Full wwPDB NMR Structure Validation Report (i)

Jun 3, 2023 – 04:27 PM EDT

PDB ID	:	6X1K
BMRB ID	:	30753
Title	:	Solution NMR structure of de novo designed TMB2.3
Authors	:	Liang, B.; Vorobieva, A.A.; Chow, C.M.; Baker, D.; Tamm, L.K.
Deposited on	:	2020-05-19

This is a Full wwPDB NMR Structure Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/NMRValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

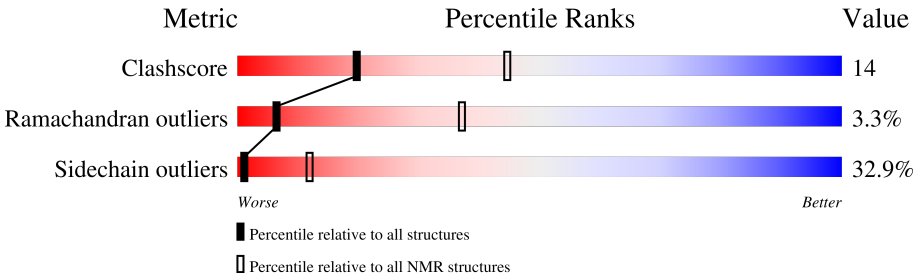
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
BMRB Restraints Analysis	:	v1.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal 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 36%.

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	124	57% 31% • 7%

2 Ensemble composition and analysis (i)

This entry contains 20 models. Model 1 is the overall representative, medoid model (most similar to other models).

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:4-A:45, A:50-A:122 (115)	0.81	1

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 4 clusters and 1 single-model cluster was found.

Cluster number	Models
1	1, 5, 7, 8, 10, 14, 15, 16, 17, 20
2	6, 11, 12, 18
3	9, 13, 19
4	3, 4
Single-model clusters	2

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 1871 atoms, of which 911 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called De novo designed transmembrane beta-barrel TMB2.3.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	124	1871	617	911	156	185	2	0

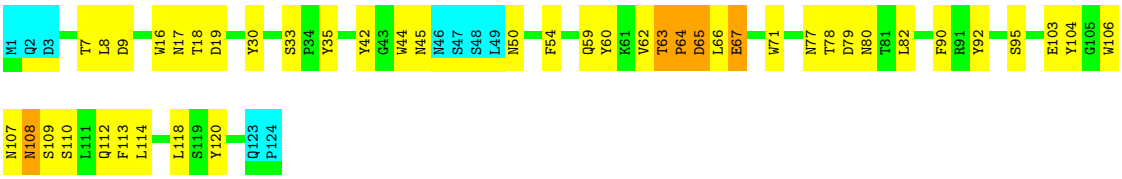
4 Residue-property plots (i)

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: De novo designed transmembrane beta-barrel TMB2.3

Chain A: 57% 31% • 7%



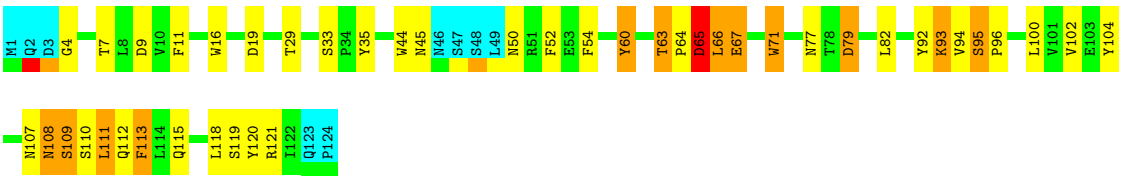
4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1 (medoid)

• Molecule 1: De novo designed transmembrane beta-barrel TMB2.3

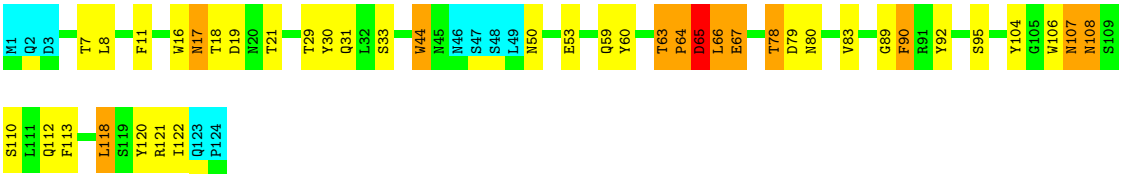
Chain A: 57% 25% 10% • 7%



4.2.2 Score per residue for model 2

• Molecule 1: De novo designed transmembrane beta-barrel TMB2.3

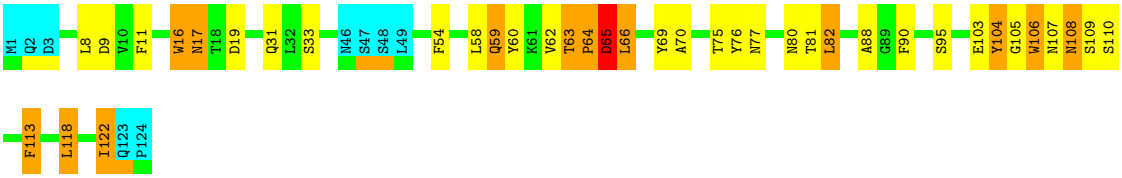
Chain A: 60% 23% 9% • 7%



4.2.3 Score per residue for model 3

- Molecule 1: De novo designed transmembrane beta-barrel TMB2.3

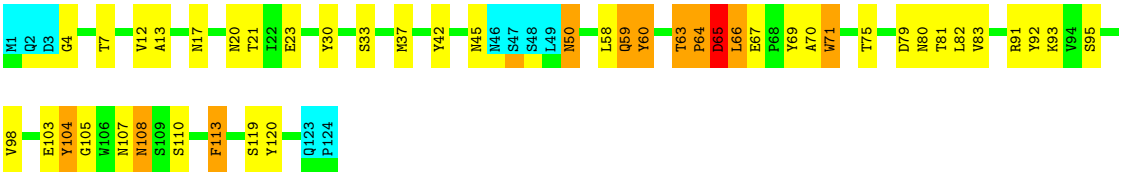
Chain A: 61% 20% 10% • 7%



4.2.4 Score per residue for model 4

- Molecule 1: De novo designed transmembrane beta-barrel TMB2.3

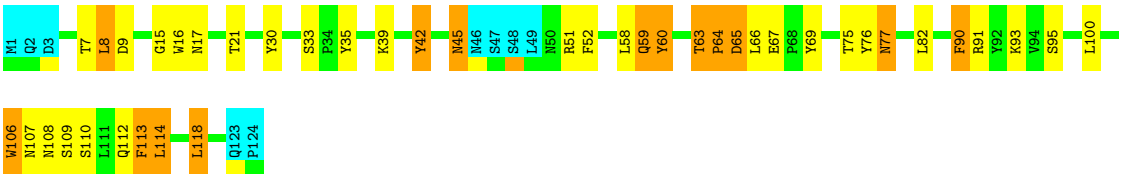
Chain A: 56% 27% 8% • 7%



4.2.5 Score per residue for model 5

- Molecule 1: De novo designed transmembrane beta-barrel TMB2.3

Chain A: 59% 23% 11% 7%



4.2.6 Score per residue for model 6

- Molecule 1: De novo designed transmembrane beta-barrel TMB2.3

Chain A: 49% 30% 13% • 7%

M1 Q2 D3 T7 L8 D9 V12 W16 N17 T18 D19 N20 I24 T25 G26 G27 A28 T29 Y30 Q31 L32 S33 Y42 N46 S47 S48 L49 N50 R51 F52 E53 F54 Q59 Y60 K61 V62 T63 P64 D65 L66 E67 T75 Y76 N77 T78 D79 L82 V83 A86 G87

A88 G89 F90 S95 P96 E97 V98 K99 L100 V101 V102 E103 Y104 G105 W106 N107 N108 S109 S110 L111 Q112 F113 L114 L118 R121 I122 Q123 P124

4.2.7 Score per residue for model 7

- Molecule 1: De novo designed transmembrane beta-barrel TMB2.3

Chain A: 52% 28% 12% • 7%

M1 Q2 D3 T7 L8 D9 V12 A13 W16 N17 T18 D19 N20 T21 I22 T25 T29 Y30 S33 P34 Y35 Y42 G43 W44 M45 N46 S47 S48 L49 F52 E53 F54 G57 L58 Q59 Y60 T63 P64 D65 L66 E67 P68 Y69 A70 W71 Y76 N77 T78 D79

N80 T81 R91 V94 S95 V102 E103 Y104 G105 W106 N107 N108 S109 S110 L111 Q112 F113 L114 S119 Q123 P124

4.2.8 Score per residue for model 8

- Molecule 1: De novo designed transmembrane beta-barrel TMB2.3

Chain A: 54% 29% 10% 7%

M1 Q2 D3 T7 N17 T18 D19 N20 T21 I22 Y30 Q31 L32 S33 P34 Y35 I36 M37 V38 K39 Y42 G43 W44 N45 N46 S47 S48 L49 F52 Q59 Y60 K61 V62 T63 P64 D65 L66 E67 P68 Y69 A70 W71 N77 T78 D79 N80 T81 L82 A88 G89 F90 R91

Y92 K93 V94 S95 V102 E103 Y104 G105 W106 N107 N108 S109 S110 L111 Q112 F113 L118 S119 Y120 R121 I122 Q123 P124

4.2.9 Score per residue for model 9

- Molecule 1: De novo designed transmembrane beta-barrel TMB2.3

Chain A: 61% 23% 7% • 7%

M1 Q2 D3 T7 L8 D9 T29 Y30 Q31 L32 S33 P34 Y35 N46 S47 S48 L49 Y60 T63 P64 D65 L66 E67 W71 A72 Y76 D79 N80 T81 L82 V83 A86 F90 R91 S95 V98 V101 V102 E103 Y104 G105 W106 N107 N108 S109 S110 L111

Q112 F113 L114 L118 S119 Y120 R121 I122 Q123 P124

4.2.10 Score per residue for model 10

- Molecule 1: De novo designed transmembrane beta-barrel TMB2.3

Chain A: 55% 28% 10% 7%

M1 Q2 D3 T7 L8 D9 V12 A13 W16 N17 T18 T25 G26 Q31 L32 S33 V38 K39 Y42 G43 W44 N45 N46 S47 S48 L49 N50 R51 F52 E53 F54 L58 Q59 V62 T63 P64 D65 L66 E67 A70 W71 A72 T75 T78 S95 V98

V102 E103 Y104 G105 W106 N107 N108 S109 S110 L111 Q112 F113 L118 S119 Y120 Q123 P124

4.2.11 Score per residue for model 11

- Molecule 1: De novo designed transmembrane beta-barrel TMB2.3

Chain A: 62% 24% 6% • 7%

M1 Q2 D3 T7 L8 D19 N20 T21 I22 T29 Y30 S33 P34 Y35 V38 Y42 N46 S47 S48 L49 F52 E53 F54 Y60 K61 V62 T63 P64 D65 L66 E67 T81 L82 V83 A86 F90 K93 V94 S95 L100 Y104 G105 W106 N107 N108

S109 S110 L111 Q112 F113 L118 S119 Y120 R121 I122 Q123 P124

4.2.12 Score per residue for model 12

- Molecule 1: De novo designed transmembrane beta-barrel TMB2.3

Chain A: 60% 21% 11% • 7%

M1 Q2 D3 G4 T7 L8 D9 W16 N17 N20 T21 T25 Y30 S33 P34 Y35 K39 Y42 N45 N46 S47 S48 L49 F54 Y60 K61 V62 T63 P64 D65 L66 E67 P68 Y69 A70 W71 N77 T78 D79 V83 A86 F90 R91 Y92

S95 L100 E103 W106 N107 N108 S109 S110 L111 Q112 F113 Q123 P124

4.2.13 Score per residue for model 13

- Molecule 1: De novo designed transmembrane beta-barrel TMB2.3

Chain A: 52% 31% 9% • 7%

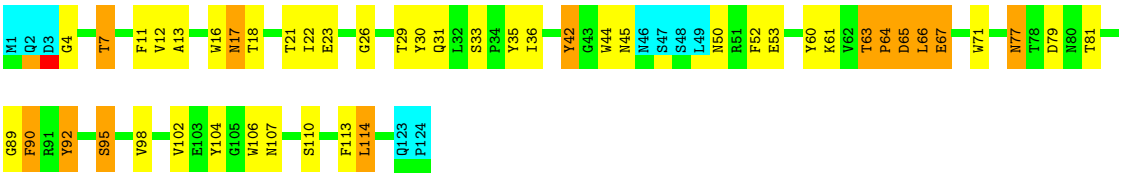
M1 Q2 D3 G4 T7 L8 D9 V10 F11 V12 A13 W16 N17 T18 D19 N20 T25 T29 Y30 S33 M37 W44 N45 N46 S47 S48 L49 N50 R51 F52 Q59 Y60 T63 P64 D65 L66 E67 T75 Y76 N77 T78 D79 N80 T81 L82 V83 G89 Y92

K93 V94 S95 V102 E103 Y104 G105 W106 N107 N108 S109 S110 L111 Q112 L118 S119 Y120 Q123 P124

4.2.14 Score per residue for model 14

• Molecule 1: De novo designed transmembrane beta-barrel TMB2.3

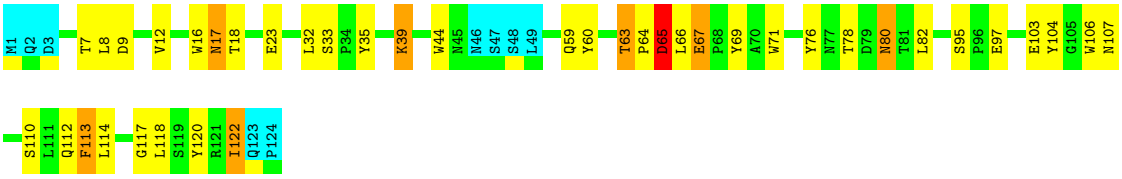
Chain A: 55% 27% 10% 7%



4.2.15 Score per residue for model 15

• Molecule 1: De novo designed transmembrane beta-barrel TMB2.3

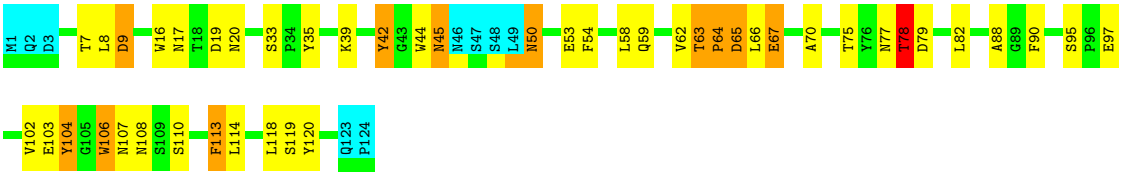
Chain A: 60% 26% 6% • 7%



4.2.16 Score per residue for model 16

• Molecule 1: De novo designed transmembrane beta-barrel TMB2.3

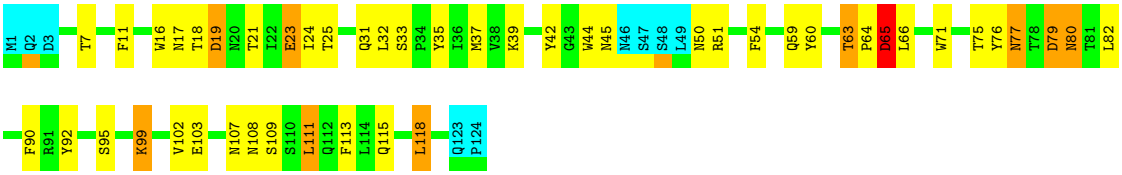
Chain A: 56% 27% 9% • 7%



4.2.17 Score per residue for model 17

• Molecule 1: De novo designed transmembrane beta-barrel TMB2.3

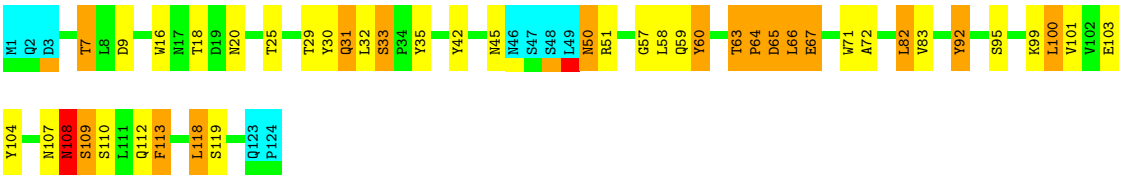
Chain A: 54% 31% 7% • 7%



4.2.18 Score per residue for model 18

• Molecule 1: De novo designed transmembrane beta-barrel TMB2.3

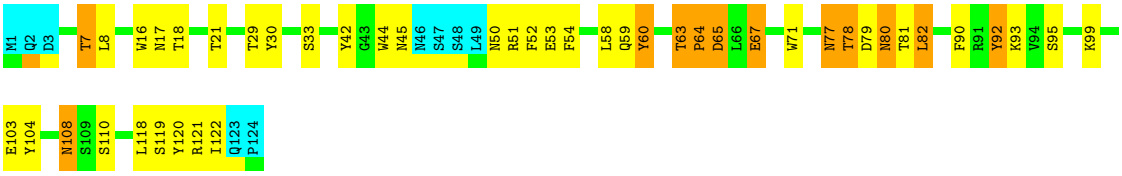
Chain A: 57% 22% 13% • 7%



4.2.19 Score per residue for model 19

• Molecule 1: De novo designed transmembrane beta-barrel TMB2.3

Chain A: 56% 27% 10% 7%



4.2.20 Score per residue for model 20

• Molecule 1: De novo designed transmembrane beta-barrel TMB2.3

Chain A: 56% 28% 9% 7%

5 Refinement protocol and experimental data overview (i)

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

Of the 200 calculated structures, 20 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 calculation	

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	549
Number of shifts mapped to atoms	549
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	36%

6 Model quality (i)

6.1 Standard geometry (i)

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	890	846	846	24±6
All	All	17800	16920	16920	484

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 14.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:111:LEU:H	1:A:111:LEU:HD22	0.80	1.33	1	1
1:A:8:LEU:HD12	1:A:8:LEU:H	0.74	1.42	12	3
1:A:8:LEU:HD11	1:A:30:TYR:CZ	0.74	2.18	13	1
1:A:118:LEU:HD12	1:A:118:LEU:H	0.74	1.43	2	3
1:A:111:LEU:HD22	1:A:111:LEU:N	0.73	1.98	1	1
1:A:82:LEU:HD12	1:A:82:LEU:H	0.71	1.45	18	2
1:A:118:LEU:HD12	1:A:118:LEU:N	0.70	2.02	17	3
1:A:114:LEU:N	1:A:114:LEU:HD23	0.70	2.02	7	3
1:A:8:LEU:HD12	1:A:8:LEU:N	0.69	2.02	5	3
1:A:82:LEU:HD12	1:A:82:LEU:N	0.69	2.02	18	3
1:A:66:LEU:HD21	1:A:92:TYR:CD1	0.68	2.23	2	1
1:A:94:VAL:HG21	1:A:100:LEU:HD13	0.68	1.65	1	1
1:A:111:LEU:HD23	1:A:111:LEU:N	0.66	2.04	10	1
1:A:104:TYR:CZ	1:A:114:LEU:HD21	0.65	2.26	9	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:22:ILE:HD13	1:A:22:ILE:N	0.64	2.06	8	1
1:A:111:LEU:HD23	1:A:111:LEU:H	0.62	1.54	10	1
1:A:111:LEU:H	1:A:111:LEU:CD2	0.62	2.07	10	2
1:A:102:VAL:HG13	1:A:102:VAL:O	0.62	1.95	16	2
1:A:16:TRP:CD1	1:A:16:TRP:N	0.62	2.68	3	3
1:A:102:VAL:O	1:A:102:VAL:HG23	0.61	1.95	17	3
1:A:108:ASN:ND2	1:A:109:SER:N	0.61	2.48	10	2
1:A:106:TRP:CG	1:A:107:ASN:N	0.61	2.68	15	4
1:A:90:PHE:CD1	1:A:90:PHE:N	0.60	2.68	14	2
1:A:76:TYR:N	1:A:76:TYR:CD2	0.60	2.70	9	1
1:A:92:TYR:N	1:A:92:TYR:CD1	0.59	2.69	19	1
1:A:8:LEU:N	1:A:8:LEU:CD1	0.58	2.66	6	3
1:A:62:VAL:HG12	1:A:62:VAL:O	0.58	1.97	3	1
1:A:113:PHE:C	1:A:114:LEU:HD23	0.58	2.17	5	3
1:A:113:PHE:CD2	1:A:113:PHE:N	0.57	2.71	15	3
1:A:66:LEU:HD11	1:A:92:TYR:CZ	0.57	2.34	2	1
1:A:81:THR:HG22	1:A:82:LEU:N	0.57	2.15	3	2
1:A:63:THR:O	1:A:65:ASP:N	0.57	2.38	13	20
1:A:42:TYR:CD1	1:A:42:TYR:N	0.57	2.72	7	2
1:A:7:THR:O	1:A:8:LEU:HD12	0.57	2.00	19	2
1:A:111:LEU:HD12	1:A:111:LEU:H	0.57	1.59	9	2
1:A:9:ASP:O	1:A:28:ALA:HB1	0.56	2.01	6	1
1:A:12:VAL:HG22	1:A:13:ALA:N	0.56	2.16	7	2
1:A:104:TYR:CE1	1:A:114:LEU:HD21	0.55	2.36	9	1
1:A:17:ASN:ND2	1:A:18:THR:N	0.55	2.54	10	2
1:A:106:TRP:CD1	1:A:107:ASN:N	0.55	2.75	7	3
1:A:122:ILE:HG23	1:A:122:ILE:O	0.55	2.02	3	1
1:A:42:TYR:CD2	1:A:42:TYR:N	0.55	2.75	16	2
1:A:82:LEU:N	1:A:82:LEU:CD1	0.54	2.68	6	3
1:A:114:LEU:N	1:A:114:LEU:CD2	0.54	2.67	7	3
1:A:17:ASN:HD22	1:A:18:THR:H	0.54	1.45	15	2
1:A:66:LEU:N	1:A:67:GLU:OE1	0.53	2.42	13	3
1:A:106:TRP:O	1:A:107:ASN:ND2	0.53	2.42	9	1
1:A:57:GLY:O	1:A:58:LEU:HD12	0.53	2.04	18	1
1:A:77:ASN:N	1:A:77:ASN:OD1	0.53	2.42	6	4
1:A:104:TYR:CD2	1:A:104:TYR:N	0.53	2.77	10	1
1:A:9:ASP:N	1:A:9:ASP:OD1	0.53	2.42	12	1
1:A:106:TRP:CZ3	1:A:107:ASN:O	0.53	2.62	16	2
1:A:120:TYR:CE1	1:A:121:ARG:O	0.52	2.62	1	4
1:A:118:LEU:N	1:A:118:LEU:CD1	0.52	2.67	17	3
1:A:39:LYS:NZ	1:A:69:TYR:OH	0.52	2.43	15	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:92:TYR:CE2	1:A:93:LYS:O	0.52	2.62	8	2
1:A:112:GLN:NE2	1:A:112:GLN:H	0.52	2.02	2	1
1:A:12:VAL:HG12	1:A:13:ALA:N	0.52	2.20	20	3
1:A:107:ASN:N	1:A:107:ASN:OD1	0.52	2.42	7	2
1:A:120:TYR:CE2	1:A:121:ARG:O	0.52	2.63	8	2
1:A:59:GLN:OE1	1:A:91:ARG:NH2	0.52	2.43	5	2
1:A:59:GLN:O	1:A:59:GLN:NE2	0.52	2.42	8	1
1:A:69:TYR:CD1	1:A:103:GLU:OE2	0.52	2.62	3	1
1:A:105:GLY:O	1:A:113:PHE:CE1	0.52	2.63	3	1
1:A:108:ASN:OD1	1:A:108:ASN:N	0.52	2.43	9	2
1:A:65:ASP:OD1	1:A:92:TYR:CE2	0.52	2.62	4	1
1:A:89:GLY:N	1:A:103:GLU:OE1	0.52	2.43	13	1
1:A:80:ASN:ND2	1:A:80:ASN:N	0.52	2.57	17	1
1:A:44:TRP:CD1	1:A:44:TRP:O	0.52	2.63	2	1
1:A:106:TRP:CE3	1:A:107:ASN:O	0.52	2.63	5	2
1:A:97:GLU:O	1:A:120:TYR:CD1	0.52	2.63	16	1
1:A:106:TRP:CZ2	1:A:112:GLN:OE1	0.51	2.63	8	2
1:A:71:TRP:CD1	1:A:72:ALA:N	0.51	2.79	18	3
1:A:66:LEU:HD21	1:A:92:TYR:CE1	0.51	2.40	2	3
1:A:65:ASP:CB	1:A:99:LYS:NZ	0.51	2.73	17	1
1:A:120:TYR:CZ	1:A:121:ARG:O	0.51	2.63	2	3
1:A:89:GLY:O	1:A:90:PHE:CD2	0.51	2.63	2	1
1:A:50:ASN:N	1:A:78:THR:OG1	0.51	2.43	2	1
1:A:58:LEU:HB2	1:A:70:ALA:HB3	0.51	1.82	4	2
1:A:17:ASN:N	1:A:17:ASN:OD1	0.51	2.42	12	1
1:A:80:ASN:N	1:A:80:ASN:OD1	0.51	2.42	19	1
1:A:17:ASN:OD1	1:A:17:ASN:N	0.51	2.43	3	1
1:A:31:GLN:NE2	1:A:121:ARG:NH1	0.51	2.59	6	1
1:A:113:PHE:CD1	1:A:113:PHE:N	0.51	2.79	9	2
1:A:106:TRP:CD2	1:A:107:ASN:N	0.50	2.79	20	2
1:A:80:ASN:N	1:A:80:ASN:ND2	0.50	2.55	15	1
1:A:64:PRO:O	1:A:65:ASP:CB	0.50	2.59	10	15
1:A:31:GLN:NE2	1:A:32:LEU:N	0.50	2.60	18	1
1:A:59:GLN:N	1:A:59:GLN:OE1	0.50	2.44	8	2
1:A:29:THR:HG23	1:A:38:VAL:O	0.50	2.07	11	1
1:A:108:ASN:HD22	1:A:109:SER:H	0.50	1.46	10	1
1:A:113:PHE:N	1:A:113:PHE:CD2	0.50	2.80	12	1
1:A:44:TRP:CG	1:A:45:ASN:N	0.50	2.79	17	2
1:A:26:GLY:O	1:A:42:TYR:CE1	0.49	2.65	14	3
1:A:20:ASN:ND2	1:A:20:ASN:O	0.49	2.45	7	2
1:A:111:LEU:H	1:A:111:LEU:CD1	0.49	2.16	9	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:66:LEU:N	1:A:67:GLU:OE2	0.49	2.46	1	1
1:A:54:PHE:O	1:A:54:PHE:CG	0.49	2.63	10	2
1:A:7:THR:HG22	1:A:8:LEU:N	0.49	2.22	10	1
1:A:76:TYR:CD2	1:A:82:LEU:HD13	0.49	2.43	13	1
1:A:104:TYR:CD2	1:A:112:GLN:OE1	0.49	2.65	1	1
1:A:58:LEU:HB3	1:A:70:ALA:HB3	0.49	1.85	3	3
1:A:15:GLY:O	1:A:16:TRP:CD1	0.49	2.66	5	1
1:A:9:ASP:OD1	1:A:9:ASP:N	0.49	2.46	9	1
1:A:30:TYR:N	1:A:30:TYR:CD2	0.49	2.80	19	1
1:A:97:GLU:O	1:A:120:TYR:CE1	0.48	2.66	15	2
1:A:59:GLN:NE2	1:A:60:TYR:O	0.48	2.46	6	1
1:A:17:ASN:ND2	1:A:18:THR:H	0.48	2.07	10	2
1:A:65:ASP:OD1	1:A:92:TYR:CD2	0.48	2.66	4	1
1:A:45:ASN:N	1:A:45:ASN:OD1	0.48	2.45	16	1
1:A:75:THR:O	1:A:75:THR:HG23	0.48	2.09	4	1
1:A:17:ASN:OD1	1:A:18:THR:N	0.48	2.47	6	2
1:A:12:VAL:CG1	1:A:13:ALA:N	0.47	2.76	20	3
1:A:108:ASN:ND2	1:A:109:SER:H	0.47	2.03	10	1
1:A:67:GLU:N	1:A:67:GLU:CD	0.47	2.66	6	6
1:A:108:ASN:O	1:A:108:ASN:ND2	0.47	2.47	7	2
1:A:11:PHE:CD2	1:A:11:PHE:C	0.47	2.88	3	2
1:A:103:GLU:N	1:A:103:GLU:CD	0.47	2.68	6	2
1:A:17:ASN:HD22	1:A:18:THR:N	0.47	2.06	15	2
1:A:62:VAL:CG1	1:A:66:LEU:O	0.47	2.63	12	1
1:A:63:THR:C	1:A:65:ASP:N	0.47	2.68	3	20
1:A:8:LEU:O	1:A:122:ILE:HG22	0.47	2.10	2	2
1:A:98:VAL:HG22	1:A:120:TYR:CD1	0.47	2.44	10	1
1:A:77:ASN:HD22	1:A:78:THR:H	0.47	1.52	19	1
1:A:12:VAL:CG2	1:A:13:ALA:N	0.47	2.77	7	2
1:A:22:ILE:O	1:A:22:ILE:HG23	0.47	2.09	14	1
1:A:66:LEU:HD11	1:A:92:TYR:CE1	0.47	2.45	18	2
1:A:21:THR:C	1:A:22:ILE:HD13	0.47	2.29	8	1
1:A:77:ASN:C	1:A:79:ASP:N	0.47	2.67	16	2
1:A:107:ASN:O	1:A:109:SER:N	0.47	2.48	3	1
1:A:31:GLN:HE22	1:A:33:SER:N	0.47	2.08	18	1
1:A:89:GLY:C	1:A:90:PHE:CG	0.47	2.88	6	4
1:A:23:GLU:OE2	1:A:24:ILE:N	0.47	2.47	17	1
1:A:17:ASN:O	1:A:19:ASP:N	0.46	2.48	7	4
1:A:44:TRP:C	1:A:45:ASN:ND2	0.46	2.68	7	1
1:A:17:ASN:C	1:A:19:ASP:N	0.46	2.68	7	7
1:A:77:ASN:O	1:A:79:ASP:N	0.46	2.48	16	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:59:GLN:N	1:A:59:GLN:CD	0.46	2.69	8	2
1:A:112:GLN:C	1:A:113:PHE:CD2	0.46	2.88	5	3
1:A:8:LEU:CD1	1:A:30:TYR:CZ	0.46	2.99	7	1
1:A:100:LEU:HD23	1:A:101:VAL:N	0.46	2.26	18	1
1:A:112:GLN:N	1:A:112:GLN:CD	0.46	2.68	10	2
1:A:95:SER:CB	1:A:96:PRO:CD	0.46	2.94	1	1
1:A:17:ASN:ND2	1:A:113:PHE:CD1	0.46	2.83	4	1
1:A:98:VAL:HG22	1:A:120:TYR:CZ	0.46	2.46	4	1
1:A:67:GLU:CD	1:A:67:GLU:N	0.46	2.67	15	3
1:A:88:ALA:O	1:A:104:TYR:CD1	0.46	2.69	8	1
1:A:67:GLU:OE1	1:A:91:ARG:NH2	0.46	2.48	12	1
1:A:107:ASN:OD1	1:A:108:ASN:N	0.46	2.49	13	1
1:A:37:MET:SD	1:A:59:GLN:OE1	0.46	2.73	13	1
1:A:71:TRP:CD1	1:A:71:TRP:O	0.46	2.68	1	2
1:A:11:PHE:CD2	1:A:11:PHE:O	0.46	2.69	3	1
1:A:62:VAL:O	1:A:62:VAL:CG1	0.46	2.64	3	1
1:A:81:THR:CG2	1:A:82:LEU:N	0.46	2.78	3	1
1:A:108:ASN:ND2	1:A:108:ASN:N	0.46	2.64	19	1
1:A:69:TYR:CE1	1:A:91:ARG:NH2	0.45	2.84	7	1
1:A:106:TRP:CE2	1:A:112:GLN:OE1	0.45	2.69	9	1
1:A:11:PHE:CD1	1:A:11:PHE:O	0.45	2.69	13	1
1:A:65:ASP:OD1	1:A:91:ARG:NH1	0.45	2.49	20	1
1:A:45:ASN:HD22	1:A:45:ASN:H	0.45	1.53	5	1
1:A:117:GLY:C	1:A:118:LEU:HD12	0.45	2.32	15	1
1:A:104:TYR:CB	1:A:113:PHE:O	0.45	2.65	4	1
1:A:104:TYR:O	1:A:104:TYR:CG	0.45	2.69	6	1
1:A:54:PHE:CD1	1:A:54:PHE:C	0.45	2.88	12	1
1:A:44:TRP:CD1	1:A:45:ASN:N	0.45	2.84	19	1
1:A:59:GLN:CD	1:A:59:GLN:H	0.45	2.15	8	1
1:A:7:THR:CG2	1:A:8:LEU:N	0.45	2.79	10	1
1:A:45:ASN:HD22	1:A:45:ASN:N	0.45	2.09	5	1
1:A:92:TYR:CD2	1:A:93:LYS:N	0.45	2.85	8	2
1:A:31:GLN:NE2	1:A:121:ARG:HH12	0.45	2.09	6	1
1:A:102:VAL:O	1:A:102:VAL:CG1	0.45	2.64	16	2
1:A:106:TRP:CD1	1:A:106:TRP:C	0.45	2.90	10	1
1:A:75:THR:C	1:A:76:TYR:CD1	0.44	2.90	6	1
1:A:77:ASN:HD22	1:A:78:THR:N	0.44	2.10	19	1
1:A:88:ALA:O	1:A:104:TYR:CE2	0.44	2.70	3	2
1:A:50:ASN:ND2	1:A:50:ASN:N	0.44	2.65	20	1
1:A:63:THR:C	1:A:65:ASP:H	0.44	2.15	4	13
1:A:9:ASP:O	1:A:28:ALA:CB	0.44	2.65	6	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:59:GLN:OE1	1:A:60:TYR:N	0.44	2.50	6	1
1:A:76:TYR:CD2	1:A:76:TYR:O	0.44	2.71	7	1
1:A:23:GLU:O	1:A:23:GLU:CG	0.44	2.66	14	1
1:A:102:VAL:O	1:A:102:VAL:CG2	0.44	2.65	17	2
1:A:50:ASN:OD1	1:A:50:ASN:N	0.44	2.51	4	1
1:A:93:LYS:CG	1:A:93:LYS:O	0.44	2.64	4	1
1:A:50:ASN:HD22	1:A:78:THR:HG23	0.44	1.72	10	1
1:A:30:TYR:CD2	1:A:30:TYR:N	0.44	2.85	8	1
1:A:107:ASN:CG	1:A:108:ASN:N	0.44	2.70	17	1
1:A:29:THR:HG22	1:A:39:LYS:HB3	0.44	1.90	20	1
1:A:32:LEU:HD12	1:A:32:LEU:N	0.44	2.27	8	1
1:A:67:GLU:N	1:A:67:GLU:OE2	0.43	2.51	16	1
1:A:112:GLN:H	1:A:112:GLN:CD	0.43	2.17	2	1
1:A:17:ASN:O	1:A:20:ASN:N	0.43	2.51	8	3
1:A:71:TRP:CD2	1:A:103:GLU:OE2	0.43	2.72	12	1
1:A:17:ASN:ND2	1:A:17:ASN:N	0.43	2.64	14	1
1:A:77:ASN:O	1:A:80:ASN:N	0.43	2.51	19	2
1:A:60:TYR:O	1:A:67:GLU:OE2	0.43	2.36	12	6
1:A:71:TRP:O	1:A:71:TRP:CG	0.43	2.71	15	1
1:A:107:ASN:O	1:A:108:ASN:O	0.43	2.37	1	1
1:A:65:ASP:O	1:A:65:ASP:CG	0.43	2.57	10	3
1:A:106:TRP:O	1:A:107:ASN:OD1	0.43	2.37	5	2
1:A:86:ALA:O	1:A:106:TRP:O	0.43	2.37	6	4
1:A:111:LEU:HD12	1:A:111:LEU:N	0.43	2.28	9	1
1:A:13:ALA:HB3	1:A:25:THR:OG1	0.43	2.13	13	1
1:A:60:TYR:O	1:A:66:LEU:O	0.43	2.37	4	2
1:A:118:LEU:HD12	1:A:118:LEU:O	0.43	2.14	5	2
1:A:112:GLN:C	1:A:113:PHE:CG	0.43	2.92	11	1
1:A:120:TYR:O	1:A:120:TYR:CG	0.43	2.69	20	1
1:A:44:TRP:CZ3	1:A:50:ASN:OD1	0.43	2.72	10	1
1:A:4:GLY:O	1:A:7:THR:OG1	0.43	2.37	14	3
1:A:67:GLU:OE1	1:A:67:GLU:O	0.43	2.37	15	1
1:A:104:TYR:CE2	1:A:114:LEU:HD21	0.43	2.49	20	1
1:A:44:TRP:CD1	1:A:44:TRP:N	0.43	2.86	8	1
1:A:105:GLY:O	1:A:113:PHE:CE2	0.43	2.72	4	1
1:A:60:TYR:O	1:A:67:GLU:OE1	0.42	2.37	7	2
1:A:64:PRO:O	1:A:65:ASP:CG	0.42	2.58	6	11
1:A:69:TYR:CE1	1:A:103:GLU:OE2	0.42	2.72	3	1
1:A:60:TYR:H	1:A:67:GLU:CD	0.42	2.16	9	1
1:A:95:SER:O	1:A:98:VAL:O	0.42	2.37	9	2
1:A:108:ASN:HD22	1:A:109:SER:N	0.42	2.09	10	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:57:GLY:O	1:A:58:LEU:HD22	0.42	2.14	7	1
1:A:108:ASN:O	1:A:109:SER:O	0.42	2.37	7	2
1:A:9:ASP:OD1	1:A:120:TYR:O	0.42	2.37	16	1
1:A:77:ASN:ND2	1:A:78:THR:N	0.42	2.67	16	1
1:A:88:ALA:O	1:A:104:TYR:CD2	0.42	2.72	6	1
1:A:9:ASP:OD1	1:A:29:THR:O	0.42	2.38	9	1
1:A:50:ASN:CB	1:A:78:THR:OG1	0.42	2.67	13	1
1:A:107:ASN:ND2	1:A:108:ASN:N	0.42	2.66	18	1
1:A:108:ASN:CG	1:A:109:SER:N	0.42	2.72	3	1
1:A:97:GLU:C	1:A:99:LYS:HZ3	0.42	2.17	6	1
1:A:94:VAL:HG12	1:A:95:SER:N	0.42	2.28	13	1
1:A:105:GLY:C	1:A:113:PHE:CE1	0.42	2.93	3	1
1:A:17:ASN:OD1	1:A:21:THR:CG2	0.42	2.67	14	1
1:A:89:GLY:C	1:A:90:PHE:CD1	0.42	2.92	20	1
1:A:107:ASN:O	1:A:110:SER:OG	0.42	2.38	4	1
1:A:62:VAL:HG13	1:A:63:THR:OG1	0.42	2.15	8	2
1:A:92:TYR:CD2	1:A:92:TYR:C	0.41	2.92	8	1
1:A:31:GLN:NE2	1:A:33:SER:O	0.41	2.50	10	1
1:A:71:TRP:CD1	1:A:71:TRP:C	0.41	2.90	4	1
1:A:17:ASN:OD1	1:A:112:GLN:O	0.41	2.38	13	1
1:A:67:GLU:O	1:A:67:GLU:OE1	0.41	2.37	14	1
1:A:9:ASP:OD2	1:A:29:THR:OG1	0.41	2.37	20	1
1:A:76:TYR:CD1	1:A:76:TYR:N	0.41	2.87	6	1
1:A:59:GLN:CD	1:A:60:TYR:N	0.41	2.73	6	1
1:A:108:ASN:O	1:A:110:SER:OG	0.41	2.38	6	1
1:A:117:GLY:O	1:A:118:LEU:HD12	0.41	2.15	15	1
1:A:44:TRP:CE3	1:A:45:ASN:O	0.41	2.74	13	1
1:A:99:LYS:O	1:A:118:LEU:CB	0.41	2.68	18	1
1:A:100:LEU:HD23	1:A:101:VAL:H	0.41	1.74	18	1
1:A:53:GLU:OE1	1:A:71:TRP:CZ3	0.41	2.74	19	1
1:A:11:PHE:O	1:A:11:PHE:CG	0.41	2.73	1	1
1:A:11:PHE:CE1	1:A:29:THR:HG23	0.41	2.51	14	1
1:A:104:TYR:CD1	1:A:104:TYR:N	0.41	2.88	20	1
1:A:79:ASP:OD1	1:A:79:ASP:N	0.41	2.54	1	1
1:A:8:LEU:O	1:A:122:ILE:CG2	0.41	2.69	2	1
1:A:71:TRP:CG	1:A:103:GLU:CD	0.40	2.94	12	1
1:A:77:ASN:C	1:A:79:ASP:H	0.40	2.20	16	1
1:A:64:PRO:O	1:A:65:ASP:OD1	0.40	2.40	8	1
1:A:30:TYR:CD1	1:A:30:TYR:N	0.40	2.89	4	1
1:A:32:LEU:N	1:A:32:LEU:CD1	0.40	2.85	8	1
1:A:19:ASP:O	1:A:20:ASN:CB	0.40	2.68	11	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:24:ILE:O	1:A:24:ILE:HG23	0.40	2.17	6	1
1:A:112:GLN:CG	1:A:113:PHE:N	0.40	2.85	18	1

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	115/124 (93%)	102±2 (89±2%)	9±2 (8±2%)	4±1 (3±1%)	6 37
All	All	2300/2480 (93%)	2046 (89%)	177 (8%)	77 (3%)	6 37

All 10 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	64	PRO	20
1	A	65	ASP	20
1	A	108	ASN	10
1	A	109	SER	9
1	A	62	VAL	5
1	A	18	THR	4
1	A	35	TYR	4
1	A	122	ILE	2
1	A	45	ASN	2
1	A	78	THR	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	89/98 (91%)	60±3 (67±4%)	29±3 (33±4%)	1 12
All	All	1780/1960 (91%)	1195 (67%)	585 (33%)	1 12

All 77 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	33	SER	20
1	A	63	THR	20
1	A	95	SER	20
1	A	7	THR	18
1	A	110	SER	18
1	A	67	GLU	17
1	A	66	LEU	16
1	A	60	TYR	15
1	A	113	PHE	15
1	A	118	LEU	15
1	A	9	ASP	13
1	A	79	ASP	13
1	A	90	PHE	13
1	A	104	TYR	13
1	A	42	TYR	13
1	A	16	TRP	12
1	A	59	GLN	12
1	A	82	LEU	11
1	A	50	ASN	10
1	A	52	PHE	10
1	A	65	ASP	10
1	A	35	TYR	9
1	A	54	PHE	9
1	A	106	TRP	9
1	A	8	LEU	9
1	A	71	TRP	8
1	A	77	ASN	8
1	A	30	TYR	8
1	A	44	TRP	8
1	A	80	ASN	8
1	A	83	VAL	8
1	A	114	LEU	8
1	A	119	SER	7
1	A	17	ASN	7
1	A	18	THR	7
1	A	21	THR	7

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Mol	Chain	Res	Type	Models (Total)
1	A	31	GLN	7
1	A	108	ASN	7
1	A	75	THR	7
1	A	81	THR	7
1	A	103	GLU	7
1	A	29	THR	6
1	A	76	TYR	6
1	A	51	ARG	6
1	A	112	GLN	6
1	A	39	LYS	6
1	A	111	LEU	5
1	A	78	THR	5
1	A	107	ASN	5
1	A	20	ASN	5
1	A	25	THR	5
1	A	102	VAL	5
1	A	92	TYR	5
1	A	93	LYS	4
1	A	53	GLU	4
1	A	45	ASN	4
1	A	100	LEU	4
1	A	99	LYS	4
1	A	19	ASP	3
1	A	23	GLU	3
1	A	37	MET	3
1	A	58	LEU	3
1	A	32	LEU	3
1	A	22	ILE	3
1	A	120	TYR	3
1	A	115	GLN	2
1	A	11	PHE	2
1	A	69	TYR	2
1	A	12	VAL	2
1	A	62	VAL	2
1	A	101	VAL	2
1	A	61	LYS	2
1	A	38	VAL	2
1	A	109	SER	1
1	A	94	VAL	1
1	A	91	ARG	1
1	A	36	ILE	1

6.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

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 36% for the well-defined parts and 34% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *chemshift_NMRSTAR31.txt*

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	549
Number of shifts mapped to atoms	549
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

7.1.2 Chemical shift referencing (i)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	115	0.56 ± 0.15	Should be checked
$^{13}C_{\beta}$	101	-0.21 ± 0.06	None needed (< 0.5 ppm)
$^{13}C'$	117	1.24 ± 0.12	Should be applied
^{15}N	108	0.73 ± 0.24	Should be applied

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 36%, i.e. 535 atoms were assigned a chemical shift out of a possible 1500. 0 out of 18 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	437/578 (76%)	106/239 (44%)	225/230 (98%)	106/109 (97%)
Sidechain	98/743 (13%)	0/487 (0%)	98/231 (42%)	0/25 (0%)

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	Total	^{1}H	^{13}C	^{15}N
Aromatic	0/179 (0%)	0/85 (0%)	0/90 (0%)	0/4 (0%)
Overall	535/1500 (36%)	106/811 (13%)	323/551 (59%)	106/138 (77%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 34%, i.e. 549 atoms were assigned a chemical shift out of a possible 1612. 0 out of 19 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	448/621 (72%)	108/256 (42%)	232/248 (94%)	108/117 (92%)
Sidechain	101/812 (12%)	0/531 (0%)	101/253 (40%)	0/28 (0%)
Aromatic	0/179 (0%)	0/85 (0%)	0/90 (0%)	0/4 (0%)
Overall	549/1612 (34%)	108/872 (12%)	333/591 (56%)	108/149 (72%)

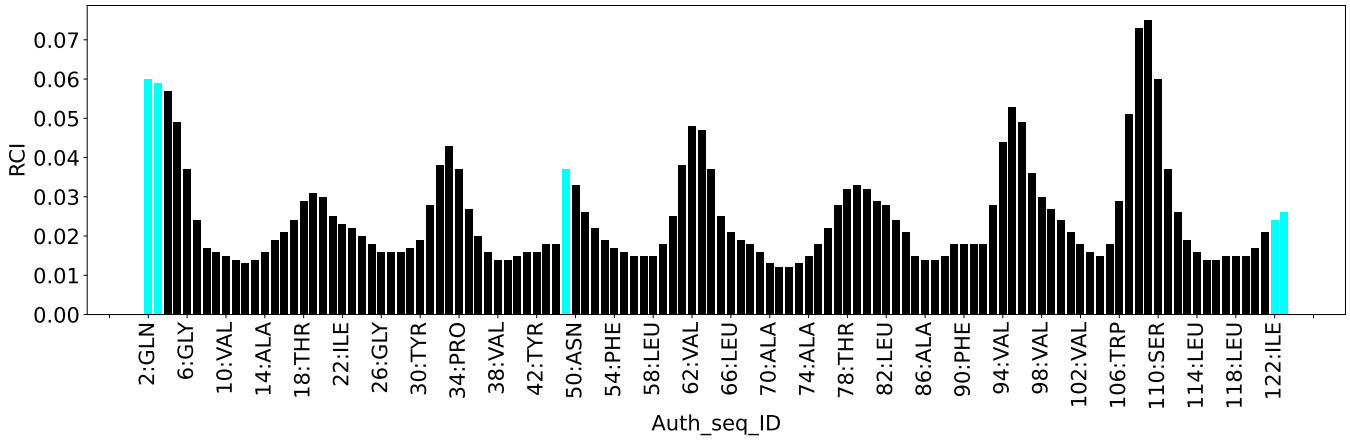
7.1.4 Statistically unusual chemical shifts (i)

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	225
Intra-residue (|i-j|=0)	0
Sequential (|i-j|=1)	28
Medium range (|i-j|>1 and |i-j|<5)	12
Long range (|i-j|≥5)	41
Inter-chain	0
Hydrogen bond restraints	144
Disulfide bond restraints	0
Total dihedral-angle restraints	204
Number of unmapped restraints	0
Number of restraints per residue	3.5
Number of long range restraints per residue[1]	1.4

[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)	1.2	0.2
0.2-0.5 (Medium)	2.2	0.39
>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.

Bins (°)	Average number of violations per model	Max (°)
1.0-10.0 (Small)	5.5	3.0
10.0-20.0 (Medium)	None	None
>20.0 (Large)	None	None

9 Distance violation analysis (i)

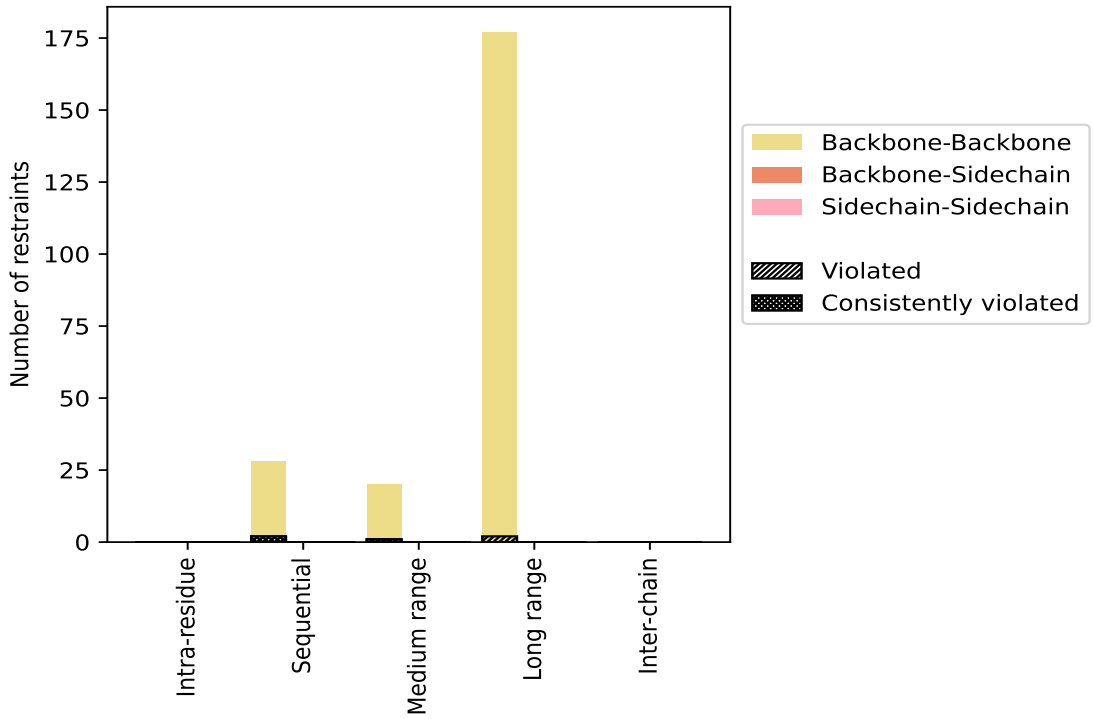
9.1 Summary of distance violations (i)

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)	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)	28	12.4	2	7.1	0.9	2	7.1	0.9
Backbone-Backbone	28	12.4	2	7.1	0.9	2	7.1	0.9
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)	12	5.3	1	8.3	0.4	1	8.3	0.4
Backbone-Backbone	12	5.3	1	8.3	0.4	1	8.3	0.4
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)	41	18.2	1	2.4	0.4	0	0.0	0.0
Backbone-Backbone	41	18.2	1	2.4	0.4	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	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	144	64.0	1	0.7	0.4	0	0.0	0.0
Disulfide bond	0	0.0	0	0.0	0.0	0	0.0	0.0
Total	225	100.0	5	2.2	2.2	3	1.3	1.3
Backbone-Backbone	225	100.0	5	2.2	2.2	3	1.3	1.3
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

[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	1	0	0	3	0.29	0.38	0.1	0.35
2	0	2	1	0	0	3	0.29	0.38	0.11	0.36
3	0	2	1	2	0	5	0.23	0.38	0.11	0.15
4	0	2	1	2	0	5	0.23	0.38	0.11	0.17
5	0	2	1	0	0	3	0.29	0.38	0.1	0.35
6	0	2	1	0	0	3	0.3	0.37	0.09	0.36
7	0	2	1	0	0	3	0.31	0.38	0.08	0.34
8	0	2	1	0	0	3	0.31	0.37	0.08	0.35
9	0	2	1	2	0	5	0.25	0.38	0.1	0.21
10	0	2	1	0	0	3	0.3	0.38	0.09	0.35
11	0	2	1	0	0	3	0.3	0.38	0.09	0.35

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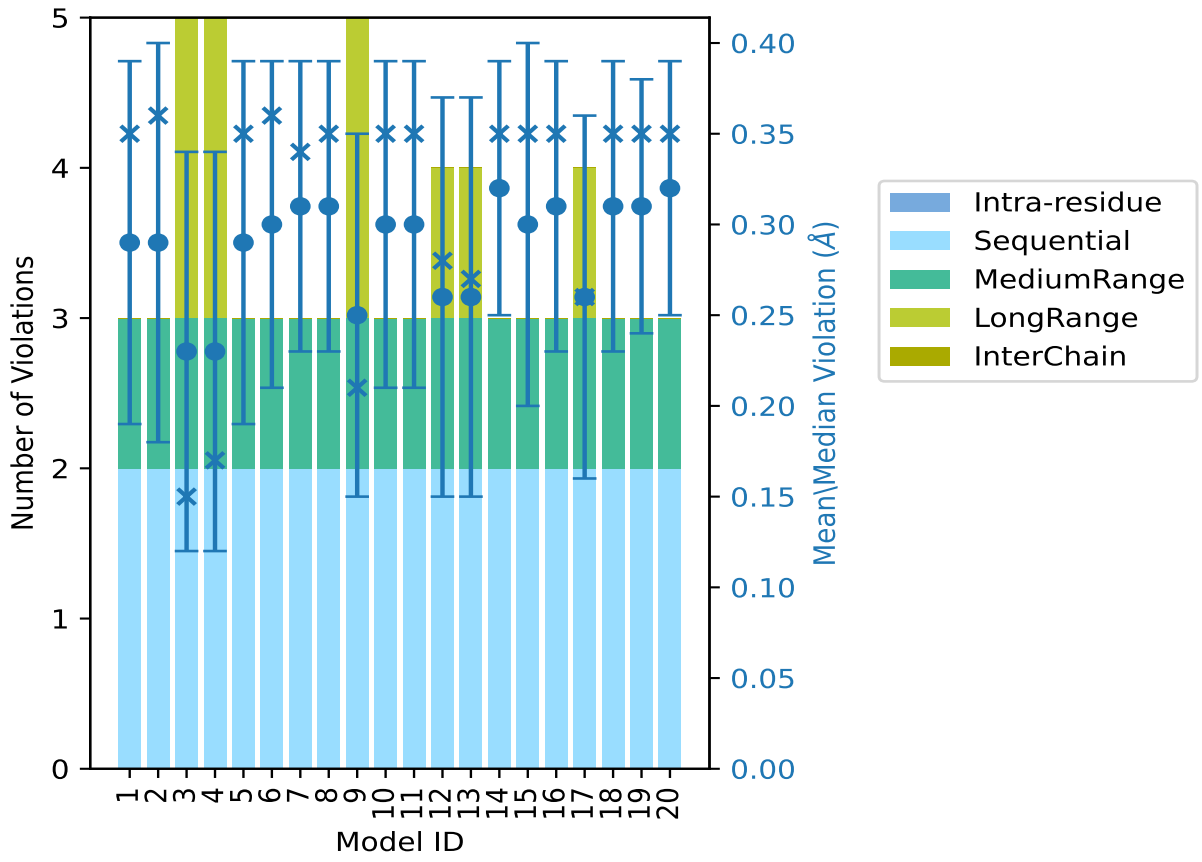
Model ID	Number of violations						Mean (Å)	Max (Å)	SD[6] (Å)	Median (Å)
	IR[1]	SQ[2]	MR[3]	LR[4]	IC[5]	Total				
12	0	2	1	1	0	4	0.26	0.38	0.11	0.28
13	0	2	1	1	0	4	0.26	0.38	0.11	0.27
14	0	2	1	0	0	3	0.32	0.38	0.07	0.35
15	0	2	1	0	0	3	0.3	0.39	0.1	0.35
16	0	2	1	0	0	3	0.31	0.39	0.08	0.35
17	0	2	1	1	0	4	0.26	0.38	0.1	0.26
18	0	2	1	0	0	3	0.31	0.38	0.08	0.35
19	0	2	1	0	0	3	0.31	0.38	0.07	0.35
20	0	2	1	0	0	3	0.32	0.38	0.07	0.35

[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

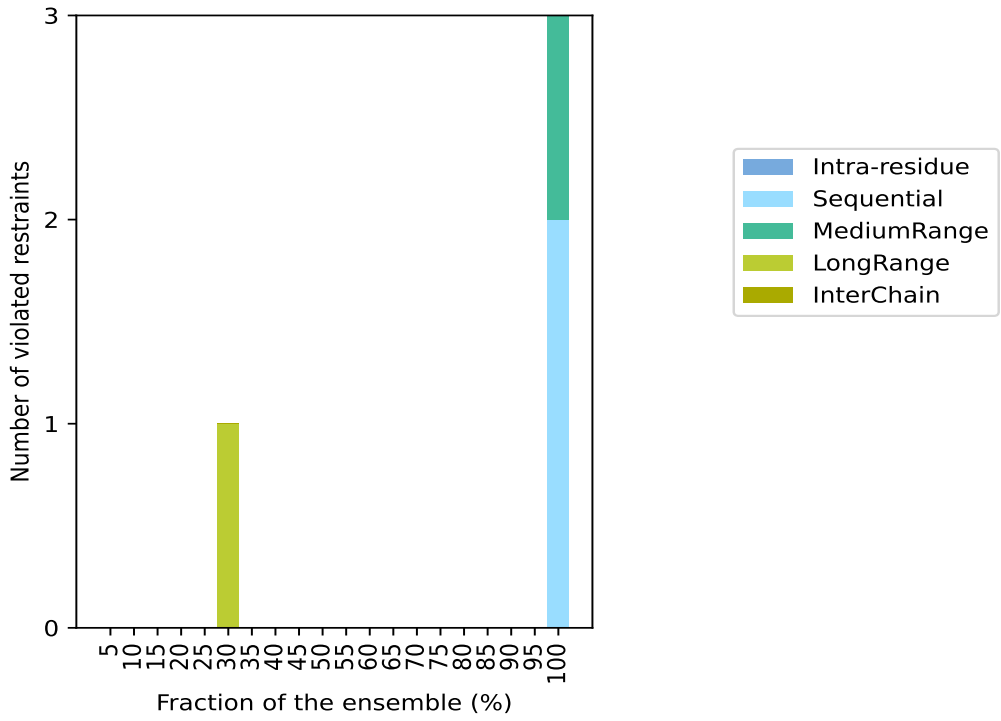
9.3 Distance violation statistics for the ensemble (i)

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, 77(IR:0, SQ:26, MR:11, LR:40, 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	0	0	0	0	1	5.0
0	0	0	0	0	0	2	10.0
0	0	0	0	0	0	3	15.0
0	0	0	0	0	0	4	20.0
0	0	0	0	0	0	5	25.0
0	0	0	1	0	1	6	30.0
0	0	0	0	0	0	7	35.0
0	0	0	0	0	0	8	40.0
0	0	0	0	0	0	9	45.0
0	0	0	0	0	0	10	50.0
0	0	0	0	0	0	11	55.0
0	0	0	0	0	0	12	60.0
0	0	0	0	0	0	13	65.0
0	0	0	0	0	0	14	70.0
0	0	0	0	0	0	15	75.0
0	0	0	0	0	0	16	80.0
0	0	0	0	0	0	17	85.0
0	0	0	0	0	0	18	90.0
0	0	0	0	0	0	19	95.0
0	2	1	0	0	3	20	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

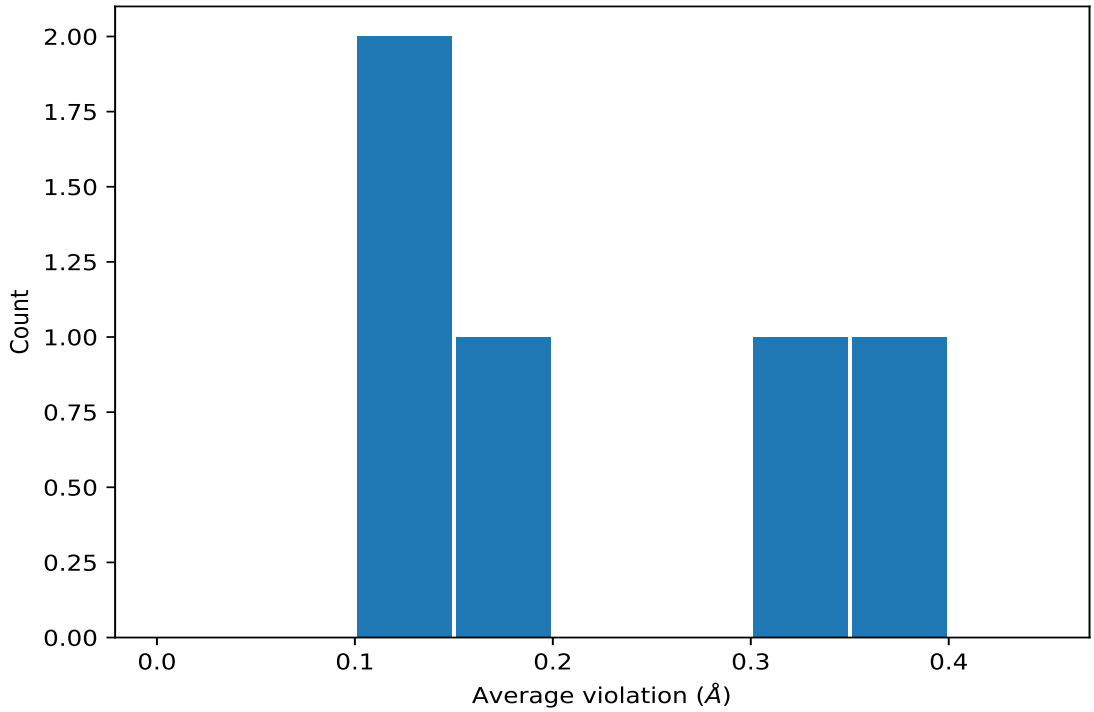
9.3.1 Bar graph : Distance violation statistics for the ensemble (i)



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.

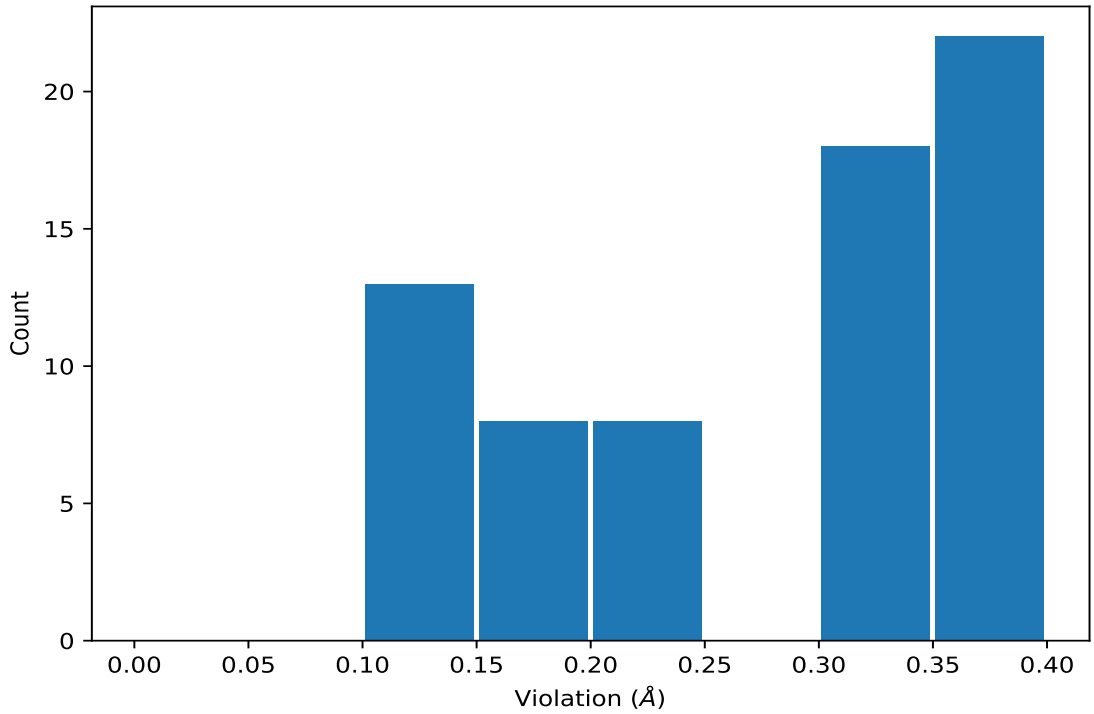
Key	Atom-1	Atom-2	Models[1]	Mean (Å)	SD[1] (Å)	Median (Å)
(1,71)	1:A:103:GLU:H	1:A:102:VAL:H	20	0.38	0.0	0.38
(1,3)	1:A:13:ALA:H	1:A:14:ALA:H	20	0.35	0.0	0.35
(1,39)	1:A:63:THR:H	1:A:65:ASP:H	20	0.18	0.03	0.18
(1,33)	1:A:60:TYR:H	1:A:66:LEU:H	6	0.14	0.03	0.14
(2,71)	1:A:70:ALA:H	1:A:58:LEU:O	3	0.14	0.01	0.14

[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)
(1,71)	1:A:103:GLU:H	1:A:102:VAL:H	15	0.39
(1,71)	1:A:103:GLU:H	1:A:102:VAL:H	16	0.39
(1,71)	1:A:103:GLU:H	1:A:102:VAL:H	1	0.38
(1,71)	1:A:103:GLU:H	1:A:102:VAL:H	2	0.38
(1,71)	1:A:103:GLU:H	1:A:102:VAL:H	3	0.38
(1,71)	1:A:103:GLU:H	1:A:102:VAL:H	4	0.38
(1,71)	1:A:103:GLU:H	1:A:102:VAL:H	5	0.38
(1,71)	1:A:103:GLU:H	1:A:102:VAL:H	7	0.38
(1,71)	1:A:103:GLU:H	1:A:102:VAL:H	9	0.38
(1,71)	1:A:103:GLU:H	1:A:102:VAL:H	10	0.38
(1,71)	1:A:103:GLU:H	1:A:102:VAL:H	11	0.38
(1,71)	1:A:103:GLU:H	1:A:102:VAL:H	12	0.38
(1,71)	1:A:103:GLU:H	1:A:102:VAL:H	13	0.38
(1,71)	1:A:103:GLU:H	1:A:102:VAL:H	14	0.38
(1,71)	1:A:103:GLU:H	1:A:102:VAL:H	17	0.38
(1,71)	1:A:103:GLU:H	1:A:102:VAL:H	18	0.38

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,71)	1:A:103:GLU:H	1:A:102:VAL:H	19	0.38
(1,71)	1:A:103:GLU:H	1:A:102:VAL:H	20	0.38
(1,71)	1:A:103:GLU:H	1:A:102:VAL:H	6	0.37
(1,71)	1:A:103:GLU:H	1:A:102:VAL:H	8	0.37
(1,3)	1:A:13:ALA:H	1:A:14:ALA:H	2	0.36
(1,3)	1:A:13:ALA:H	1:A:14:ALA:H	6	0.36
(1,3)	1:A:13:ALA:H	1:A:14:ALA:H	1	0.35
(1,3)	1:A:13:ALA:H	1:A:14:ALA:H	3	0.35
(1,3)	1:A:13:ALA:H	1:A:14:ALA:H	4	0.35
(1,3)	1:A:13:ALA:H	1:A:14:ALA:H	5	0.35
(1,3)	1:A:13:ALA:H	1:A:14:ALA:H	8	0.35
(1,3)	1:A:13:ALA:H	1:A:14:ALA:H	9	0.35
(1,3)	1:A:13:ALA:H	1:A:14:ALA:H	10	0.35
(1,3)	1:A:13:ALA:H	1:A:14:ALA:H	11	0.35
(1,3)	1:A:13:ALA:H	1:A:14:ALA:H	12	0.35
(1,3)	1:A:13:ALA:H	1:A:14:ALA:H	13	0.35
(1,3)	1:A:13:ALA:H	1:A:14:ALA:H	14	0.35
(1,3)	1:A:13:ALA:H	1:A:14:ALA:H	15	0.35
(1,3)	1:A:13:ALA:H	1:A:14:ALA:H	16	0.35
(1,3)	1:A:13:ALA:H	1:A:14:ALA:H	17	0.35
(1,3)	1:A:13:ALA:H	1:A:14:ALA:H	18	0.35
(1,3)	1:A:13:ALA:H	1:A:14:ALA:H	19	0.35
(1,3)	1:A:13:ALA:H	1:A:14:ALA:H	20	0.35
(1,3)	1:A:13:ALA:H	1:A:14:ALA:H	7	0.34
(1,39)	1:A:63:THR:H	1:A:65:ASP:H	14	0.22
(1,39)	1:A:63:THR:H	1:A:65:ASP:H	20	0.22
(1,39)	1:A:63:THR:H	1:A:65:ASP:H	19	0.21
(1,33)	1:A:60:TYR:H	1:A:66:LEU:H	9	0.21
(1,39)	1:A:63:THR:H	1:A:65:ASP:H	7	0.2
(1,39)	1:A:63:THR:H	1:A:65:ASP:H	8	0.2
(1,39)	1:A:63:THR:H	1:A:65:ASP:H	12	0.2
(1,39)	1:A:63:THR:H	1:A:65:ASP:H	16	0.2
(1,39)	1:A:63:THR:H	1:A:65:ASP:H	13	0.19
(1,39)	1:A:63:THR:H	1:A:65:ASP:H	18	0.19
(1,39)	1:A:63:THR:H	1:A:65:ASP:H	6	0.18
(1,39)	1:A:63:THR:H	1:A:65:ASP:H	9	0.18
(1,39)	1:A:63:THR:H	1:A:65:ASP:H	10	0.18
(1,39)	1:A:63:THR:H	1:A:65:ASP:H	11	0.18
(1,39)	1:A:63:THR:H	1:A:65:ASP:H	17	0.18
(1,39)	1:A:63:THR:H	1:A:65:ASP:H	4	0.17
(2,71)	1:A:70:ALA:H	1:A:58:LEU:O	4	0.15
(1,39)	1:A:63:THR:H	1:A:65:ASP:H	1	0.15

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,39)	1:A:63:THR:H	1:A:65:ASP:H	5	0.15
(1,39)	1:A:63:THR:H	1:A:65:ASP:H	15	0.15
(1,33)	1:A:60:TYR:H	1:A:66:LEU:H	3	0.15
(2,71)	1:A:70:ALA:H	1:A:58:LEU:O	3	0.14
(1,39)	1:A:63:THR:H	1:A:65:ASP:H	2	0.14
(1,33)	1:A:60:TYR:H	1:A:66:LEU:H	17	0.14
(1,33)	1:A:60:TYR:H	1:A:66:LEU:H	13	0.13
(2,71)	1:A:70:ALA:H	1:A:58:LEU:O	9	0.12
(1,39)	1:A:63:THR:H	1:A:65:ASP:H	3	0.12
(1,33)	1:A:60:TYR:H	1:A:66:LEU:H	12	0.12
(1,33)	1:A:60:TYR:H	1:A:66:LEU:H	4	0.11

10 Dihedral-angle violation analysis (i)

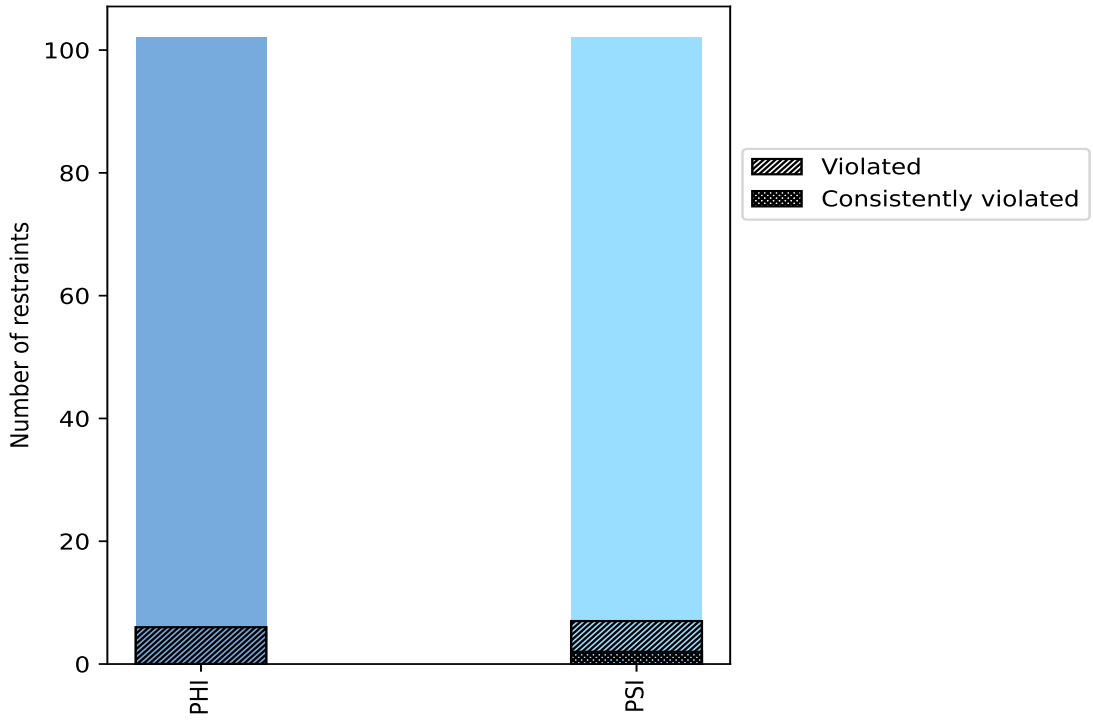
10.1 Summary of dihedral-angle violations (i)

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	102	50.0	6	5.9	2.9	0	0.0	0.0
PSI	102	50.0	7	6.9	3.4	2	2.0	1.0
Total	204	100.0	13	6.4	6.4	2	1.0	1.0

[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 (i)



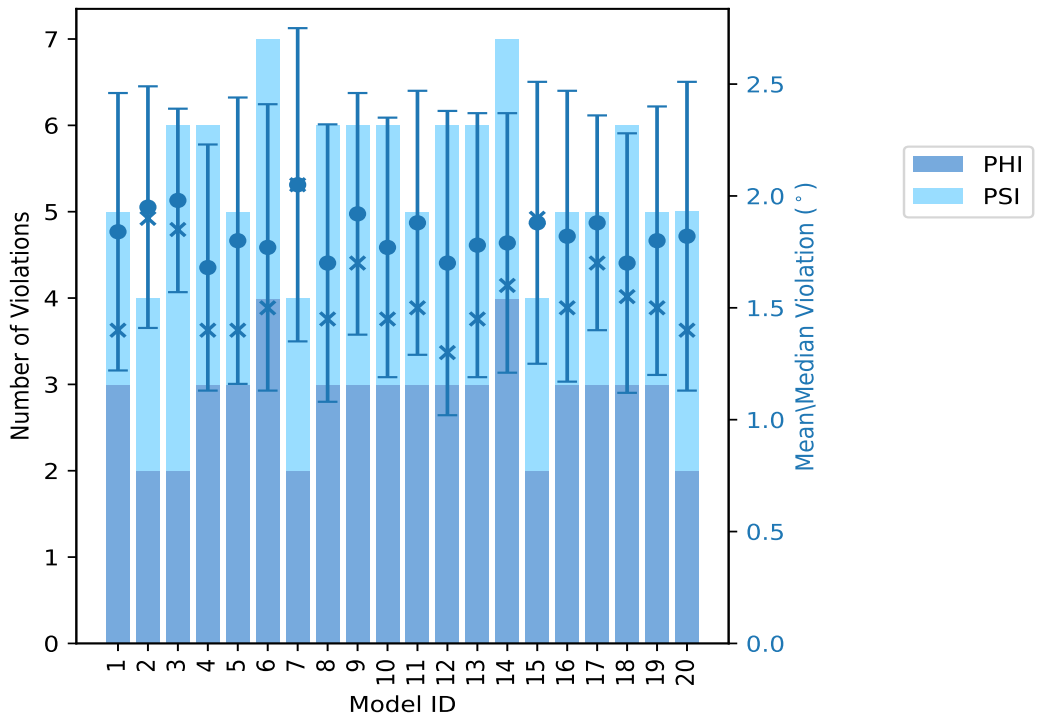
Violated and consistently violated restraints are shown using different hatch patterns in their respective categories

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	3	2	5	1.84	2.7	0.62	1.4
2	2	2	4	1.95	2.7	0.54	1.9
3	2	4	6	1.98	2.7	0.41	1.85
4	3	3	6	1.68	2.5	0.55	1.4
5	3	2	5	1.8	2.8	0.64	1.4
6	4	3	7	1.77	3.0	0.64	1.5
7	2	2	4	2.05	2.8	0.7	2.05
8	3	3	6	1.7	2.7	0.62	1.45
9	3	3	6	1.92	2.8	0.54	1.7
10	3	3	6	1.77	2.8	0.58	1.45
11	3	2	5	1.88	2.6	0.59	1.5
12	3	3	6	1.7	2.7	0.68	1.3
13	3	3	6	1.78	2.8	0.59	1.45
14	4	3	7	1.79	2.7	0.58	1.6
15	2	2	4	1.88	2.5	0.63	1.9
16	3	2	5	1.82	2.6	0.65	1.5
17	3	2	5	1.88	2.5	0.48	1.7
18	3	3	6	1.7	2.7	0.58	1.55
19	3	2	5	1.8	2.7	0.6	1.5
20	2	3	5	1.82	2.7	0.69	1.4

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]	%
1	3	4	1	5.0
1	1	2	2	10.0
0	0	0	3	15.0
1	0	1	4	20.0
0	0	0	5	25.0
0	0	0	6	30.0
0	1	1	7	35.0
0	0	0	8	40.0
0	0	0	9	45.0
0	0	0	10	50.0
0	0	0	11	55.0

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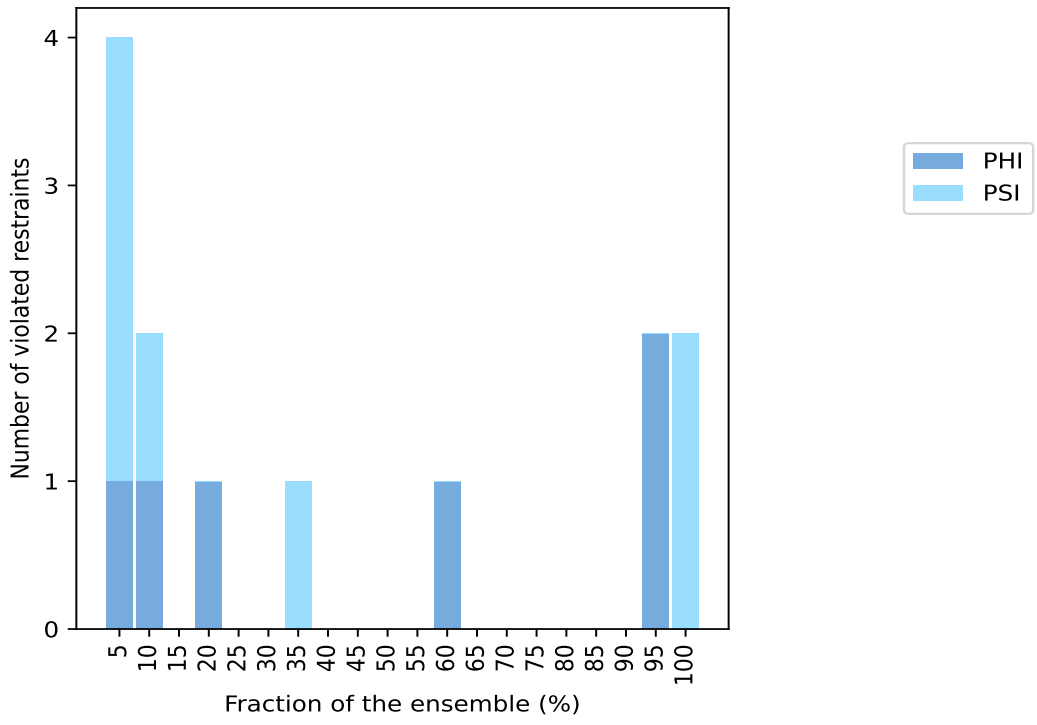
Number of violated restraints			Fraction of the ensemble	
PHI	PSI	Total	Count[1]	%
1	0	1	12	60.0
0	0	0	13	65.0
0	0	0	14	70.0
0	0	0	15	75.0
0	0	0	16	80.0
0	0	0	17	85.0
0	0	0	18	90.0
2	0	2	19	95.0
0	2	2	20	100.0

[1] Number of models with violations

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

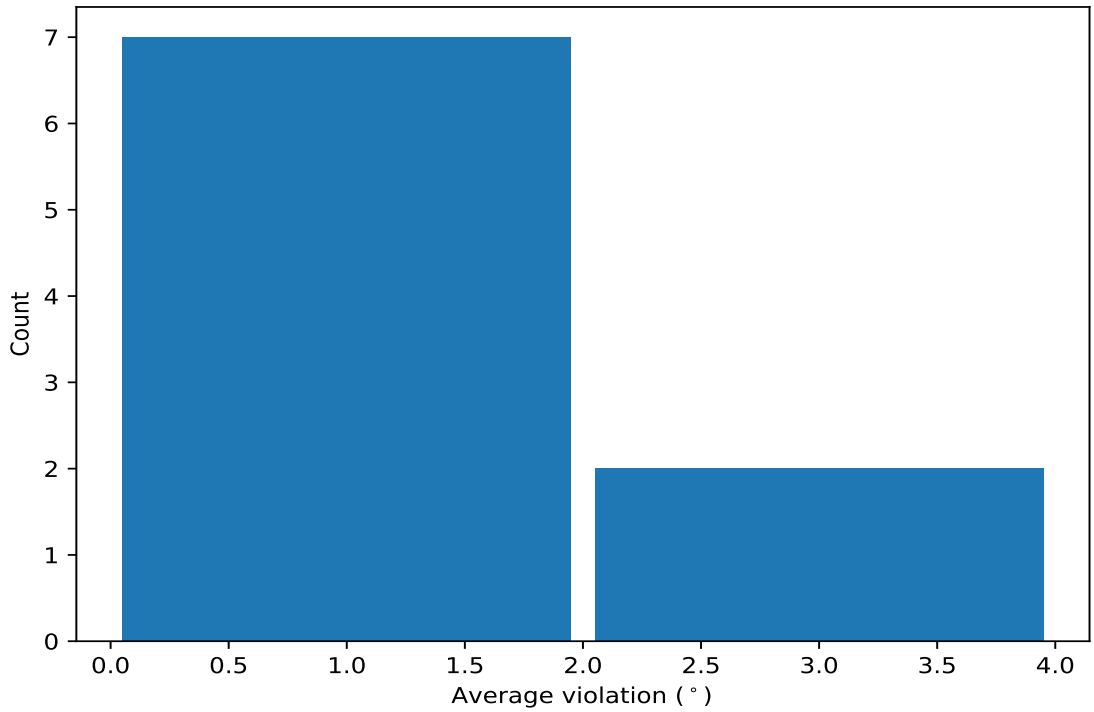


10.4 Most violated dihedral-angle restraints in the ensemble (i)

10.4.1 Histogram : Distribution of mean dihedral-angle 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



10.4.2 Table: Most violated dihedral-angle 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.

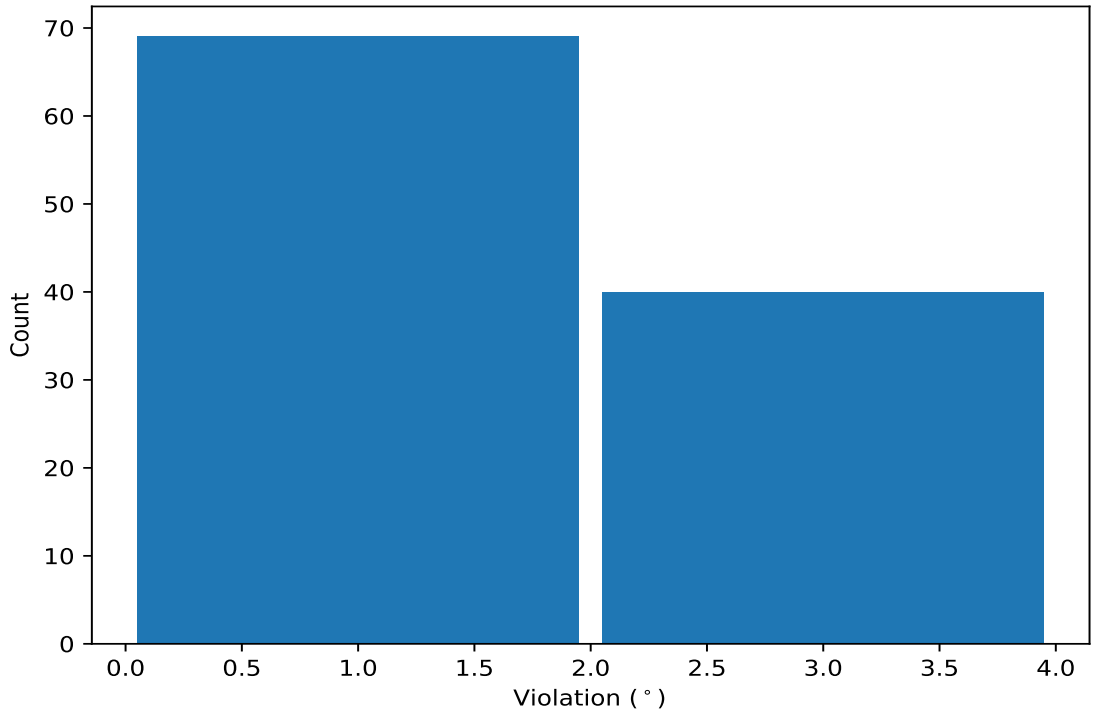
Key	Atom-1	Atom-2	Atom-3	Atom-4	Models[1]	Mean	SD[2]	Median
(1,170)	1:A:102:VAL:N	1:A:102:VAL:CA	1:A:102:VAL:C	1:A:103:GLU:N	20	2.67	0.16	2.7
(1,20)	1:A:13:ALA:N	1:A:13:ALA:CA	1:A:13:ALA:C	1:A:14:ALA:N	20	2.48	0.15	2.5
(1,169)	1:A:101:VAL:C	1:A:102:VAL:N	1:A:102:VAL:CA	1:A:102:VAL:C	19	1.45	0.16	1.4
(1,19)	1:A:12:VAL:C	1:A:13:ALA:N	1:A:13:ALA:CA	1:A:13:ALA:C	19	1.35	0.08	1.3
(1,103)	1:A:65:ASP:C	1:A:66:LEU:N	1:A:66:LEU:CA	1:A:66:LEU:C	12	1.29	0.18	1.3
(1,104)	1:A:66:LEU:N	1:A:66:LEU:CA	1:A:66:LEU:C	1:A:67:GLU:N	7	1.31	0.18	1.3
(1,105)	1:A:66:LEU:C	1:A:67:GLU:N	1:A:67:GLU:CA	1:A:67:GLU:C	4	1.4	0.25	1.35
(1,110)	1:A:69:TYR:N	1:A:69:TYR:CA	1:A:69:TYR:C	1:A:70:ALA:N	2	1.6	0.2	1.6
(1,107)	1:A:67:GLU:C	1:A:68:PRO:N	1:A:68:PRO:CA	1:A:68:PRO:C	2	1.4	0.3	1.4

[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 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.

Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,170)	1:A:102:VAL:N	1:A:102:VAL:CA	1:A:102:VAL:C	1:A:103:GLU:N	6	3.0
(1,170)	1:A:102:VAL:N	1:A:102:VAL:CA	1:A:102:VAL:C	1:A:103:GLU:N	5	2.8
(1,170)	1:A:102:VAL:N	1:A:102:VAL:CA	1:A:102:VAL:C	1:A:103:GLU:N	7	2.8
(1,170)	1:A:102:VAL:N	1:A:102:VAL:CA	1:A:102:VAL:C	1:A:103:GLU:N	9	2.8
(1,170)	1:A:102:VAL:N	1:A:102:VAL:CA	1:A:102:VAL:C	1:A:103:GLU:N	10	2.8
(1,170)	1:A:102:VAL:N	1:A:102:VAL:CA	1:A:102:VAL:C	1:A:103:GLU:N	13	2.8
(1,20)	1:A:13:ALA:N	1:A:13:ALA:CA	1:A:13:ALA:C	1:A:14:ALA:N	3	2.7
(1,20)	1:A:13:ALA:N	1:A:13:ALA:CA	1:A:13:ALA:C	1:A:14:ALA:N	7	2.7
(1,20)	1:A:13:ALA:N	1:A:13:ALA:CA	1:A:13:ALA:C	1:A:14:ALA:N	14	2.7
(1,170)	1:A:102:VAL:N	1:A:102:VAL:CA	1:A:102:VAL:C	1:A:103:GLU:N	1	2.7
(1,170)	1:A:102:VAL:N	1:A:102:VAL:CA	1:A:102:VAL:C	1:A:103:GLU:N	2	2.7
(1,170)	1:A:102:VAL:N	1:A:102:VAL:CA	1:A:102:VAL:C	1:A:103:GLU:N	8	2.7
(1,170)	1:A:102:VAL:N	1:A:102:VAL:CA	1:A:102:VAL:C	1:A:103:GLU:N	12	2.7
(1,170)	1:A:102:VAL:N	1:A:102:VAL:CA	1:A:102:VAL:C	1:A:103:GLU:N	18	2.7
(1,170)	1:A:102:VAL:N	1:A:102:VAL:CA	1:A:102:VAL:C	1:A:103:GLU:N	19	2.7
(1,170)	1:A:102:VAL:N	1:A:102:VAL:CA	1:A:102:VAL:C	1:A:103:GLU:N	20	2.7
(1,20)	1:A:13:ALA:N	1:A:13:ALA:CA	1:A:13:ALA:C	1:A:14:ALA:N	11	2.6
(1,20)	1:A:13:ALA:N	1:A:13:ALA:CA	1:A:13:ALA:C	1:A:14:ALA:N	12	2.6
(1,20)	1:A:13:ALA:N	1:A:13:ALA:CA	1:A:13:ALA:C	1:A:14:ALA:N	16	2.6
(1,20)	1:A:13:ALA:N	1:A:13:ALA:CA	1:A:13:ALA:C	1:A:14:ALA:N	20	2.6
(1,170)	1:A:102:VAL:N	1:A:102:VAL:CA	1:A:102:VAL:C	1:A:103:GLU:N	11	2.6

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,170)	1:A:102:VAL:N	1:A:102:VAL:CA	1:A:102:VAL:C	1:A:103:GLU:N	14	2.6
(1,170)	1:A:102:VAL:N	1:A:102:VAL:CA	1:A:102:VAL:C	1:A:103:GLU:N	16	2.6
(1,20)	1:A:13:ALA:N	1:A:13:ALA:CA	1:A:13:ALA:C	1:A:14:ALA:N	1	2.5
(1,20)	1:A:13:ALA:N	1:A:13:ALA:CA	1:A:13:ALA:C	1:A:14:ALA:N	4	2.5
(1,20)	1:A:13:ALA:N	1:A:13:ALA:CA	1:A:13:ALA:C	1:A:14:ALA:N	6	2.5
(1,20)	1:A:13:ALA:N	1:A:13:ALA:CA	1:A:13:ALA:C	1:A:14:ALA:N	9	2.5
(1,20)	1:A:13:ALA:N	1:A:13:ALA:CA	1:A:13:ALA:C	1:A:14:ALA:N	15	2.5
(1,170)	1:A:102:VAL:N	1:A:102:VAL:CA	1:A:102:VAL:C	1:A:103:GLU:N	15	2.5
(1,170)	1:A:102:VAL:N	1:A:102:VAL:CA	1:A:102:VAL:C	1:A:103:GLU:N	17	2.5
(1,20)	1:A:13:ALA:N	1:A:13:ALA:CA	1:A:13:ALA:C	1:A:14:ALA:N	8	2.4
(1,20)	1:A:13:ALA:N	1:A:13:ALA:CA	1:A:13:ALA:C	1:A:14:ALA:N	13	2.4
(1,20)	1:A:13:ALA:N	1:A:13:ALA:CA	1:A:13:ALA:C	1:A:14:ALA:N	17	2.4
(1,170)	1:A:102:VAL:N	1:A:102:VAL:CA	1:A:102:VAL:C	1:A:103:GLU:N	4	2.4
(1,20)	1:A:13:ALA:N	1:A:13:ALA:CA	1:A:13:ALA:C	1:A:14:ALA:N	5	2.3
(1,20)	1:A:13:ALA:N	1:A:13:ALA:CA	1:A:13:ALA:C	1:A:14:ALA:N	10	2.3
(1,20)	1:A:13:ALA:N	1:A:13:ALA:CA	1:A:13:ALA:C	1:A:14:ALA:N	19	2.3
(1,170)	1:A:102:VAL:N	1:A:102:VAL:CA	1:A:102:VAL:C	1:A:103:GLU:N	3	2.3
(1,20)	1:A:13:ALA:N	1:A:13:ALA:CA	1:A:13:ALA:C	1:A:14:ALA:N	2	2.2
(1,20)	1:A:13:ALA:N	1:A:13:ALA:CA	1:A:13:ALA:C	1:A:14:ALA:N	18	2.2
(1,106)	1:A:67:GLU:N	1:A:67:GLU:CA	1:A:67:GLU:C	1:A:68:PRO:N	3	1.9
(1,169)	1:A:101:VAL:C	1:A:102:VAL:N	1:A:102:VAL:CA	1:A:102:VAL:C	3	1.8
(1,110)	1:A:69:TYR:N	1:A:69:TYR:CA	1:A:69:TYR:C	1:A:70:ALA:N	3	1.8
(1,105)	1:A:66:LEU:C	1:A:67:GLU:N	1:A:67:GLU:CA	1:A:67:GLU:C	9	1.8
(1,169)	1:A:101:VAL:C	1:A:102:VAL:N	1:A:102:VAL:CA	1:A:102:VAL:C	17	1.7
(1,107)	1:A:67:GLU:C	1:A:68:PRO:N	1:A:68:PRO:CA	1:A:68:PRO:C	14	1.7
(1,169)	1:A:101:VAL:C	1:A:102:VAL:N	1:A:102:VAL:CA	1:A:102:VAL:C	2	1.6
(1,169)	1:A:101:VAL:C	1:A:102:VAL:N	1:A:102:VAL:CA	1:A:102:VAL:C	18	1.6
(1,104)	1:A:66:LEU:N	1:A:66:LEU:CA	1:A:66:LEU:C	1:A:67:GLU:N	14	1.6
(1,103)	1:A:65:ASP:C	1:A:66:LEU:N	1:A:66:LEU:CA	1:A:66:LEU:C	9	1.6
(1,19)	1:A:12:VAL:C	1:A:13:ALA:N	1:A:13:ALA:CA	1:A:13:ALA:C	10	1.5
(1,19)	1:A:12:VAL:C	1:A:13:ALA:N	1:A:13:ALA:CA	1:A:13:ALA:C	18	1.5
(1,169)	1:A:101:VAL:C	1:A:102:VAL:N	1:A:102:VAL:CA	1:A:102:VAL:C	6	1.5
(1,169)	1:A:101:VAL:C	1:A:102:VAL:N	1:A:102:VAL:CA	1:A:102:VAL:C	8	1.5
(1,169)	1:A:101:VAL:C	1:A:102:VAL:N	1:A:102:VAL:CA	1:A:102:VAL:C	14	1.5
(1,169)	1:A:101:VAL:C	1:A:102:VAL:N	1:A:102:VAL:CA	1:A:102:VAL:C	16	1.5
(1,169)	1:A:101:VAL:C	1:A:102:VAL:N	1:A:102:VAL:CA	1:A:102:VAL:C	19	1.5
(1,104)	1:A:66:LEU:N	1:A:66:LEU:CA	1:A:66:LEU:C	1:A:67:GLU:N	6	1.5
(1,103)	1:A:65:ASP:C	1:A:66:LEU:N	1:A:66:LEU:CA	1:A:66:LEU:C	11	1.5
(1,103)	1:A:65:ASP:C	1:A:66:LEU:N	1:A:66:LEU:CA	1:A:66:LEU:C	13	1.5
(1,103)	1:A:65:ASP:C	1:A:66:LEU:N	1:A:66:LEU:CA	1:A:66:LEU:C	17	1.5
(1,19)	1:A:12:VAL:C	1:A:13:ALA:N	1:A:13:ALA:CA	1:A:13:ALA:C	1	1.4
(1,19)	1:A:12:VAL:C	1:A:13:ALA:N	1:A:13:ALA:CA	1:A:13:ALA:C	3	1.4
(1,19)	1:A:12:VAL:C	1:A:13:ALA:N	1:A:13:ALA:CA	1:A:13:ALA:C	5	1.4
(1,19)	1:A:12:VAL:C	1:A:13:ALA:N	1:A:13:ALA:CA	1:A:13:ALA:C	8	1.4
(1,19)	1:A:12:VAL:C	1:A:13:ALA:N	1:A:13:ALA:CA	1:A:13:ALA:C	9	1.4
(1,19)	1:A:12:VAL:C	1:A:13:ALA:N	1:A:13:ALA:CA	1:A:13:ALA:C	13	1.4
(1,19)	1:A:12:VAL:C	1:A:13:ALA:N	1:A:13:ALA:CA	1:A:13:ALA:C	19	1.4
(1,169)	1:A:101:VAL:C	1:A:102:VAL:N	1:A:102:VAL:CA	1:A:102:VAL:C	4	1.4
(1,169)	1:A:101:VAL:C	1:A:102:VAL:N	1:A:102:VAL:CA	1:A:102:VAL:C	5	1.4
(1,169)	1:A:101:VAL:C	1:A:102:VAL:N	1:A:102:VAL:CA	1:A:102:VAL:C	7	1.4
(1,169)	1:A:101:VAL:C	1:A:102:VAL:N	1:A:102:VAL:CA	1:A:102:VAL:C	10	1.4

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,169)	1:A:101:VAL:C	1:A:102:VAL:N	1:A:102:VAL:CA	1:A:102:VAL:C	11	1.4
(1,169)	1:A:101:VAL:C	1:A:102:VAL:N	1:A:102:VAL:CA	1:A:102:VAL:C	20	1.4
(1,158)	1:A:96:PRO:N	1:A:96:PRO:CA	1:A:96:PRO:C	1:A:97:GLU:N	10	1.4
(1,110)	1:A:69:TYR:N	1:A:69:TYR:CA	1:A:69:TYR:C	1:A:70:ALA:N	4	1.4
(1,105)	1:A:66:LEU:C	1:A:67:GLU:N	1:A:67:GLU:CA	1:A:67:GLU:C	6	1.4
(1,104)	1:A:66:LEU:N	1:A:66:LEU:CA	1:A:66:LEU:C	1:A:67:GLU:N	9	1.4
(1,19)	1:A:12:VAL:C	1:A:13:ALA:N	1:A:13:ALA:CA	1:A:13:ALA:C	2	1.3
(1,19)	1:A:12:VAL:C	1:A:13:ALA:N	1:A:13:ALA:CA	1:A:13:ALA:C	4	1.3
(1,19)	1:A:12:VAL:C	1:A:13:ALA:N	1:A:13:ALA:CA	1:A:13:ALA:C	7	1.3
(1,19)	1:A:12:VAL:C	1:A:13:ALA:N	1:A:13:ALA:CA	1:A:13:ALA:C	11	1.3
(1,19)	1:A:12:VAL:C	1:A:13:ALA:N	1:A:13:ALA:CA	1:A:13:ALA:C	12	1.3
(1,19)	1:A:12:VAL:C	1:A:13:ALA:N	1:A:13:ALA:CA	1:A:13:ALA:C	15	1.3
(1,19)	1:A:12:VAL:C	1:A:13:ALA:N	1:A:13:ALA:CA	1:A:13:ALA:C	16	1.3
(1,19)	1:A:12:VAL:C	1:A:13:ALA:N	1:A:13:ALA:CA	1:A:13:ALA:C	17	1.3
(1,19)	1:A:12:VAL:C	1:A:13:ALA:N	1:A:13:ALA:CA	1:A:13:ALA:C	20	1.3
(1,169)	1:A:101:VAL:C	1:A:102:VAL:N	1:A:102:VAL:CA	1:A:102:VAL:C	1	1.3
(1,169)	1:A:101:VAL:C	1:A:102:VAL:N	1:A:102:VAL:CA	1:A:102:VAL:C	13	1.3
(1,105)	1:A:66:LEU:C	1:A:67:GLU:N	1:A:67:GLU:CA	1:A:67:GLU:C	14	1.3
(1,104)	1:A:66:LEU:N	1:A:66:LEU:CA	1:A:66:LEU:C	1:A:67:GLU:N	13	1.3
(1,103)	1:A:65:ASP:C	1:A:66:LEU:N	1:A:66:LEU:CA	1:A:66:LEU:C	1	1.3
(1,103)	1:A:65:ASP:C	1:A:66:LEU:N	1:A:66:LEU:CA	1:A:66:LEU:C	6	1.3
(1,103)	1:A:65:ASP:C	1:A:66:LEU:N	1:A:66:LEU:CA	1:A:66:LEU:C	12	1.3
(1,19)	1:A:12:VAL:C	1:A:13:ALA:N	1:A:13:ALA:CA	1:A:13:ALA:C	6	1.2
(1,169)	1:A:101:VAL:C	1:A:102:VAL:N	1:A:102:VAL:CA	1:A:102:VAL:C	15	1.2
(1,159)	1:A:96:PRO:C	1:A:97:GLU:N	1:A:97:GLU:CA	1:A:97:GLU:C	10	1.2
(1,104)	1:A:66:LEU:N	1:A:66:LEU:CA	1:A:66:LEU:C	1:A:67:GLU:N	12	1.2
(1,169)	1:A:101:VAL:C	1:A:102:VAL:N	1:A:102:VAL:CA	1:A:102:VAL:C	12	1.1
(1,138)	1:A:83:VAL:N	1:A:83:VAL:CA	1:A:83:VAL:C	1:A:84:PRO:N	20	1.1
(1,107)	1:A:67:GLU:C	1:A:68:PRO:N	1:A:68:PRO:CA	1:A:68:PRO:C	4	1.1
(1,105)	1:A:66:LEU:C	1:A:67:GLU:N	1:A:67:GLU:CA	1:A:67:GLU:C	8	1.1
(1,104)	1:A:66:LEU:N	1:A:66:LEU:CA	1:A:66:LEU:C	1:A:67:GLU:N	8	1.1
(1,104)	1:A:66:LEU:N	1:A:66:LEU:CA	1:A:66:LEU:C	1:A:67:GLU:N	18	1.1
(1,103)	1:A:65:ASP:C	1:A:66:LEU:N	1:A:66:LEU:CA	1:A:66:LEU:C	5	1.1
(1,103)	1:A:65:ASP:C	1:A:66:LEU:N	1:A:66:LEU:CA	1:A:66:LEU:C	14	1.1
(1,103)	1:A:65:ASP:C	1:A:66:LEU:N	1:A:66:LEU:CA	1:A:66:LEU:C	16	1.1
(1,103)	1:A:65:ASP:C	1:A:66:LEU:N	1:A:66:LEU:CA	1:A:66:LEU:C	18	1.1
(1,103)	1:A:65:ASP:C	1:A:66:LEU:N	1:A:66:LEU:CA	1:A:66:LEU:C	19	1.1