

Full wwPDB NMR Structure Validation Report (i)

Jan 11, 2024 – 04:22 PM JST

PDB ID : 8X1V BMRB ID : 36612

Title: NMR structure of a bimolecular parallel G-quadruplex formed by AAGGG

repeats from pathogenic RFC1 gene

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Deposited on : 2023-11-08

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:

Cyrange : Kirchner and Güntert (2011)

NmrClust : Kelley et al. (1996)

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)

 $\begin{array}{ccc} wwPDB\text{-ShiftChecker} &:& v1.2\\ BMRB \ Restraints \ Analysis &:& v1.2 \end{array}$

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

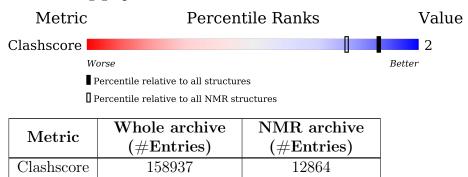
Validation Pipeline (wwPDB-VP) : 2.36

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 40%.

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.



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	12	8%	58%		25%	8%	
1	В	12	25%		67%		8%	



2 Ensemble composition and analysis (i)

This entry contains 10 models. This entry does not contain polypeptide chains, therefore identification of well-defined residues and clustering analysis are not possible. All residues are included in the validation scores.



3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 778 atoms, of which 268 are hydrogens and 0 are deuteriums.

• Molecule 1 is a DNA chain called DNA (5'-D(*AP*AP*GP*GP*GP*AP*AP*GP*GP*GP*AP*A)-3').

Mol	Chain	Residues		Atoms					Trace	
1	Λ	19	Total	С	Н	N	О	Р	0	
	12	389	120	134	60	64	11	0		
1	1 D	B	19	Total	С	Н	N	О	Р	0
	Б	В 12		120	134	60	64	11	U	

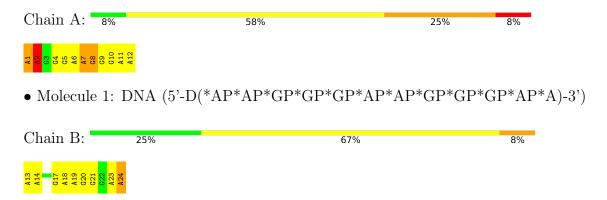


4 Residue-property plots (i)

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: DNA (5'-D(*AP*AP*GP*GP*GP*AP*AP*AP*GP*GP*GP*AP*A)-3')



4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

• Molecule 1: DNA (5'-D(*AP*AP*GP*GP*GP*AP*AP*AP*GP*GP*AP*A)-3')





4.2.2 Score per residue for model 2

• Molecule 1: DNA (5'-D(*AP*AP*GP*GP*GP*AP*AP*AP*GP*GP*GP*AP*A)-3')

Chain A: 17% 42% 33% 8%

A1 A2 G3 G4 G5 A6 A7 G8 G9 G10 A11

• Molecule 1: DNA (5'-D(*AP*AP*GP*GP*GP*AP*AP*AP*GP*GP*GP*AP*A)-3')

Chain B: 25% 67% 8%

A13 A14 A18 A18 A23 A23 A24

4.2.3 Score per residue for model 3

• Molecule 1: DNA (5'-D(*AP*AP*GP*GP*GP*AP*AP*AP*GP*GP*GP*AP*A)-3')

Chain A: 67% 25% 8%

A1 G3 G4 G5 A7 A7 G8 G9 G10 A11

• Molecule 1: DNA (5'-D(*AP*AP*GP*GP*GP*AP*AP*AP*GP*GP*GP*AP*A)-3')

Chain B: 33% 50% 17%

A13 A14 A18 A19 G20 G21 A23 A23

4.2.4 Score per residue for model 4

• Molecule 1: DNA (5'-D(*AP*AP*GP*GP*GP*AP*AP*AP*GP*GP*GP*AP*A)-3')

Chain A: 8% 50% 33% 8%

A12 A12 A12 A12 A12 A12

 \bullet Molecule 1: DNA (5'-D(*AP*AP*GP*GP*GP*AP*AP*AP*GP*GP*GP*AP*A)-3')

Chain B: 25% 58% 17%

A13 A14 A14 G16 G16 G17 A18 A19 G20 G21 G21 A23 A23



4.2.5 Score per residue for model 5

• Molecule 1: DNA (5'-D(*AP*AP*GP*GP*GP*AP*AP*AP*GP*GP*AP*A)-3')

Chain A: 8% 58% 25% 8%

A1 A2 G4 G5 A6 A7 G10 G10 A11

• Molecule 1: DNA (5'-D(*AP*AP*GP*GP*GP*AP*AP*AP*GP*GP*GP*AP*A)-3')

Chain B: 25% 33% 42%

A13 A14 G20 G20 G21 A23 A23

4.2.6 Score per residue for model 6

 \bullet Molecule 1: DNA (5'-D(*AP*AP*GP*GP*GP*AP*AP*AP*GP*GP*GP*AP*A)-3')

Chain A: 58% 33% 8%

A1 G3 G4 G5 A6 A7 G9 G10 A11

• Molecule 1: DNA (5'-D(*AP*AP*GP*GP*GP*AP*AP*AP*GP*GP*GP*AP*A)-3')

Chain B: 17% 67% 17%

A13 A14 A18 A19 G20 G21 G22 A23 A23

4.2.7 Score per residue for model 7

 \bullet Molecule 1: DNA (5'-D(*AP*AP*GP*GP*GP*AP*AP*AP*GP*GP*GP*AP*A)-3')

Chain A: 8% 50% 8%

A12 A6 A7 A7 A7 G9 G9 G9 G10 A11

 \bullet Molecule 1: DNA (5'-D(*AP*AP*GP*GP*GP*AP*AP*AP*GP*GP*GP*AP*A)-3')

Chain B: 25% 67% 8%

A13 A14 A14 A18 A19 G20 G21 G22 A23 A23



4.2.8 Score per residue for model 8

• Molecule 1: DNA (5'-D(*AP*AP*GP*GP*GP*AP*AP*AP*GP*GP*AP*A)-3')

Chain A: 8% 67% 17% 8%

A1 A2 G3 G4 G5 A6 A7 G8 G9 G10 G10 A11

• Molecule 1: DNA (5'-D(*AP*AP*GP*GP*GP*AP*AP*AP*GP*GP*GP*AP*A)-3')

Chain B: 50% 42% 8%

A13 A18 G20 G21 G22 A23 A23

4.2.9 Score per residue for model 9

• Molecule 1: DNA (5'-D(*AP*AP*GP*GP*GP*AP*AP*AP*GP*GP*GP*AP*A)-3')

Chain A: 17% 50% 25% 8%

A1 A2 G3 G4 G5 A6 A7 G8 G9 G10 A11

• Molecule 1: DNA (5'-D(*AP*AP*GP*GP*GP*AP*AP*AP*GP*GP*GP*AP*A)-3')

Chain B: 25% 50% 25%

A13 A14 G17 A18 A19 G20 G21 G21 A23 A23

4.2.10 Score per residue for model 10

• Molecule 1: DNA (5'-D(*AP*AP*GP*GP*GP*AP*AP*AP*GP*GP*GP*AP*A)-3')

Chain A: 17% 25% 50% 8%



 \bullet Molecule 1: DNA (5'-D(*AP*AP*GP*GP*GP*AP*AP*AP*GP*GP*GP*AP*A)-3')

Chain B: 25% 67% 8%





5 Refinement protocol and experimental data overview (i)

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

Of the 500 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
Amber	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	196
Number of shifts mapped to atoms	196
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	40%



6 Model quality (i)

6.1 Standard geometry (i)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with |Z| > 5 is considered an outlier worth inspection. RMSZ is the (average) root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	В	Sond lengths	Bond angles		
		RMSZ	#Z>5	RMSZ	#Z>5	
1	A	1.39 ± 0.02	$0\pm0/290~(~0.0\pm~0.0\%)$	2.32 ± 0.06	$20\pm4/448$ ($4.4\pm$ 0.9%)	
1	В	1.37 ± 0.02	$0\pm0/290~(~0.0\pm~0.0\%)$	2.10 ± 0.08	14±3/448 (3.2± 0.7%)	
All	All	1.38	0/5800 (0.0%)	2.22	341/8960 (3.8%)	

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

Mol	Chain	Chirality	Planarity
1	A	0.0 ± 0.0	5.5 ± 1.4
1	В	0.0 ± 0.0	2.6 ± 0.7
All	All	0	81

There are no bond-length outliers.

All unique angle outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mal	Chain	Dag	Trino	Atoma	\mathbf{Z}	Observed(0)	Ideal(0)	Mod	dels
Mol	Chain	Res	Type	Atoms		$Observed(^o)$	$\operatorname{Ideal}({}^{o})$	Worst	Total
1	A	8	DG	O4'-C1'-N9	12.32	116.62	108.00	2	10
1	A	7	DA	N1-C6-N6	-10.61	112.23	118.60	1	8
1	В	20	DG	O4'-C1'-N9	10.47	115.33	108.00	1	10
1	A	10	DG	O4'-C1'-N9	10.42	115.29	108.00	10	10
1	A	6	DA	N1-C6-N6	-10.19	112.48	118.60	8	9
1	В	13	DA	O4'-C1'-N9	10.09	115.06	108.00	10	10
1	A	1	DA	O4'-C1'-N9	9.92	114.95	108.00	8	10
1	В	17	DG	O4'-C1'-N9	9.42	114.60	108.00	7	6
1	A	11	DA	O4'-C1'-N9	9.14	114.40	108.00	5	7
1	A	5	DG	O4'-C1'-N9	8.49	113.94	108.00	9	8
1	В	24	DA	N1-C6-N6	-7.95	113.83	118.60	1	7
1	В	23	DA	O4'-C1'-C2'	-7.76	99.69	105.90	8	10
1	В	14	DA	N1-C6-N6	-7.68	113.99	118.60	1	8

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Mal	Chain	Dog	Treno		Z	Observed(0)	Ideal(0)	Mod	dels
Mol	Chain	Res	Type	Atoms		$Observed(^o)$	$Ideal(^{o})$	Worst	Total
1	A	1	DA	N1-C6-N6	-7.58	114.06	118.60	1	10
1	В	14	DA	O4'-C1'-N9	7.57	113.30	108.00	6	1
1	A	12	DA	N1-C6-N6	-7.54	114.08	118.60	1	3
1	A	2	DA	N1-C6-N6	-7.43	114.14	118.60	1	10
1	В	13	DA	N1-C6-N6	-7.39	114.16	118.60	1	10
1	В	18	DA	O4'-C1'-N9	7.35	113.15	108.00	7	2
1	A	7	DA	C5-C6-N1	7.04	121.22	117.70	1	9
1	A	11	DA	N1-C6-N6	-6.90	114.46	118.60	1	10
1	A	7	DA	O4'-C1'-N9	6.84	112.79	108.00	1	8
1	В	19	DA	O4'-C1'-N9	6.84	112.79	108.00	10	6
1	A	7	DA	C4-C5-C6	-6.76	113.62	117.00	1	3
1	A	6	DA	C5-C6-N1	6.67	121.04	117.70	1	9
1	В	23	DA	N1-C6-N6	-6.53	114.68	118.60	1	10
1	A	1	DA	C5-C6-N1	6.50	120.95	117.70	1	10
1	A	3	DG	O4'-C1'-N9	6.49	112.54	108.00	1	1
1	В	18	DA	C5-C6-N1	6.46	120.93	117.70	1	9
1	A	6	DA	C4-C5-C6	-6.33	113.84	117.00	8	7
1	В	23	DA	O4'-C1'-N9	6.25	112.37	108.00	8	7
1	В	23	DA	C1'-O4'-C4'	-6.23	103.87	110.10	5	8
1	В	19	DA	C5-C6-N1	6.14	120.77	117.70	1	7
1	A	1	DA	C1'-O4'-C4'	-6.07	104.03	110.10	1	7
1	A	12	DA	C4-C5-C6	-6.04	113.98	117.00	1	1
1	A	12	DA	C5-C6-N1	5.94	120.67	117.70	1	6
1	В	17	DG	C1'-O4'-C4'	-5.87	104.23	110.10	7	7
1	A	11	DA	C5-C6-N1	5.83	120.62	117.70	1	4
1	В	13	DA	C5-C6-N1	5.70	120.55	117.70	1	7
1	В	23	DA	C5-C6-N1	5.69	120.55	117.70	1	1
1	В	23	DA	C4-C5-C6	-5.58	114.21	117.00	1	1
1	A	2	DA	O4'-C1'-N9	5.57	111.90	108.00	3	5
1	A	3	DG	P-O3'-C3'	5.53	126.34	119.70	8	2
1	В	24	DA	C5-C6-N1	5.49	120.45	117.70	1	2
1	A	11	DA	O4'-C1'-C2'	-5.49	101.51	105.90	4	1
1	В	14	DA	O4'-C1'-C2'	-5.47	101.52	105.90	4	1
1	A	1	DA	C4-C5-C6	-5.47	114.26	117.00	1	1
1	A	11	DA	P-O3'-C3'	5.47	126.27	119.70	1	1
1	В	24	DA	C4-C5-C6	-5.44	114.28	117.00	1	1
1	A	11	DA	C4-C5-C6	-5.41	114.30	117.00	1	2
1	A	4	DG	N3-C4-C5	-5.39	125.91	128.60	4	2
1	A	9	DG	C5-C6-N1	5.37	114.19	111.50	4	5
1	В	13	DA	O4'-C1'-C2'	-5.33	101.64	105.90	8	1
1	В	20	DG	N3-C2-N2	-5.32	116.18	119.90	1	1

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Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$\mathrm{Ideal}(^{o})$	Mod	dels
IVIOI	Chain	nes	Type	Atoms	L	Observed()	ideai()	Worst	Total
1	A	10	DG	O4'-C1'-C2'	-5.29	101.67	105.90	9	1
1	В	18	DA	P-O3'-C3'	5.25	126.00	119.70	3	3
1	A	7	DA	O4'-C4'-C3'	5.23	109.14	106.00	4	3
1	A	10	DG	C1'-O4'-C4'	-5.22	104.88	110.10	7	4
1	A	2	DA	C8-N9-C4	-5.20	103.72	105.80	1	1
1	A	10	DG	N3-C2-N2	-5.20	116.26	119.90	3	2
1	В	24	DA	O4'-C1'-N9	5.19	111.63	108.00	6	1
1	A	12	DA	O4'-C1'-N9	5.16	111.61	108.00	7	2
1	A	8	DG	C5-C6-N1	5.15	114.07	111.50	1	1
1	В	18	DA	C4-C5-C6	-5.14	114.43	117.00	1	1
1	В	14	DA	C5-C6-N1	5.14	120.27	117.70	1	1
1	A	2	DA	C4-C5-C6	-5.13	114.43	117.00	5	2
1	В	14	DA	C4-C5-C6	-5.13	114.43	117.00	1	2
1	A	6	DA	C6-C5-N7	5.10	135.87	132.30	8	1
1	A	3	DG	N3-C2-N2	-5.09	116.33	119.90	6	1
1	В	16	DG	O4'-C1'-N9	5.09	111.56	108.00	4	1
1	В	21	DG	N3-C2-N2	-5.05	116.36	119.90	6	1
1	A	2	DA	C5-C6-N1	5.03	120.22	117.70	1	1

There are no chirality outliers.

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

Mol	Chain	Res	Type	Group	Models (Total)
1	A	2	DA	Sidechain	10
1	В	24	DA	Sidechain	10
1	A	9	DG	Sidechain	9
1	A	4	DG	Sidechain	8
1	A	7	DA	Sidechain	8
1	В	21	DG	Sidechain	6
1	A	8	DG	Sidechain	6
1	A	6	DA	Sidechain	4
1	A	12	DA	Sidechain	4
1	В	22	DG	Sidechain	4
1	В	18	DA	Sidechain	3
1	A	11	DA	Sidechain	2
1	В	19	DA	Sidechain	2
1	A	10	DG	Sidechain	2
1	A	3	DG	Sidechain	1
1	A	5	DG	Sidechain	1
1	В	14	DA	Sidechain	1



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	255	134	134	1±0
1	В	255	134	134	0±1
All	All	5100	2680	2680	15

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 2.

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

Atom-1	Atom-2	Clash(Å)	$\mathbf{Distance}(\mathbf{\mathring{A}})$	Mod	${f Models}$	
Atom-1	Atom-2	Clash(A)	Distance(A)	Worst	Total	
1:A:1:DA:H1'	1:A:2:DA:C4	0.56	2.36	3	10	
1:B:13:DA:H1'	1:B:14:DA:C4	0.46	2.46	5	4	
1:B:13:DA:C4	1:B:14:DA:C2	0.40	3.09	1	1	

6.3 Torsion angles (i)

6.3.1 Protein backbone (i)

There are no protein molecules in this entry.

6.3.2 Protein sidechains (i)

There are no protein molecules in this entry.

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 40% for the well-defined parts and 40% for the entire structure.

7.1 Chemical shift list 1

File name: working cs.cif

Chemical shift list name: starch_output

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	196
Number of shifts mapped to atoms	196
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)

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

7.1.3 Completeness of resonance assignments (i)

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 40%, i.e. 196 atoms were assigned a chemical shift out of a possible 492. 0 out of 0 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^{1}\mathbf{H}$	$^{13}\mathbf{C}$	$^{15}{ m N}$
Sugar	148/288 (51%)	148/168 (88%)	0/120 (0%)	0/0 (%)
Base	48/204 (24%)	$48/132 \ (36\%)$	0/36~(0%)	0/36 (0%)
Overall	196/492 (40%)	196/300 (65%)	0/156 (0%)	0/36 (0%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 40%, i.e. 196 atoms were assigned a chemical shift out of a possible 492. 0 out of 0 assigned methyl groups (LEU and VAL) were assigned stereospecifically.



	Total	$^{1}{ m H}$	$^{13}\mathbf{C}$	$^{15}{ m N}$
Sugar	148/288 (51%)	148/168 (88%)	0/120 (0%)	0/0 (%)
Base	48/204 (24%)	48/132 (36%)	0/36 (0%)	0/36 (0%)
Overall	196/492 (40%)	196/300~(65%)	0/156~(0%)	0/36 (0%)

7.1.4 Statistically unusual chemical shifts (i)

There are no statistically unusual chemical shifts.

7.1.5 Random Coil Index (RCI) plots (i)

No random coil index(RCI) plot could be generated from the current chemical shift list. RCI is only applicable to proteins



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	276
Intra-residue ($ i-j =0$)	138
Sequential ($ i-j =1$)	82
Medium range ($ i-j >1$ and $ i-j <5$)	8
Long range (i-j ≥5)	12
Inter-chain	12
Hydrogen bond restraints	24
Disulfide bond restraints	0
Total dihedral-angle restraints	100
Number of unmapped restraints	0
Number of restraints per residue	15.7
Number of long range restraints per residue ¹	1.0

¹Long 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)	1.6	0.19
0.2-0.5 (Medium)	None	None
>0.5 (Large)	None	None



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

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

Bins $(^{\circ})$	Average number of violations per model	$\operatorname{Max}(^{\circ})$
1.0-10.0 (Small)	0.1	1.2
10.0-20.0 (Medium)	None	None
>20.0 (Large)	None	None



9 Distance violation analysis (i)

9.1 Summary of distance violations (i)

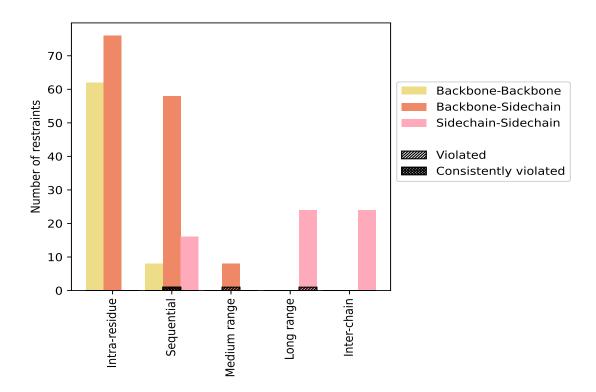
The following table shows the summary of distance violations in different restraint categories based on the sequence separation of the atoms involved. Each category is further sub-divided into three sub-categories based on the atoms involved. Violations less than 0.1 Å are not included in the statistics.

Donton into topo o	Commit	% ¹	Vic	olated ⁵	3	Consis	tentl	y Violated ⁴
Restraints type	Count	70	Count	$\%^2$	$ \%^1$	Count	$ \%^2$	$\%^1$
Intra-residue (i-j =0)	138	50.0	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	62	22.5	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	76	27.5	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)	82	29.7	1	1.2	0.4	1	1.2	0.4
Backbone-Backbone	8	2.9	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	58	21.0	1	1.7	0.4	1	1.7	0.4
Sidechain-Sidechain	16	5.8	0	0.0	0.0	0	0.0	0.0
Medium range ($ i-j >1 \& i-j <5$)	8	2.9	1	12.5	0.4	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	8	2.9	1	12.5	0.4	0	0.0	0.0
Sidechain-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Long range ($ i-j \ge 5$)	12	4.3	1	8.3	0.4	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	12	4.3	1	8.3	0.4	0	0.0	0.0
Inter-chain	12	4.3	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	12	4.3	0	0.0	0.0	0	0.0	0.0
Hydrogen bond	24	8.7	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	276	100.0	3	1.1	1.1	1	0.4	0.4
Backbone-Backbone	70	25.4	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	142	51.4	2	1.4	0.7	1	0.7	0.4
Sidechain-Sidechain	64	23.2	1	1.6	0.4	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.

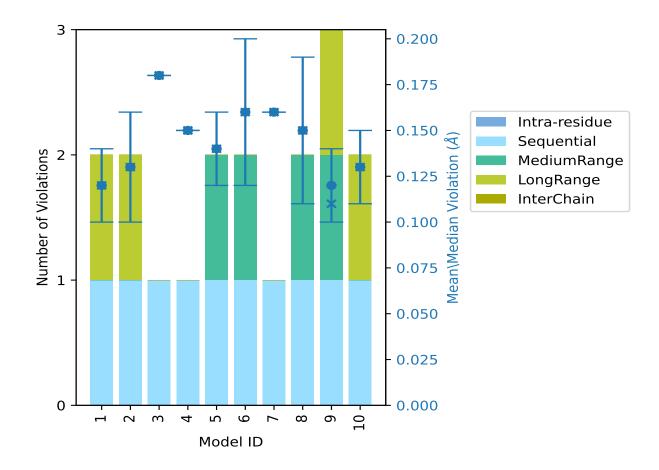
Model ID	IR^1	Nun SQ ²	nber o	f viola	${f tions}$	Total	Mean (Å)	Max (Å)	\mathbf{SD}^6 (Å)	Median (Å)
1	0	1	0	1	0	2	0.12	0.14	0.02	0.12
2	0	1	0	1	0	2	0.13	0.16	0.03	0.13
3	0	1	0	0	0	1	0.18	0.18	0.0	0.18
4	0	1	0	0	0	1	0.15	0.15	0.0	0.15
5	0	1	1	0	0	2	0.14	0.15	0.02	0.14
6	0	1	1	0	0	2	0.16	0.19	0.04	0.16
7	0	1	0	0	0	1	0.16	0.16	0.0	0.16
8	0	1	1	0	0	2	0.15	0.19	0.04	0.15
9	0	1	1	1	0	3	0.12	0.15	0.02	0.11
10	0	1	0	1	0	2	0.13	0.15	0.02	0.13

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



⁵Inter-chain restraints, ⁶Standard 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, 249(IR:138, SQ:81, MR:7, LR:11, IC:12) restraints are not violated in the ensemble.

Nu	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	10.0		
0	0	0	0	0	0	2	20.0		
0	0	0	0	0	0	3	30.0		
0	0	1	1	0	2	4	40.0		

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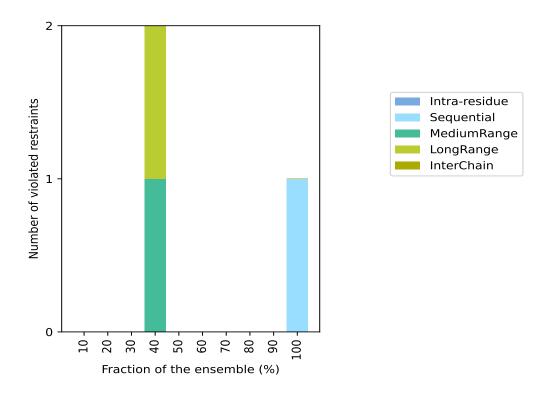


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Nu	mber	of vio	lated	Fraction of the ensemble			
IR^1	SQ^2	MR^3	LR^4	IC^5	Total	Count ⁶	%
0	0	0	0	0	0	5	50.0
0	0	0	0	0	0	6	60.0
0	0	0	0	0	0	7	70.0
0	0	0	0	0	0	8	80.0
0	0	0	0	0	0	9	90.0
0	1	0	0	0	1	10	100.0

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

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

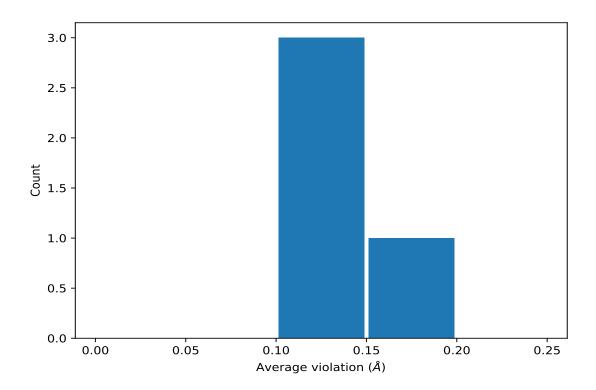


9.4 Most violated distance restraints in the ensemble (i)

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	${f Models}^1$	Mean (Å)	${ m SD}^1\ (m \AA)$	Median (Å)
(1,117)	1:1:A:DA:H3'	1:2:A:DA:H8	10	0.16	0.02	0.16
(1,245)	1:18:B:DA:H2	1:20:B:DG:H2'	4	0.11	0.01	0.12
(1,245)	1:18:B:DA:H2	1:20:B:DG:H2"	4	0.11	0.01	0.12
(1,11)	1:16:B:DG:H1	1:21:B:DG:H8	4	0.11	0.0	0.11

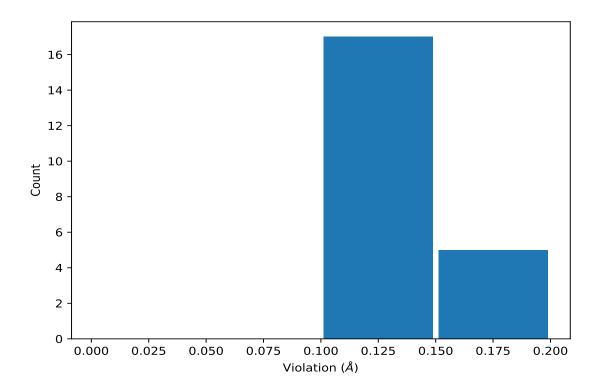
¹Number of violated models, ²Standard deviation

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)
(1,117)	1:1:A:DA:H3'	1:2:A:DA:H8	6	0.19
(1,117)	1:1:A:DA:H3'	1:2:A:DA:H8	8	0.19
(1,117)	1:1:A:DA:H3'	1:2:A:DA:H8	3	0.18
(1,117)	1:1:A:DA:H3'	1:2:A:DA:H8	2	0.16
(1,117)	1:1:A:DA:H3'	1:2:A:DA:H8	7	0.16
(1,117)	1:1:A:DA:H3'	1:2:A:DA:H8	4	0.15
(1,117)	1:1:A:DA:H3'	1:2:A:DA:H8	5	0.15
(1,117)	1:1:A:DA:H3'	1:2:A:DA:H8	9	0.15
(1,117)	1:1:A:DA:H3'	1:2:A:DA:H8	10	0.15
(1,117)	1:1:A:DA:H3'	1:2:A:DA:H8	1	0.14
(1,245)	1:18:B:DA:H2	1:20:B:DG:H2'	5	0.12
(1,245)	1:18:B:DA:H2	1:20:B:DG:H2"	5	0.12
(1,245)	1:18:B:DA:H2	1:20:B:DG:H2'	6	0.12
(1,245)	1:18:B:DA:H2	1:20:B:DG:H2"	6	0.12
(1,245)	1:18:B:DA:H2	1:20:B:DG:H2'	9	0.11
(1,245)	1:18:B:DA:H2	1:20:B:DG:H2"	9	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,11)	1:16:B:DG:H1	1:21:B:DG:H8	1	0.11
(1,11)	1:16:B:DG:H1	1:21:B:DG:H8	9	0.11
(1,11)	1:16:B:DG:H1	1:21:B:DG:H8	10	0.11
(1,245)	1:18:B:DA:H2	1:20:B:DG:H2'	8	0.1
(1,245)	1:18:B:DA:H2	1:20:B:DG:H2"	8	0.1
(1,11)	1:16:B:DG:H1	1:21:B:DG:H8	2	0.1



10 Dihedral-angle violation analysis (i)

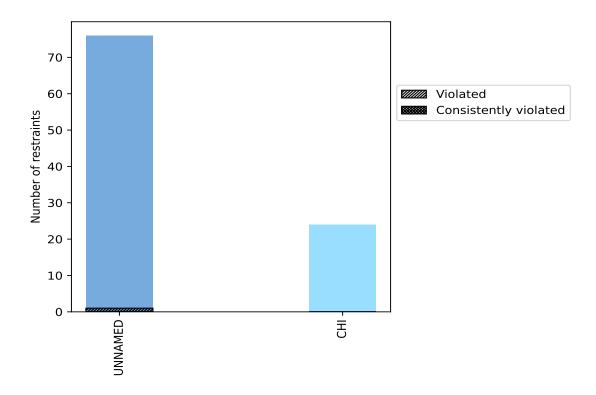
10.1 Summary of dihedral-angle violations (i)

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 true	Count	$\%^{1}$	${f Violated^3}$			Consistently Violated ⁴		
Angle type	Count	70	Count	$\%^2$	$\%^1$	Count	$\%^2$	$\%^1$
UNNAMED	76	76.0	1	1.3	1.0	0	0.0	0.0
CHI	24	24.0	0	0.0	0.0	0	0.0	0.0
Total	100	100.0	1	1.0	1.0	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 (i)



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

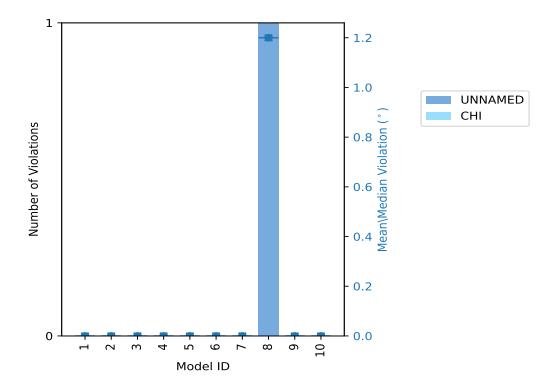


10.2 Dihedral-angle violation statistics for each model (i)

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 (°)	Modion (°)
Wiodei 1D	UNNAMED	CHI	Total	Mean ()	Max ()	SD ()	$ \text{Median } (^{\circ}) $
1	0	0	0	0.0	0.0	0.0	0.0
2	0	0	0	0.0	0.0	0.0	0.0
3	0	0	0	0.0	0.0	0.0	0.0
4	0	0	0	0.0	0.0	0.0	0.0
5	0	0	0	0.0	0.0	0.0	0.0
6	0	0	0	0.0	0.0	0.0	0.0
7	0	0	0	0.0	0.0	0.0	0.0
8	1	0	1	1.2	1.2	0.0	1.2
9	0	0	0	0.0	0.0	0.0	0.0
10	0	0	0	0.0	0.0	0.0	0.0

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



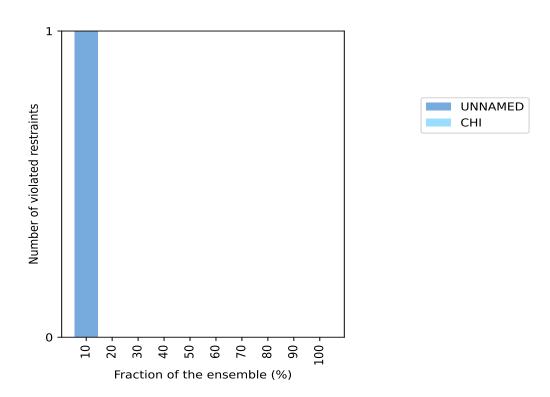
10.3 Dihedral-angle violation statistics for the ensemble (i)

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	violat	ed restraints	Fraction of the ensemble			
UNNAMED	CHI	Total	$Count^1$	%		
1	0	1	1	10.0		
0	0	0	2	20.0		
0	0	0	3	30.0		
0	0	0	4	40.0		
0	0	0	5	50.0		
0	0	0	6	60.0		
0	0	0	7	70.0		
0	0	0	8	80.0		
0	0	0	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 (i)

No violations found

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.

Data insufficient to plot histogram

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 (°)
(1,100)	1:16:B:DG:H1'	1:16:B:DG:C1'	1:16:B:DG:C2'	1:16:B:DG:H2'	8	1.2

