wwPDB NMR Structure Validation Summary Report

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EMDB ID	:	EMD-2324
BMRB ID	:	19157
Title	:	Atomic-resolution structure of a quadruplet cross-beta amyloid fibril.
Authors	:	Fitzpatrick, A.W.P.; Debelouchina, G.T.; Bayro, M.J.; Clare, D.K.; Caporini, M.A.; Bajaj, V.S.; Jaroniec, C.P.; Wang, L.; Ladizhansky, V.; Muller, S.A.; MacPhee, C.E.; Waudby, C.A.; Mott, H.R.; de Simone, A.; Knowles, T.P.J.; Saibil, H.R.; Vendruscolo, M.; Orlova, E.V.; Griffin, R.G.; Dobson, C.M.
Deposited on	:	2013-02-28

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:

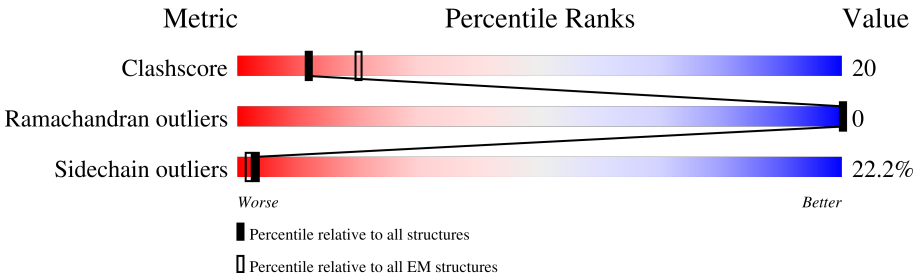
EMDB validation analysis	:	NOT EXECUTED
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	NOT EXECUTED
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.33

1 Overall quality at a glance

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

The overall completeness of chemical shifts assignment is 3%.

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	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	11	55% 36% 9%
1	B	11	55% 36% 9%
1	C	11	55% 27% 18%
1	D	11	55% 36% 9%
1	E	11	55% 27% 18%
1	F	11	64% 27% 9%
1	G	11	55% 36% 9%
1	H	11	64% 27% 9%
1	I	11	55% 27% 18%

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Mol	Chain	Length	Quality of chain
1	J	11	55% 36% 9%
1	K	11	55% 36% 9%
1	L	11	55% 36% 9%
1	M	11	55% 36% 9%
1	N	11	55% 36% 9%
1	O	11	55% 36% 9%
1	P	11	64% 27% 9%

2 Ensemble composition and analysis (i)

This entry contains 1 models. Identification of well-defined residues and clustering analysis are not possible.

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 2752 atoms, of which 1392 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called TRANSTHYRETIN.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	11	Total	C	H	N	O	0	
			172	57	87	11	17		
1	B	11	Total	C	H	N	O	0	
			172	57	87	11	17		
1	C	11	Total	C	H	N	O	0	
			172	57	87	11	17		
1	D	11	Total	C	H	N	O	0	
			172	57	87	11	17		
1	E	11	Total	C	H	N	O	0	
			172	57	87	11	17		
1	F	11	Total	C	H	N	O	0	
			172	57	87	11	17		
1	G	11	Total	C	H	N	O	0	
			172	57	87	11	17		
1	H	11	Total	C	H	N	O	0	
			172	57	87	11	17		
1	I	11	Total	C	H	N	O	0	
			172	57	87	11	17		
1	J	11	Total	C	H	N	O	0	
			172	57	87	11	17		
1	K	11	Total	C	H	N	O	0	
			172	57	87	11	17		
1	L	11	Total	C	H	N	O	0	
			172	57	87	11	17		
1	M	11	Total	C	H	N	O	0	
			172	57	87	11	17		
1	N	11	Total	C	H	N	O	0	
			172	57	87	11	17		
1	O	11	Total	C	H	N	O	0	
			172	57	87	11	17		
1	P	11	Total	C	H	N	O	0	
			172	57	87	11	17		

4 Residue-property plots (i)

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: TRANSTHYRETIN

Chain A:

• Molecule 1: TRANSTHYRETIN

Chain B:

• Molecule 1: TRANSTHYRETIN

Chain C:

• Molecule 1: TRANSTHYRETIN

Chain D:

• Molecule 1: TRANSTHYRETIN

Chain E:

• Molecule 1: TRANSTHYRETIN

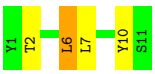
Chain F:

• Molecule 1: TRANSTHYRETIN

Chain G:

• Molecule 1: TRANSTHYRETIN

Chain H:



• Molecule 1: TRANSTHYRETIN

Chain I:

• Molecule 1: TRANSTHYRETIN

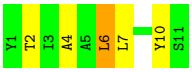
Chain J:

• Molecule 1: TRANSTHYRETIN

Chain K:

• Molecule 1: TRANSTHYRETIN

Chain L:



• Molecule 1: TRANSTHYRETIN

Chain M:

• Molecule 1: TRANSTHYRETIN

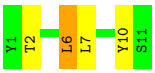
Chain N:

• Molecule 1: TRANSTHYRETIN

Chain O:

• Molecule 1: TRANSTHYRETIN

Chain P:



5 Refinement protocol and experimental data overview

Of the ? calculated structures, 1 were deposited, based on the following criterion: *?*.

The authors did not provide any information on software used for structure solution, optimization or refinement.

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

Chemical shift file(s)	working_cs.cif
Number of chemical shift lists	1
Total number of shifts	66
Number of shifts mapped to atoms	66
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	3%

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

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

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	85	87	87	5
1	B	85	87	87	6
1	C	85	87	87	7
1	D	85	87	87	7
1	E	85	87	87	6
1	F	85	87	87	6
1	G	85	87	87	5
1	H	85	87	87	6
1	I	85	87	87	6
1	J	85	87	87	6
1	K	85	87	87	6
1	L	85	87	87	7
1	M	85	87	87	6
1	N	85	87	87	7
1	O	85	87	87	5
1	P	85	87	87	6
All	All	1360	1392	1392	54

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 20.

5 of 54 clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)
1:E:3:ILE:HD11	1:F:10:TYR:OH	0.57	2.00
1:M:3:ILE:HD11	1:N:10:TYR:OH	0.57	2.00
1:K:3:ILE:HD11	1:L:10:TYR:OH	0.56	2.00
1:C:3:ILE:HD11	1:D:10:TYR:OH	0.56	2.00
1:G:3:ILE:HD11	1:H:10:TYR:OH	0.56	2.01

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	9/11 (82%)	9 (100%)	0 (0%)	0 (0%)	100	100
1	B	9/11 (82%)	9 (100%)	0 (0%)	0 (0%)	100	100
1	C	9/11 (82%)	9 (100%)	0 (0%)	0 (0%)	100	100
1	D	9/11 (82%)	9 (100%)	0 (0%)	0 (0%)	100	100
1	E	9/11 (82%)	9 (100%)	0 (0%)	0 (0%)	100	100
1	F	9/11 (82%)	9 (100%)	0 (0%)	0 (0%)	100	100
1	G	9/11 (82%)	9 (100%)	0 (0%)	0 (0%)	100	100
1	H	9/11 (82%)	9 (100%)	0 (0%)	0 (0%)	100	100
1	I	9/11 (82%)	9 (100%)	0 (0%)	0 (0%)	100	100
1	J	9/11 (82%)	9 (100%)	0 (0%)	0 (0%)	100	100
1	K	9/11 (82%)	9 (100%)	0 (0%)	0 (0%)	100	100
1	L	9/11 (82%)	9 (100%)	0 (0%)	0 (0%)	100	100
1	M	9/11 (82%)	9 (100%)	0 (0%)	0 (0%)	100	100
1	N	9/11 (82%)	9 (100%)	0 (0%)	0 (0%)	100	100
1	O	9/11 (82%)	9 (100%)	0 (0%)	0 (0%)	100	100
1	P	9/11 (82%)	9 (100%)	0 (0%)	0 (0%)	100	100
All	All	144/176 (82%)	144 (100%)	0 (0%)	0 (0%)	100	100

There are no Ramachandran outliers.

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	9/9 (100%)	7 (78%)	2 (22%)	3	30
1	B	9/9 (100%)	7 (78%)	2 (22%)	3	30
1	C	9/9 (100%)	7 (78%)	2 (22%)	3	30
1	D	9/9 (100%)	7 (78%)	2 (22%)	3	30
1	E	9/9 (100%)	7 (78%)	2 (22%)	3	30
1	F	9/9 (100%)	7 (78%)	2 (22%)	3	30
1	G	9/9 (100%)	7 (78%)	2 (22%)	3	30
1	H	9/9 (100%)	7 (78%)	2 (22%)	3	30
1	I	9/9 (100%)	7 (78%)	2 (22%)	3	30
1	J	9/9 (100%)	7 (78%)	2 (22%)	3	30
1	K	9/9 (100%)	7 (78%)	2 (22%)	3	30
1	L	9/9 (100%)	7 (78%)	2 (22%)	3	30
1	M	9/9 (100%)	7 (78%)	2 (22%)	3	30
1	N	9/9 (100%)	7 (78%)	2 (22%)	3	30
1	O	9/9 (100%)	7 (78%)	2 (22%)	3	30
1	P	9/9 (100%)	7 (78%)	2 (22%)	3	30
All	All	144/144 (100%)	112 (78%)	32 (22%)	3	30

5 of 32 residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type
1	A	6	LEU
1	A	7	LEU
1	B	6	LEU
1	B	7	LEU
1	C	6	LEU

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

The completeness of assignment taking into account all chemical shift lists is 3% for the well-defined parts and 3% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *assigned_chemical_shifts_1*

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	66
Number of shifts mapped to atoms	66
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	1

7.1.2 Chemical shift referencing

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

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 3%, i.e. 63 atoms were assigned a chemical shift out of a possible 2320. 0 out of 32 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	31/848 (4%)	0/336 (0%)	22/352 (6%)	9/160 (6%)
Sidechain	22/1184 (2%)	0/816 (0%)	22/368 (6%)	0/0 (—%)
Aromatic	10/288 (3%)	0/128 (0%)	10/160 (6%)	0/0 (—%)
Overall	63/2320 (3%)	0/1280 (0%)	54/880 (6%)	9/160 (6%)

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)

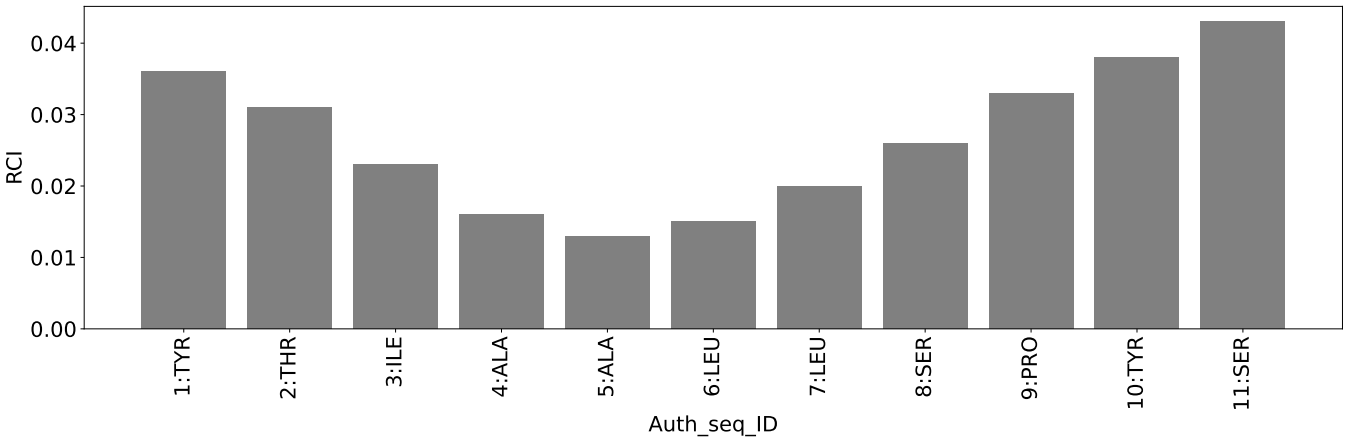
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, *ppm*	Expected range, *ppm*	Z-score
1	A	1	TYR	N	39.20	100.12 – 140.79	-20.0

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	2880
Intra-residue (|i-j|=0)	768
Sequential (|i-j|=1)	1344
Medium range (|i-j|>1 and |i-j|<5)	320
Long range (|i-j|≥5)	256
Inter-chain	192
Hydrogen bond restraints	0
Disulfide bond restraints	0
Total dihedral-angle restraints	144
Number of unmapped restraints	0
Number of restraints per residue	17.2
Number of long range restraints per residue[1]	1.5

[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)	64.0	0.14
0.2-0.5 (Medium)	None	None
>0.5 (Large)	640.0	11.99

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)	25.0	3.3
10.0-20.0 (Medium)	None	None
>20.0 (Large)	None	None

9 Distance violation analysis (i)

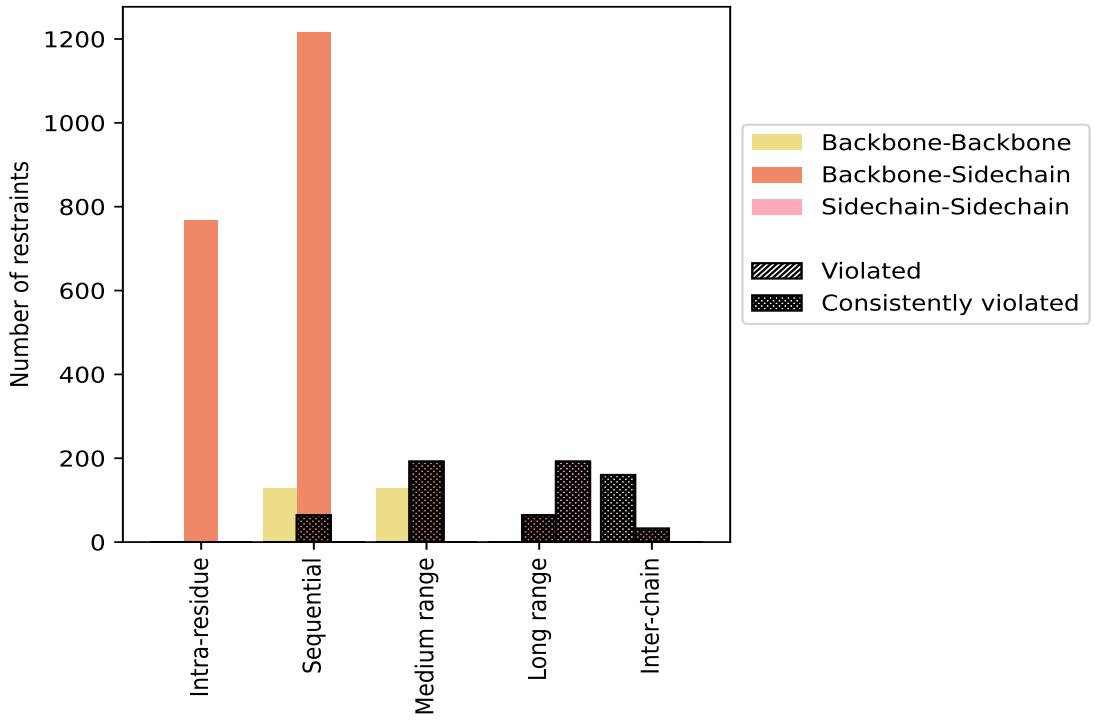
9.1 Summary of distance violations (i)

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)	768	26.7	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	768	26.7	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)	1344	46.7	64	4.8	2.2	64	4.8	2.2
Backbone-Backbone	128	4.4	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	1216	42.2	64	5.3	2.2	64	5.3	2.2
Sidechain-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Medium range (|i-j|>1 & |i-j|<5)	320	11.1	192	60.0	6.7	192	60.0	6.7
Backbone-Backbone	128	4.4	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	192	6.7	192	100.0	6.7	192	100.0	6.7
Sidechain-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Long range (|i-j|≥5)	256	8.9	256	100.0	8.9	256	100.0	8.9
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	64	2.2	64	100.0	2.2	64	100.0	2.2
Sidechain-Sidechain	192	6.7	192	100.0	6.7	192	100.0	6.7
Inter-chain	192	6.7	192	100.0	6.7	192	100.0	6.7
Backbone-Backbone	160	5.6	160	100.0	5.6	160	100.0	5.6
Backbone-Sidechain	32	1.1	32	100.0	1.1	32	100.0	1.1
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	2880	100.0	704	24.4	24.4	704	24.4	24.4
Backbone-Backbone	416	14.4	160	38.5	5.6	160	38.5	5.6
Backbone-Sidechain	2272	78.9	352	15.5	12.2	352	15.5	12.2
Sidechain-Sidechain	192	6.7	192	100.0	6.7	192	100.0	6.7

[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

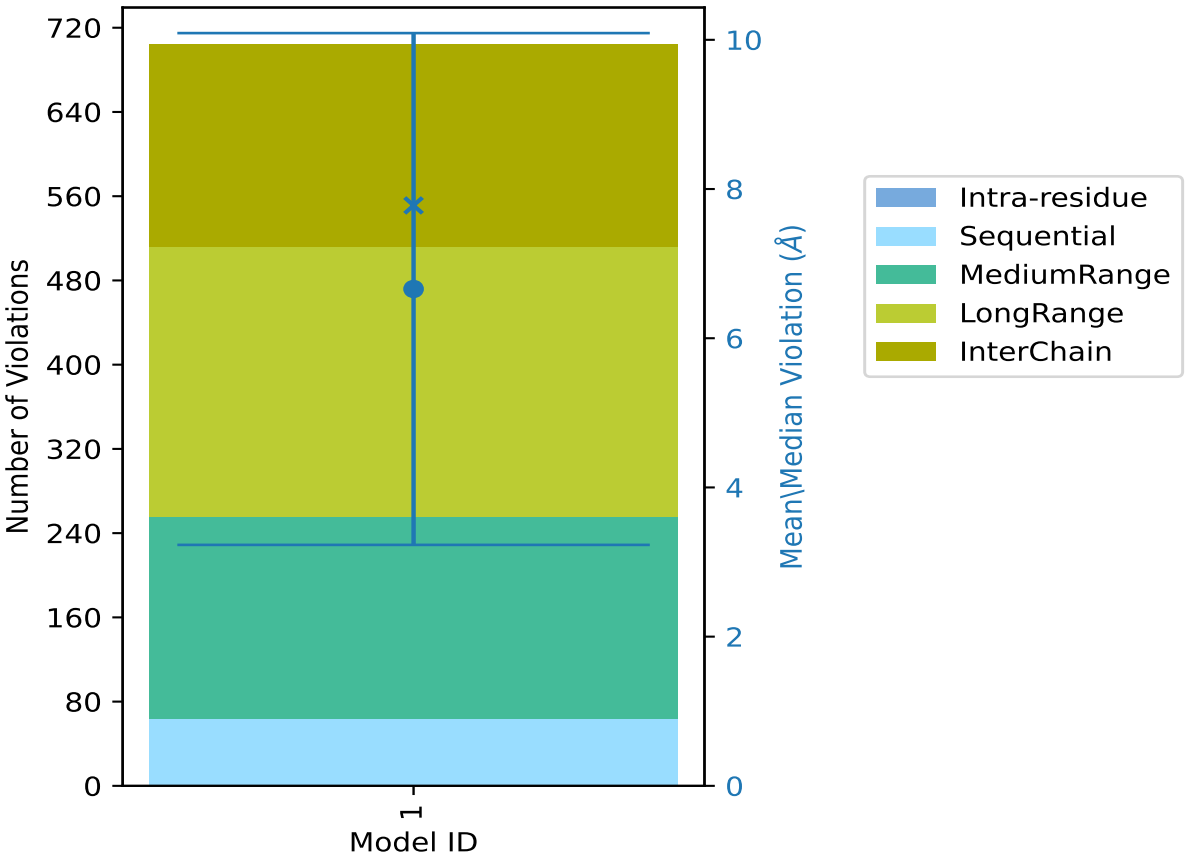
9.2 Distance violation statistics for each model

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	0	64	192	256	192	704	6.66	11.99	3.43	7.78

[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



The mean(dot),median(x) and the standard deviation are shown in blue with respect to the y axis on the right

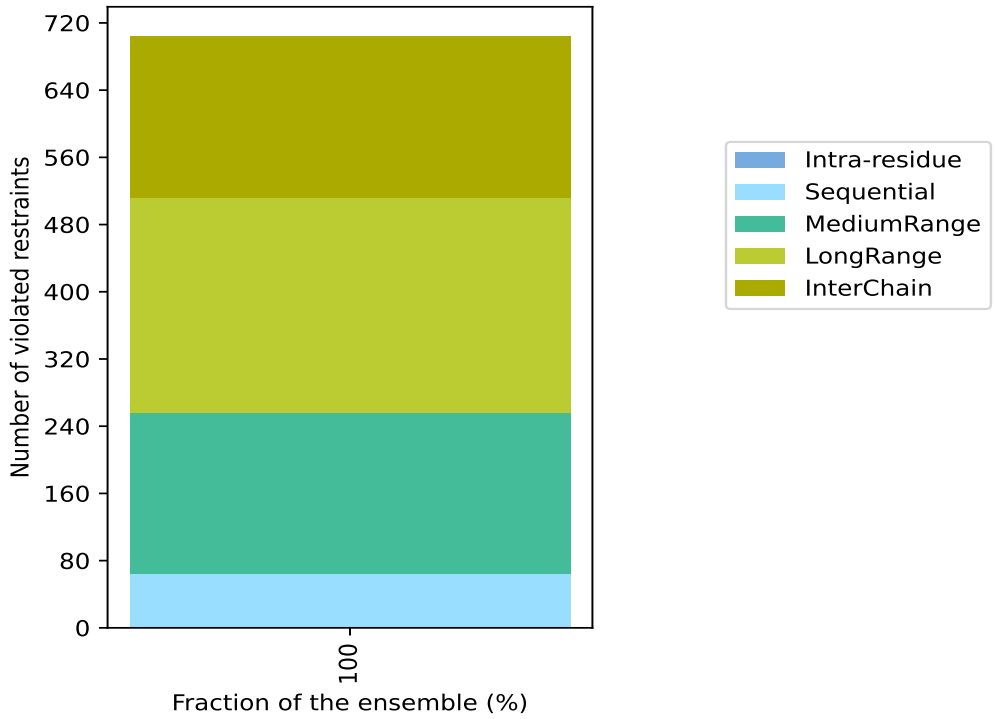
9.3 Distance violation statistics for the ensemble

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, 2176(IR:768, SQ:1280, MR:128, LR:0, 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	64	192	256	192	704	1	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



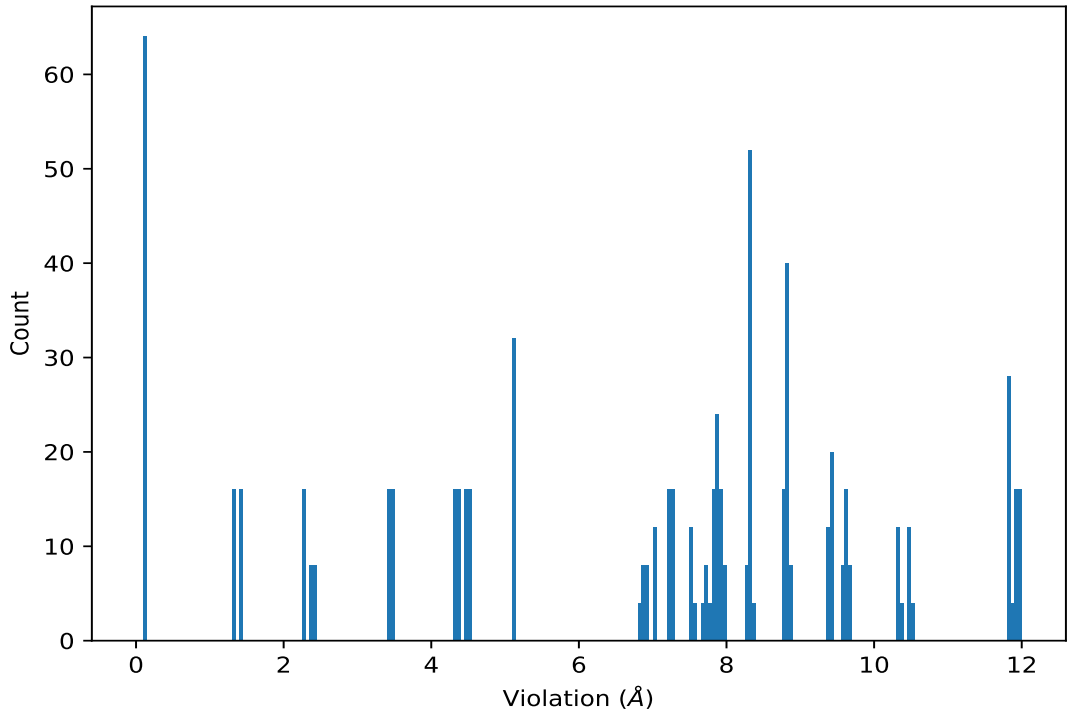
9.4 Most violated distance restraints in the ensemble

No violations found

9.5 All violated distance restraints

9.5.1 Histogram : Distribution of distance violations

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)
(1,3313)	1:A:4:ALA:CB	1:A:9:PRO:CG	1	11.99
(1,3131)	1:A:4:ALA:CB	1:A:9:PRO:CG	1	11.99
(1,2949)	1:A:4:ALA:CB	1:A:9:PRO:CG	1	11.99
(1,2767)	1:A:4:ALA:CB	1:A:9:PRO:CG	1	11.99
(1,3451)	1:G:4:ALA:CB	1:G:9:PRO:CG	1	11.98
(1,3405)	1:E:4:ALA:CB	1:E:9:PRO:CG	1	11.98
(1,3359)	1:C:4:ALA:CB	1:C:9:PRO:CG	1	11.98
(1,3269)	1:G:4:ALA:CB	1:G:9:PRO:CG	1	11.98
(1,3223)	1:E:4:ALA:CB	1:E:9:PRO:CG	1	11.98
(1,3177)	1:C:4:ALA:CB	1:C:9:PRO:CG	1	11.98

10 Dihedral-angle violation analysis

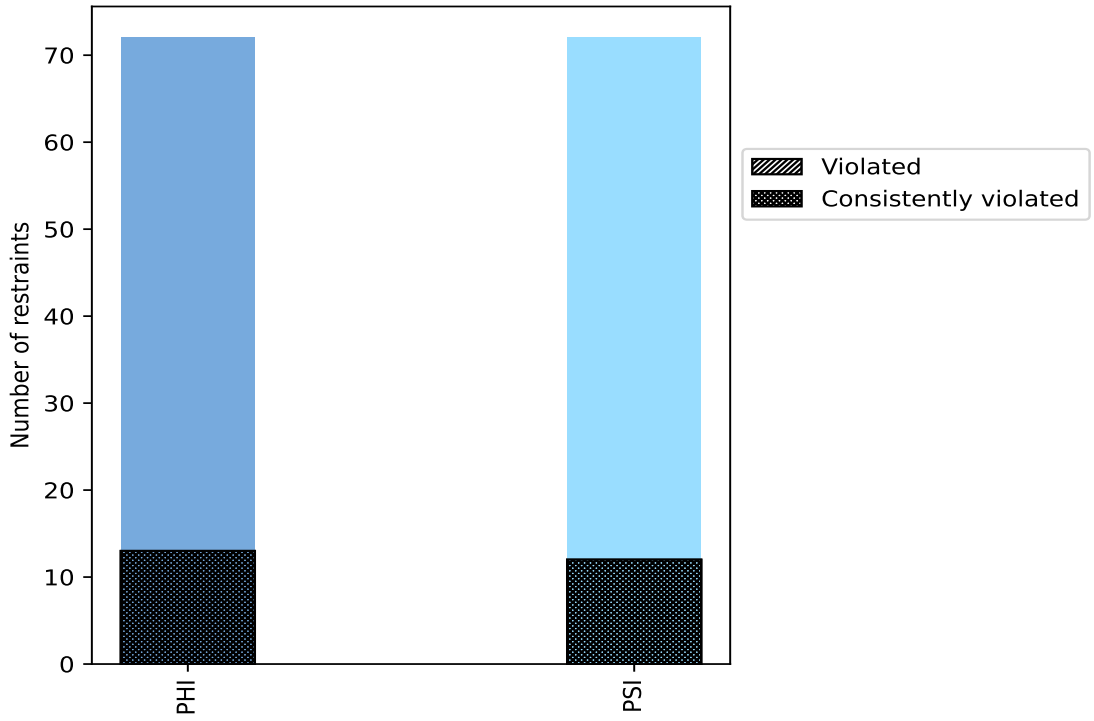
10.1 Summary of dihedral-angle violations

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	72	50.0	13	18.1	9.0	13	18.1	9.0
PSI	72	50.0	12	16.7	8.3	12	16.7	8.3
Total	144	100.0	25	17.4	17.4	25	17.4	17.4

[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



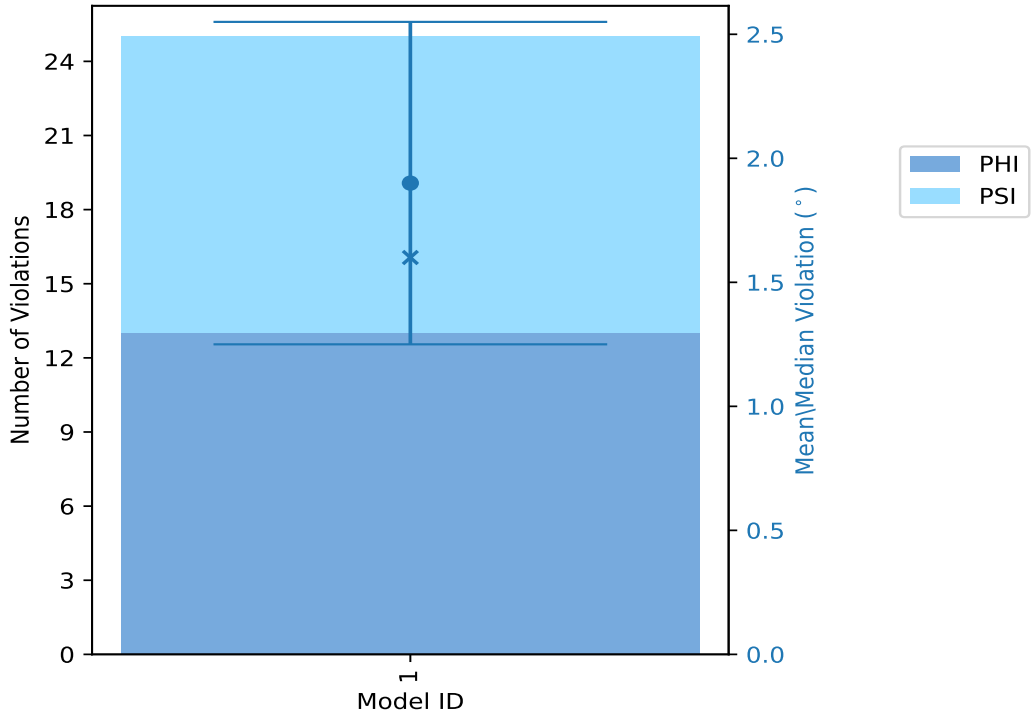
Violated and consistently violated restraints are shown using different hatch patterns in their respective categories

10.2 Dihedral-angle violation statistics for each model

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	13	12	25	1.9	3.3	0.65	1.6

10.2.1 Bar graph : Dihedral violation statistics for each model



The mean(dot),median(x) and the standard deviation are shown in blue with respect to the y axis on the right

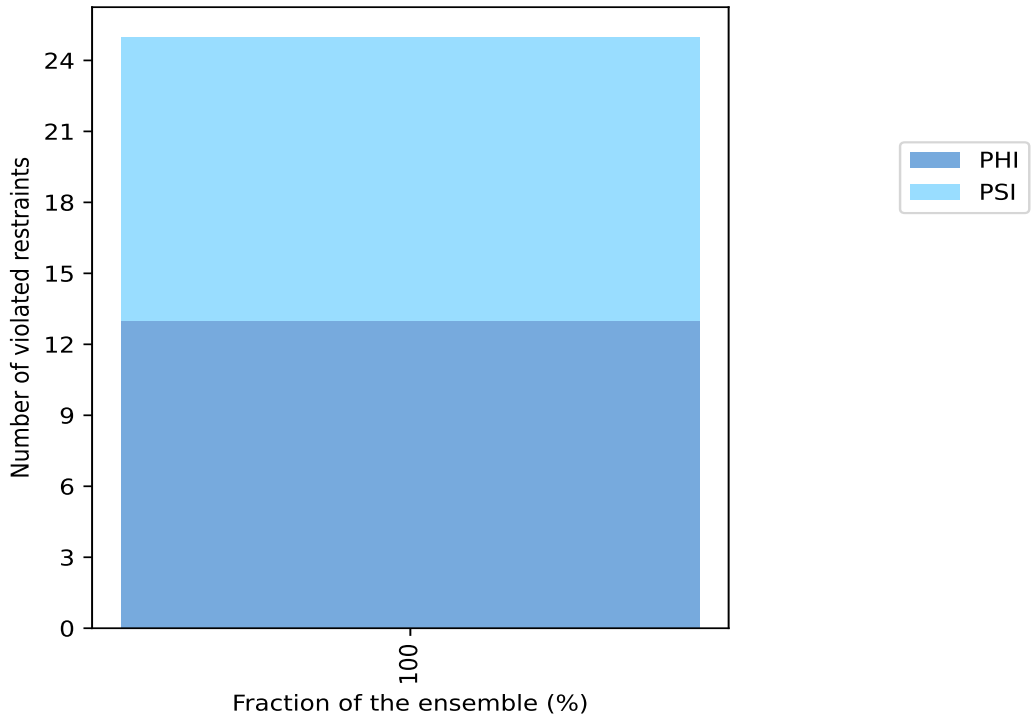
10.3 Dihedral-angle violation statistics for the ensemble

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]	%
13	12	25	1	100.0

[1] Number of models with violations

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



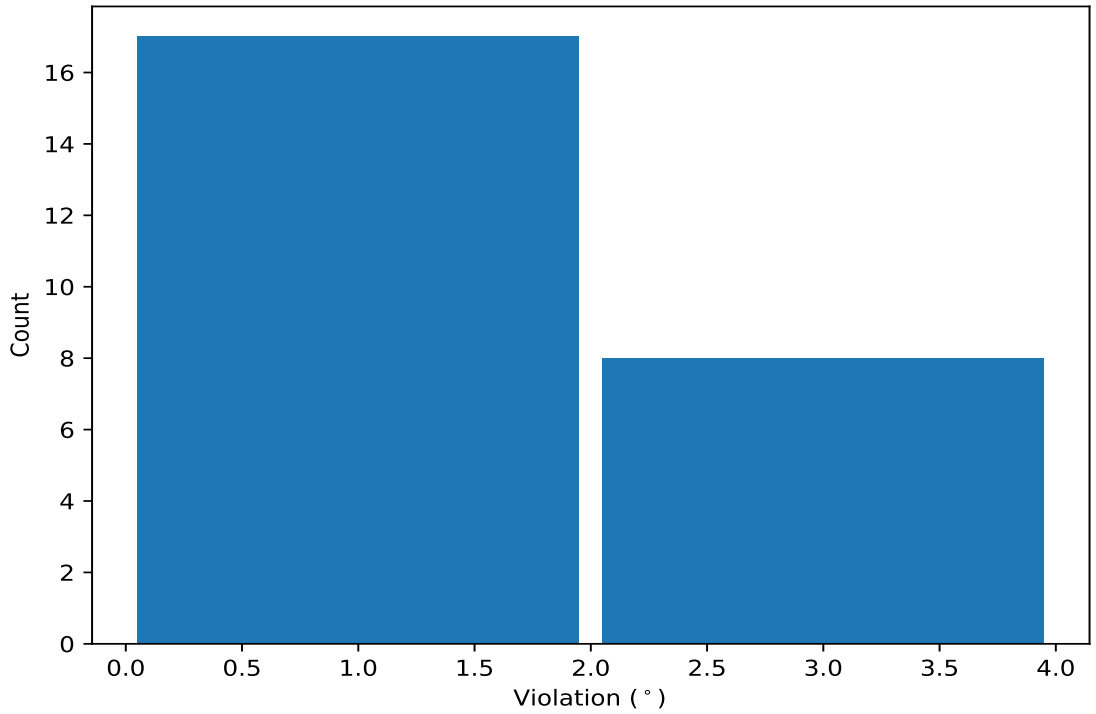
10.4 Most violated dihedral-angle restraints in the ensemble

No violations found

10.5 All violated dihedral-angle restraints

10.5.1 Histogram : Distribution of violations

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

The following table provides the list of violationsfor 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 (°)
(1,40)	1:C:4:ALA:N	1:C:4:ALA:CA	1:C:4:ALA:C	1:C:5:ALA:N	1	3.3
(1,76)	1:E:4:ALA:N	1:E:4:ALA:CA	1:E:4:ALA:C	1:E:5:ALA:N	1	3.0
(1,4)	1:A:4:ALA:N	1:A:4:ALA:CA	1:A:4:ALA:C	1:A:5:ALA:N	1	3.0
(1,112)	1:G:4:ALA:N	1:G:4:ALA:CA	1:G:4:ALA:C	1:G:5:ALA:N	1	3.0
(1,121)	1:G:4:ALA:C	1:G:5:ALA:N	1:G:5:ALA:CA	1:G:5:ALA:C	1	2.7
(1,85)	1:E:4:ALA:C	1:E:5:ALA:N	1:E:5:ALA:CA	1:E:5:ALA:C	1	2.5
(1,49)	1:C:4:ALA:C	1:C:5:ALA:N	1:C:5:ALA:CA	1:C:5:ALA:C	1	2.3
(1,13)	1:A:4:ALA:C	1:A:5:ALA:N	1:A:5:ALA:CA	1:A:5:ALA:C	1	2.3
(1,58)	1:D:4:ALA:N	1:D:4:ALA:CA	1:D:4:ALA:C	1:D:5:ALA:N	1	1.9
(1,130)	1:H:4:ALA:N	1:H:4:ALA:CA	1:H:4:ALA:C	1:H:5:ALA:N	1	1.9