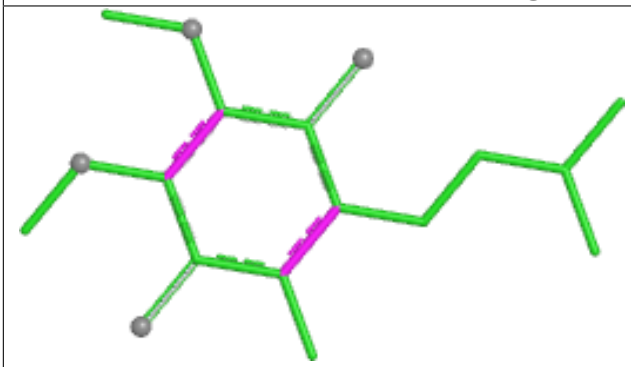


Torsions

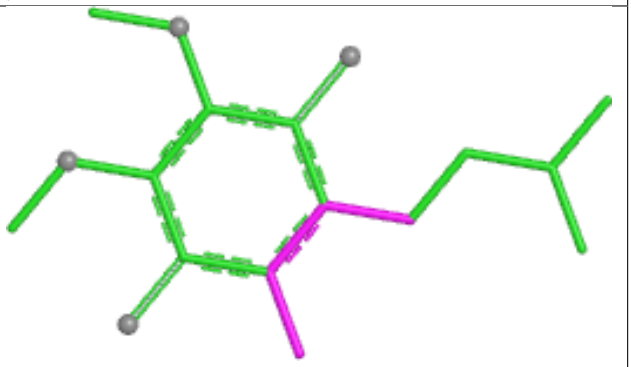


Rings

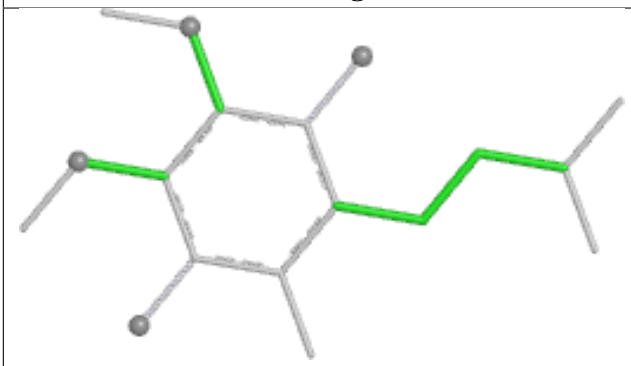
Ligand UQ8 D 201



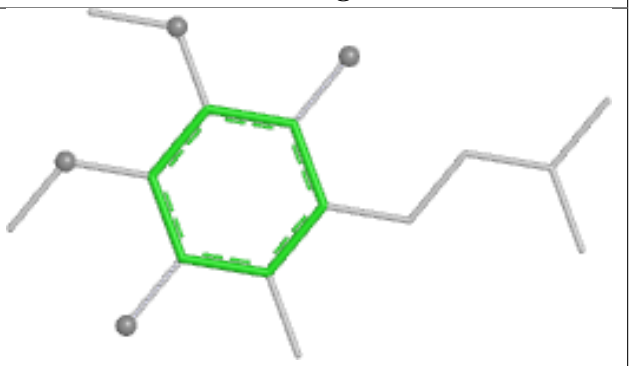
Bond lengths



Bond angles



Torsions



Rings

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 2% for the well-defined parts and 4% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *assigned_chemical_shifts_list_DsbB*

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	744
Number of shifts mapped to atoms	671
Number of unparsed shifts	0
Number of shifts with mapping errors	73
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	1

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 73) occurrences are reported below.

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	6	ASN	C	179.258	0.145	1
1	A	6	ASN	CA	57.564	0.300	1
1	A	6	ASN	CB	38.167	0.300	1
1	A	7	GLN	C	180.404	0.092	1
1	A	7	GLN	CA	57.611	0.012	1
1	A	7	GLN	CB	26.649	0.210	1
1	A	7	GLN	CG	31.228	0.300	1
1	A	7	GLN	H	9.338	0.026	1
1	A	7	GLN	N	120.525	0.189	1
1	A	8	ALA	C	179.313	0.300	1
1	A	8	ALA	CA	54.645	0.300	1
1	A	8	ALA	CB	17.967	0.300	1
1	A	8	ALA	H	9.436	0.052	1
1	A	8	ALA	N	123.894	0.176	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	9	SER	C	173.894	0.126	1
1	A	9	SER	CA	60.565	0.137	1
1	A	9	SER	CB	63.79	0.070	1
1	A	109	ARG	N	112.15	0.050	1
1	A	110	PHE	CA	58.681	0.114	1
1	A	111	PRO	CA	65.848	0.300	1
1	A	111	PRO	CD	51.081	0.220	1
1	A	112	GLU	C	177.165	0.300	1
1	A	113	TRP	CA	53.381	0.091	1
1	A	113	TRP	H	9.706	0.060	1
1	A	113	TRP	N	111.82	0.076	1
1	A	163	SER	CA	60.441	0.222	1
1	A	163	SER	CB	63.788	0.300	1
1	A	163	SER	H	9.427	0.022	1
1	A	163	SER	N	112.832	0.300	1
1	A	165	PRO	CA	62.249	0.011	1
1	A	165	PRO	CD	51.723	0.128	1
1	A	165	PRO	N	134.035	0.022	1
1	A	168	ALA	CA	51.195	0.007	1
1	A	168	ALA	CB	18.891	0.003	1
1	A	201	UQ1	C12	30.3	0.643	4
1	A	201	UQ1	C17	29.8	0.643	4
1	A	201	UQ1	C22	29.3	0.643	4
1	A	201	UQ1	C27	28.8	0.643	4
1	A	201	UQ1	C32	28.3	0.643	4
1	A	201	UQ1	C37	27.8	0.643	4
1	A	201	UQ1	C11	43.4	0.643	4
1	A	201	UQ1	C16	43.0	0.643	4
1	A	201	UQ1	C21	42.6	0.643	4
1	A	201	UQ1	C26	42.2	0.643	4
1	A	201	UQ1	C31	41.8	0.643	4
1	A	201	UQ1	C36	41.4	0.643	4
1	A	201	UQ1	C15	20.7	0.643	4
1	A	201	UQ1	C20	20.2	0.643	4
1	A	201	UQ1	C25	19.7	0.643	4
1	A	201	UQ1	C30	19.2	0.643	4
1	A	201	UQ1	C35	18.7	0.643	4
1	A	201	UQ1	C40	18.2	0.643	4
1	A	201	UQ1	C38	124.75	0.300	4
1	A	201	UQ1	C39	136.254	0.051	4
1	A	201	UQ1	C41	41.517	0.095	4

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	201	UQ1	C42	28.26	0.020	4
1	A	201	UQ1	C43	126.157	0.271	4
1	A	201	UQ1	C44	135.212	0.112	4
1	A	201	UQ1	C45	17.92	0.069	4
1	A	201	UQ1	C46	28.177	0.074	4
1	A	201	UQ1	C1	135.534	0.060	1
1	A	201	UQ1	C1M	15.859	0.061	4
1	A	201	UQ1	C6	127.427	0.300	1
1	A	201	UQ1	C7	26.58	0.011	4
1	A	201	UQ1	C8	123.68	0.098	4
1	A	201	UQ1	C9	140.1	0.117	4
1	A	201	UQ1	C10	20.609	0.118	4
1	A	201	UQ1	C5	154.709	0.300	4
1	A	201	UQ1	C2	154.709	0.300	1
1	A	201	UQ1	C4	142.41	0.300	1
1	A	201	UQ1	C3	142.41	0.300	4
1	A	201	UQ1	C4M	63.804	0.193	4
1	A	201	UQ1	C3M	63.804	0.193	4

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	130	-0.89 ± 0.11	Should be checked
$^{13}C_{\beta}$	114	0.43 ± 0.15	None needed (< 0.5 ppm)
$^{13}C'$	116	-0.46 ± 0.26	None needed (< 0.5 ppm)
^{15}N	125	1.13 ± 0.36	Should be applied

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 2%, i.e. 225 atoms were assigned a chemical shift out of a possible 12014. 0 out of 143 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	140/4666 (3%)	21/1899 (1%)	78/1874 (4%)	41/893 (5%)
Sidechain	82/6296 (1%)	0/4124 (0%)	82/1972 (4%)	0/200 (0%)
Aromatic	3/1052 (0%)	0/501 (0%)	3/510 (1%)	0/41 (0%)
Overall	225/12014 (2%)	21/6524 (0%)	163/4356 (4%)	41/1134 (4%)

Note: This is a solid-state NMR structure, where hydrogen atoms are typically not assigned a chemical shift value, which may lead to lower completeness of assignment measure.

7.1.4 Statistically unusual chemical shifts (i)

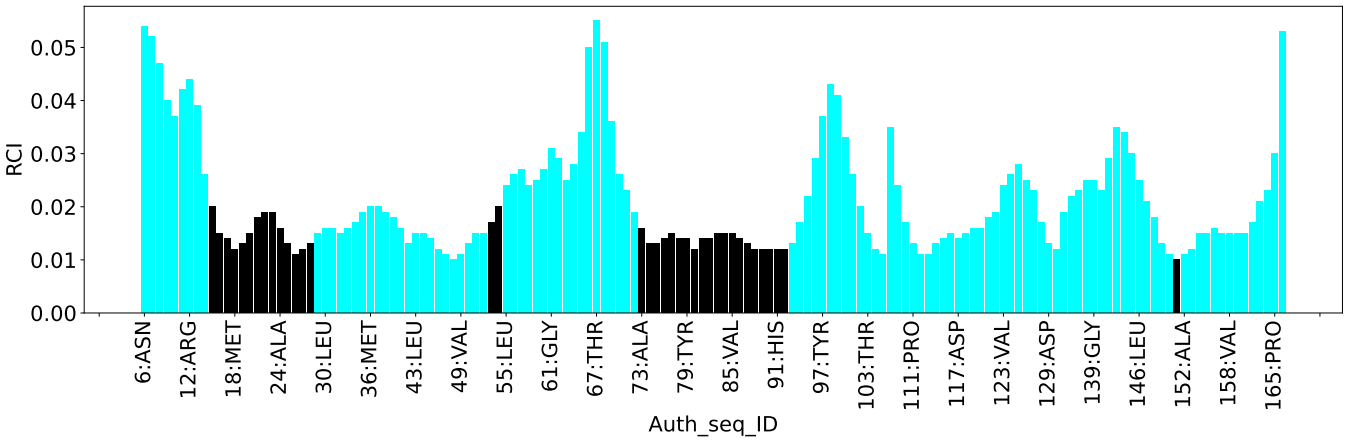
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, *ppm*	Expected range, *ppm*	Z-score
1	A	92	THR	CG2	27.48	16.06 – 27.03	5.4

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

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	1334
Intra-residue (|i-j|=0)	374
Sequential (|i-j|=1)	526
Medium range (|i-j|>1 and |i-j|<5)	426
Long range (|i-j|≥5)	8
Inter-chain	0
Hydrogen bond restraints	0
Disulfide bond restraints	0
Total dihedral-angle restraints	372
Number of unmapped restraints	6
Number of restraints per residue	1.3
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)	40.2	0.2
0.2-0.5 (Medium)	48.9	0.33
>0.5 (Large)	0.5	0.85

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

Dihedral-angle violations less than 1° are not included in the calculation.

Bins (°)	Average number of violations per model	Max (°)
1.0-10.0 (Small)	11.4	6.17
10.0-20.0 (Medium)	None	None
>20.0 (Large)	None	None

9 Distance violation analysis (i)

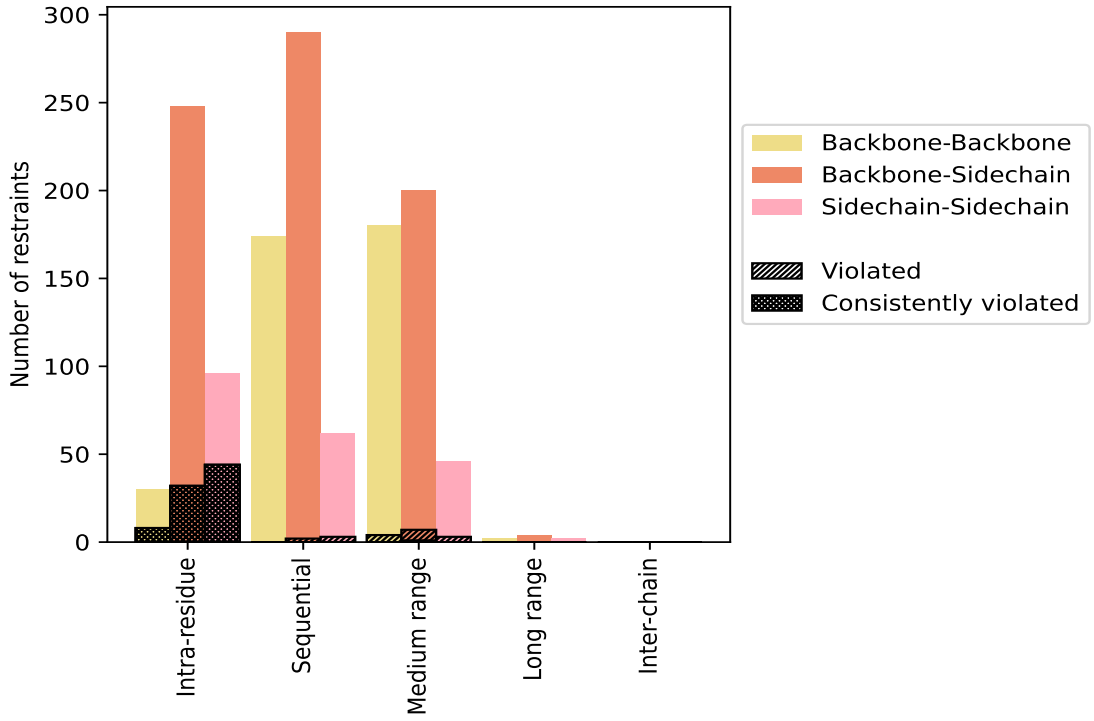
9.1 Summary of distance violations (i)

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)	374	28.0	84	22.5	6.3	84	22.5	6.3
Backbone-Backbone	30	2.2	8	26.7	0.6	8	26.7	0.6
Backbone-Sidechain	248	18.6	32	12.9	2.4	32	12.9	2.4
Sidechain-Sidechain	96	7.2	44	45.8	3.3	44	45.8	3.3
Sequential (|i-j|=1)	526	39.4	5	1.0	0.4	0	0.0	0.0
Backbone-Backbone	174	13.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	290	21.7	2	0.7	0.1	0	0.0	0.0
Sidechain-Sidechain	62	4.6	3	4.8	0.2	0	0.0	0.0
Medium range (|i-j|>1 & |i-j|<5)	426	31.9	14	3.3	1.0	1	0.2	0.1
Backbone-Backbone	180	13.5	4	2.2	0.3	0	0.0	0.0
Backbone-Sidechain	200	15.0	7	3.5	0.5	1	0.5	0.1
Sidechain-Sidechain	46	3.4	3	6.5	0.2	0	0.0	0.0
Long range (|i-j|≥5)	8	0.6	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	2	0.1	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	4	0.3	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	2	0.1	0	0.0	0.0	0	0.0	0.0
Inter-chain	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
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	1334	100.0	103	7.7	7.7	85	6.4	6.4
Backbone-Backbone	386	28.9	12	3.1	0.9	8	2.1	0.6
Backbone-Sidechain	742	55.6	41	5.5	3.1	33	4.4	2.5
Sidechain-Sidechain	206	15.4	50	24.3	3.7	44	21.4	3.3

[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

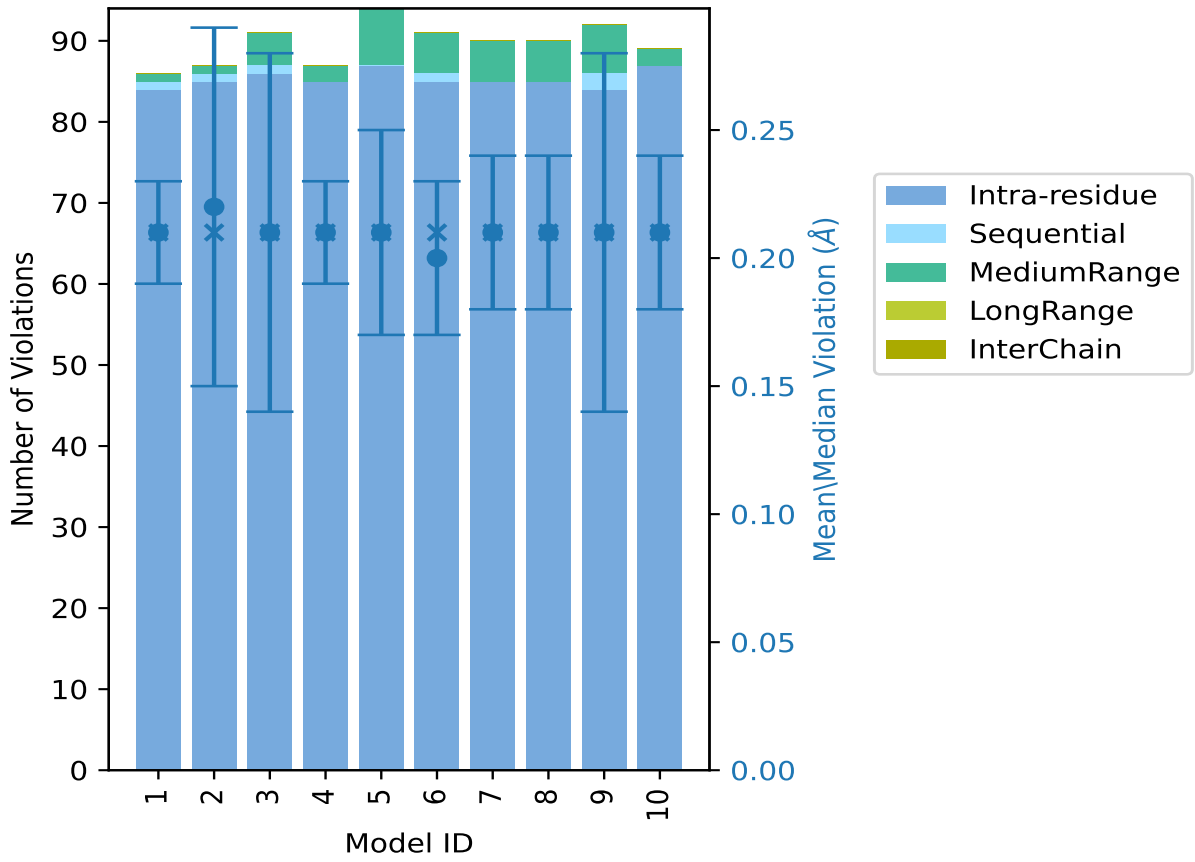
9.2 Distance violation statistics for each model

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	84	1	1	0	0	86	0.21	0.24	0.02	0.21
2	85	1	1	0	0	87	0.22	0.85	0.07	0.21
3	86	1	4	0	0	91	0.21	0.83	0.07	0.21
4	85	0	2	0	0	87	0.21	0.24	0.02	0.21
5	87	0	7	0	0	94	0.21	0.51	0.04	0.21
6	85	1	5	0	0	91	0.2	0.25	0.03	0.21
7	85	0	5	0	0	90	0.21	0.28	0.03	0.21
8	85	0	5	0	0	90	0.21	0.24	0.03	0.21
9	84	2	6	0	0	92	0.21	0.7	0.07	0.21
10	87	0	2	0	0	89	0.21	0.32	0.03	0.21

[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, 1231(IR:290, SQ:521, MR:412, LR:8, IC:0) 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	5	0	0	5	1	10.0
0	3	3	0	0	6	2	20.0
0	1	2	0	0	3	3	30.0

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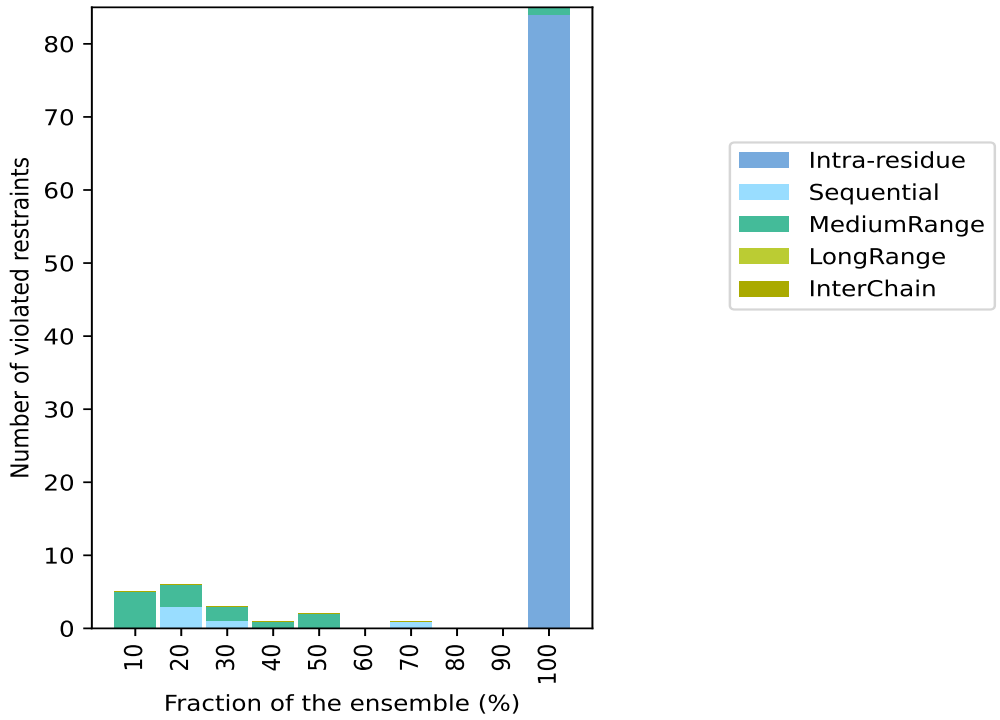
Number of violated restraints						Fraction of the ensemble	
IR[1]	SQ[2]	MR[3]	LR[4]	IC[5]	Total	Count[6]	%
0	0	1	0	0	1	4	40.0
0	0	2	0	0	2	5	50.0
0	0	0	0	0	0	6	60.0
0	1	0	0	0	1	7	70.0
0	0	0	0	0	0	8	80.0
0	0	0	0	0	0	9	90.0
84	0	1	0	0	85	10	100.0

[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

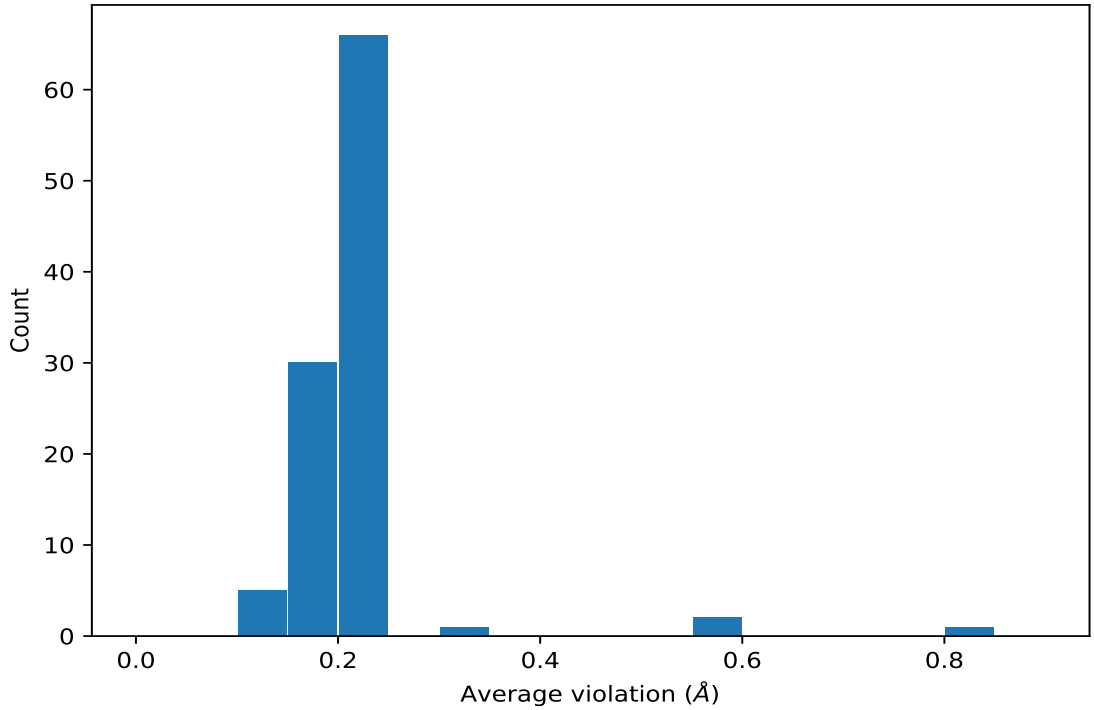


9.4 Most violated distance restraints in the ensemble

9.4.1 Histogram : Distribution of mean distance violations

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 ⓘ

The following table provides the mean and the standard deviation of the violations for the 10 worst performing restraints, sorted by number of violated models and the mean 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.

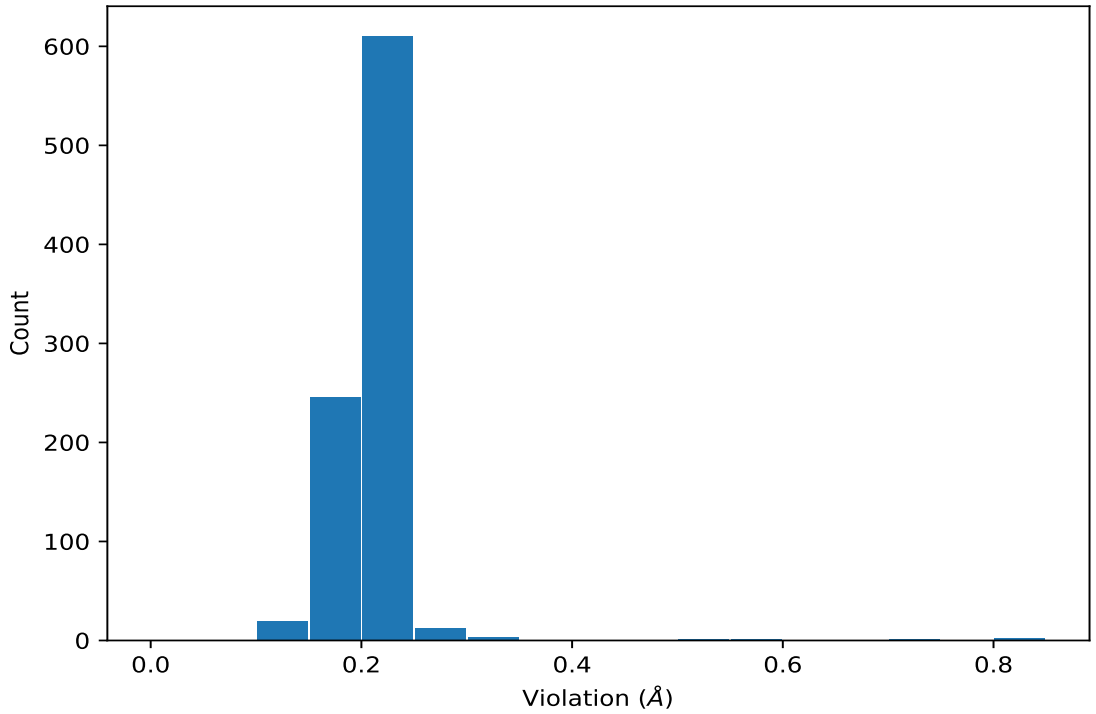
Key	Atom-1	Atom-2	Models[1]	Mean (Å)	SD[1] (Å)	Median (Å)
(1,1311)	1:151:D:ILE:CD1	1:151:D:ILE:CG1	10	0.24	0.0	0.24
(1,743)	1:68:D:PRO:CB	1:68:D:PRO:CA	10	0.24	0.01	0.24
(1,767)	1:68:D:PRO:CB	1:68:D:PRO:CA	10	0.24	0.01	0.24
(1,782)	1:48:D:ARG:CB	1:48:D:ARG:CA	10	0.24	0.0	0.24
(1,1205)	1:68:D:PRO:CB	1:70:D:ARG:C	10	0.24	0.06	0.24
(1,644)	1:151:A:ILE:CD1	1:151:A:ILE:CG1	10	0.24	0.0	0.24
(1,168)	1:48:A:ARG:CG	1:48:A:ARG:CD	10	0.24	0.01	0.24
(1,483)	1:115:A:PRO:CG	1:115:A:PRO:CB	10	0.24	0.0	0.24
(1,484)	1:115:A:PRO:CG	1:115:A:PRO:CB	10	0.24	0.0	0.24
(1,97)	1:93:A:MET:CB	1:93:A:MET:CA	10	0.23	0.0	0.23

[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)
(1,1260)	1:75:D:VAL:CG1	1:76:D:ILE:CG1	2	0.85
(1,1260)	1:75:D:VAL:CG1	1:76:D:ILE:CG1	3	0.83
(1,593)	1:75:A:VAL:CG1	1:76:A:ILE:CG1	9	0.7
(1,161)	1:49:A:VAL:CB	1:48:A:ARG:CD	9	0.55
(1,593)	1:158:A:VAL:CG1	1:162:A:ILE:CG1	5	0.51
(1,1205)	1:68:D:PRO:CB	1:70:D:ARG:C	3	0.33
(1,1205)	1:68:D:PRO:CB	1:70:D:ARG:C	10	0.32
(1,1205)	1:68:D:PRO:CB	1:70:D:ARG:C	2	0.31
(1,671)	1:68:D:PRO:CA	1:65:D:PRO:CA	7	0.28
(1,1205)	1:68:D:PRO:CB	1:70:D:ARG:C	9	0.27

10 Dihedral-angle violation analysis

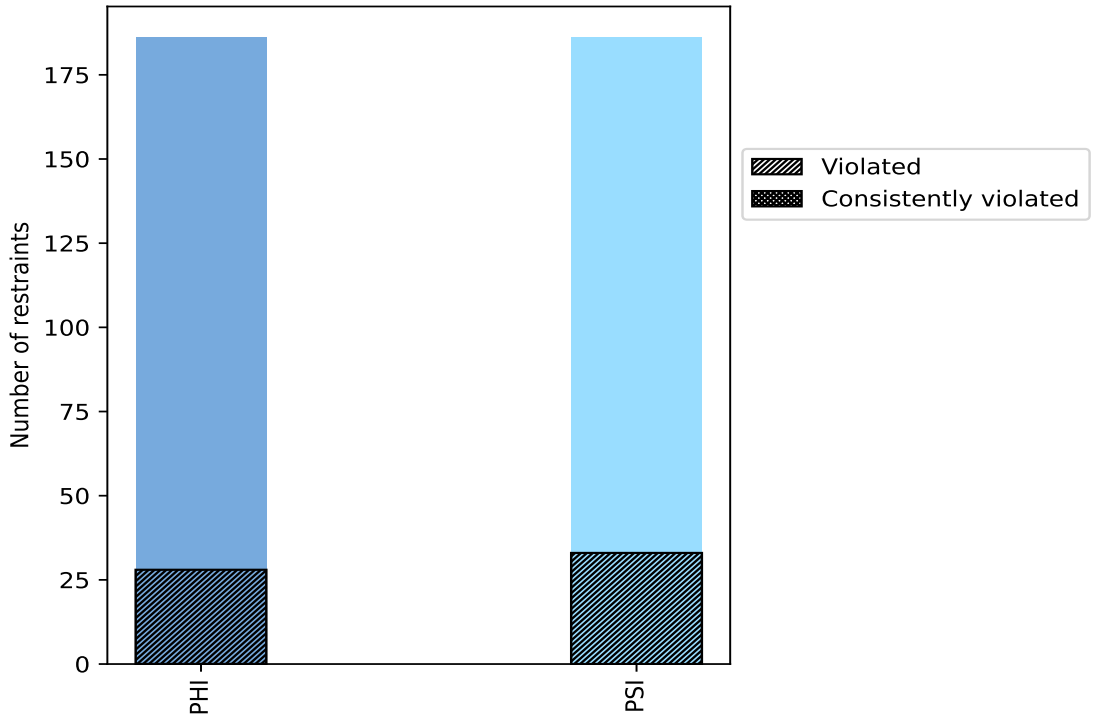
10.1 Summary of dihedral-angle violations

The following table provides the summary of dihedral-angle violations in different dihedral-angle types. Violations less than 1° are not included in the calculation.

Angle type	Count	%[1]	Violated[3]			Consistently Violated[4]		
			Count	%[2]	%[1]	Count	%[2]	%[1]
PHI	186	50.0	28	15.1	7.5	0	0.0	0.0
PSI	186	50.0	33	17.7	8.9	0	0.0	0.0
Total	372	100.0	61	16.4	16.4	0	0.0	0.0

[1] percentage calculated with respect to total number of dihedral-angle restraints, [2] percentage calculated with respect to number of restraints in a particular dihedral-angle type, [3] violated in at least one model, [4] violated in all the models

10.1.1 Bar chart : Distribution of dihedral-angles and violations



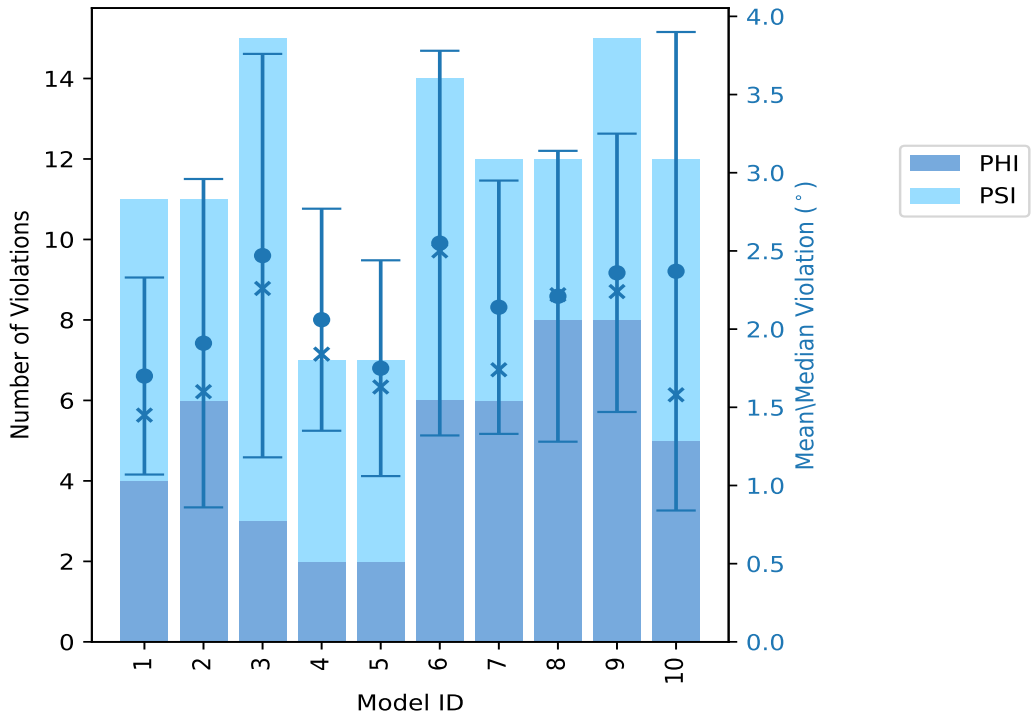
Violated and consistently violated restraints are shown using different hatch patterns in their respective categories

10.2 Dihedral-angle violation statistics for each model (i)

The following table provides the dihedral-angle violation statistics for each model in the ensemble. Violations less than 1° are not included in the statistics.

Model ID	Number of violations			Mean (°)	Max (°)	SD (°)	Median (°)
	PHI	PSI	Total				
1	4	7	11	1.7	3.01	0.63	1.45
2	6	5	11	1.91	4.89	1.05	1.6
3	3	12	15	2.47	5.61	1.29	2.26
4	2	5	7	2.06	3.49	0.71	1.84
5	2	5	7	1.75	3.19	0.69	1.63
6	6	8	14	2.55	5.35	1.23	2.5
7	6	6	12	2.14	3.77	0.81	1.74
8	8	4	12	2.21	3.93	0.93	2.22
9	8	7	15	2.36	3.77	0.89	2.24
10	5	7	12	2.37	6.17	1.53	1.58

10.2.1 Bar graph : Dihedral 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

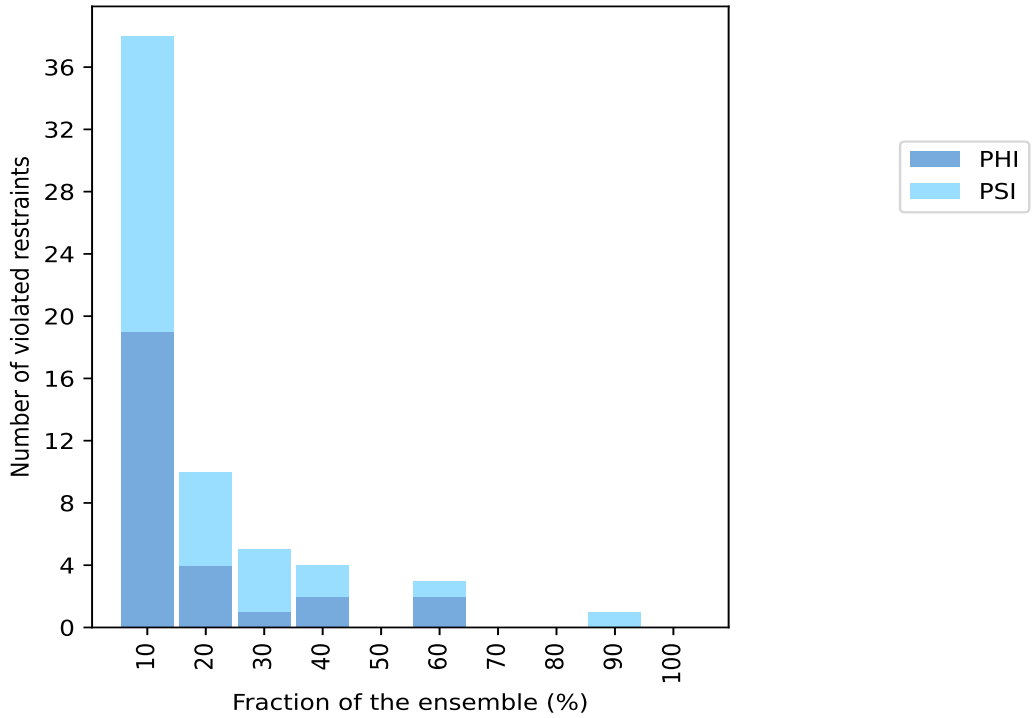
10.3 Dihedral-angle violation statistics for the ensemble (i)

Violation analysis may find that some restraints are violated in very 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 ensemble.

Number of violated restraints			Fraction of the ensemble	
PHI	PSI	Total	Count[1]	%
19	19	38	1	10.0
4	6	10	2	20.0
1	4	5	3	30.0
2	2	4	4	40.0
0	0	0	5	50.0
2	1	3	6	60.0
0	0	0	7	70.0
0	0	0	8	80.0
0	1	1	9	90.0
0	0	0	10	100.0

[1] Number of models with violations

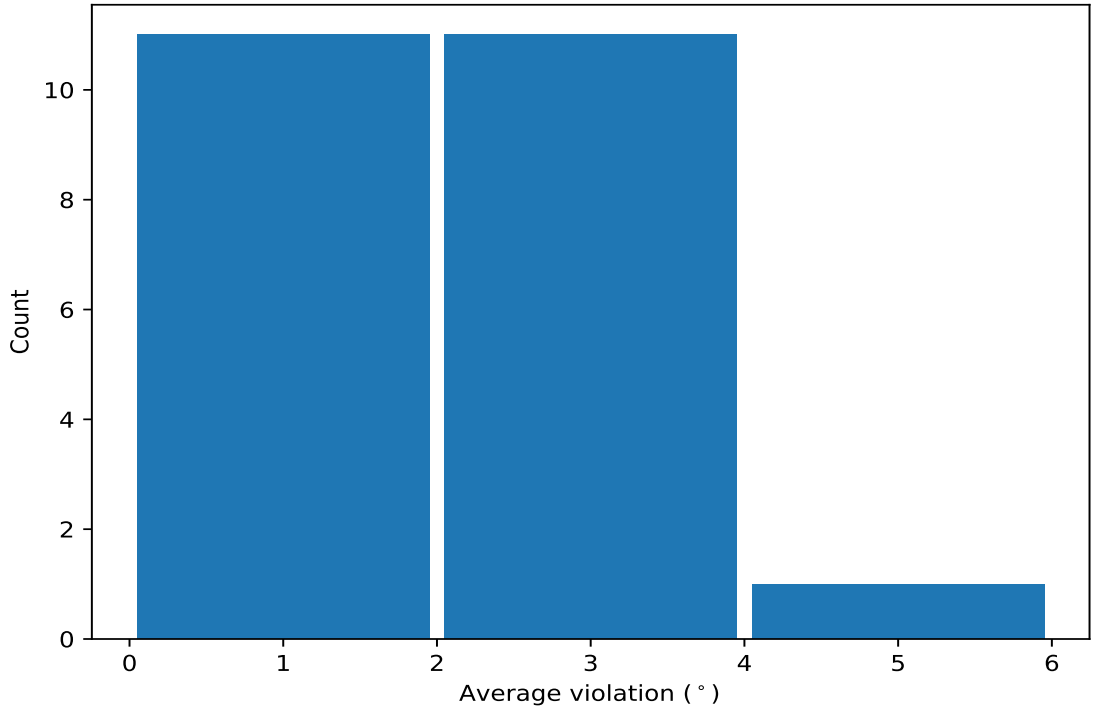
10.3.1 Bar graph : Dihedral-angle Violation statistics for the ensemble (i)



10.4 Most violated dihedral-angle restraints in the ensemble

10.4.1 Histogram : Distribution of mean dihedral-angle violations

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



10.4.2 Table: Most violated dihedral-angle restraints

The following table provides the mean and the standard deviation of the violations for the 10 worst performing restraints, sorted by number of violated models and the mean violation value. The Key (restraint list ID, restraint ID) is the unique identifier for a given restraint.

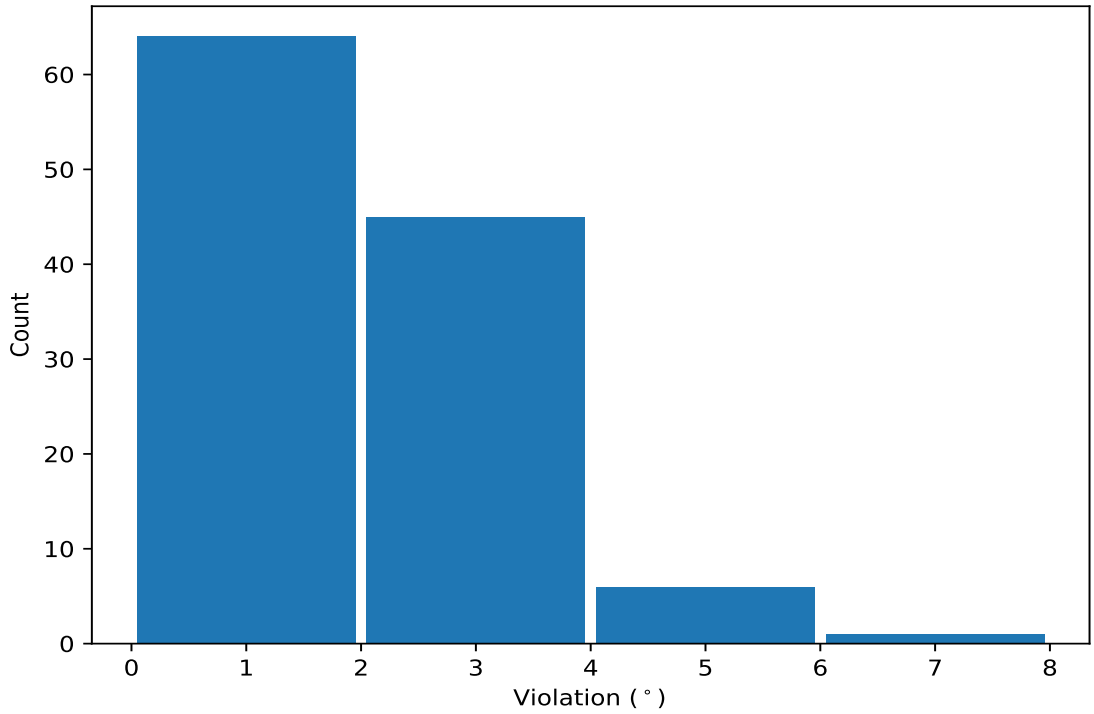
Key	Atom-1	Atom-2	Atom-3	Atom-4	Models[1]	Mean	SD[2]	Median
(1,140)	1:120:A:VAL:N	1:120:A:VAL:CA	1:120:A:VAL:C	1:121:A:PRO:N	9	2.58	0.68	2.69
(1,237)	1:43:D:LEU:C	1:44:D:CYS:N	1:44:D:CYS:CA	1:44:D:CYS:C	6	2.88	0.79	2.84
(1,238)	1:44:D:CYS:N	1:44:D:CYS:CA	1:44:D:CYS:C	1:45:D:ILE:N	6	2.84	0.46	3.0
(1,135)	1:103:A:THR:C	1:104:A:CYS:N	1:104:A:CYS:CA	1:104:A:CYS:C	6	1.66	0.52	1.51
(1,150)	1:130:A:CYS:N	1:130:A:CYS:CA	1:130:A:CYS:C	1:131:A:ALA:N	4	4.97	1.02	5.12
(1,321)	1:103:D:THR:C	1:104:D:CYS:N	1:104:D:CYS:CA	1:104:D:CYS:C	4	2.64	0.67	2.34
(1,362)	1:156:D:VAL:N	1:156:D:VAL:CA	1:156:D:VAL:C	1:157:D:ALA:N	4	2.0	0.81	2.01
(1,341)	1:145:D:TRP:C	1:146:D:LEU:N	1:146:D:LEU:CA	1:146:D:LEU:C	4	1.79	0.78	1.54
(1,368)	1:159:D:LEU:N	1:159:D:LEU:CA	1:159:D:LEU:C	1:160:D:VAL:N	3	2.42	0.59	2.78
(1,138)	1:105:A:ASP:N	1:105:A:ASP:CA	1:105:A:ASP:C	1:106:A:PHE:N	3	1.52	0.21	1.63

[1] Number of violated models, [2]Standard deviation, All angle values are in degree (°)

10.5 All violated dihedral-angle restraints (i)

10.5.1 Histogram : Distribution of violations (i)

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



10.5.2 Table: All violated dihedral-angle restraints (i)

The following table provides the list of violations for 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.

Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,150)	1:130:A:CYS:N	1:130:A:CYS:CA	1:130:A:CYS:C	1:131:A:ALA:N	10	6.17
(1,150)	1:130:A:CYS:N	1:130:A:CYS:CA	1:130:A:CYS:C	1:131:A:ALA:N	3	5.61
(1,367)	1:158:D:VAL:C	1:159:D:LEU:N	1:159:D:LEU:CA	1:159:D:LEU:C	6	5.35
(1,151)	1:130:A:CYS:C	1:131:A:ALA:N	1:131:A:ALA:CA	1:131:A:ALA:C	2	4.89
(1,150)	1:130:A:CYS:N	1:130:A:CYS:CA	1:130:A:CYS:C	1:131:A:ALA:N	6	4.62
(1,139)	1:119:A:TRP:C	1:120:A:VAL:N	1:120:A:VAL:CA	1:120:A:VAL:C	10	4.53
(1,237)	1:43:D:LEU:C	1:44:D:CYS:N	1:44:D:CYS:CA	1:44:D:CYS:C	3	4.15
(1,320)	1:103:D:THR:N	1:103:D:THR:CA	1:103:D:THR:C	1:104:D:CYS:N	8	3.93
(1,336)	1:130:D:CYS:N	1:130:D:CYS:CA	1:130:D:CYS:C	1:131:D:ALA:N	3	3.81
(1,321)	1:103:D:THR:C	1:104:D:CYS:N	1:104:D:CYS:CA	1:104:D:CYS:C	7	3.77