



wwPDB NMR Structure Validation Summary Report ⓘ

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PDB ID : 9ZDL / pdb_00009zdl
BMRB ID : 31285
Title : A6-A11 diselenide glargine insulin
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Deposited on : 2025-11-25

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

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with specific help available everywhere you see the ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
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) : 2.50

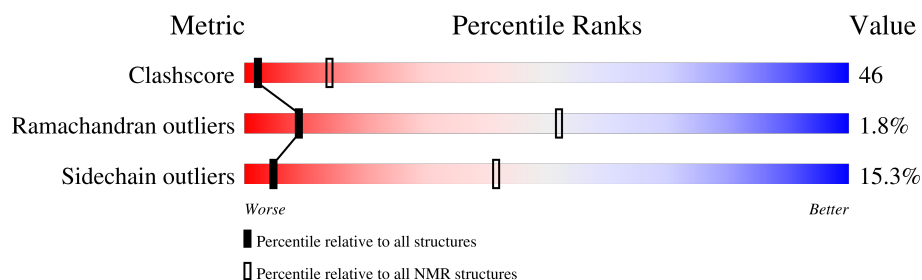
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 52%.

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	229148	14424
Ramachandran outliers	224038	12848
Sidechain outliers	223484	12823

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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	21	33% 38% 14% 14%
2	B	32	19% 47% . 31%

2 Ensemble composition and analysis

This entry contains 20 models. Model 4 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *closest to the average*.

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:2-A:5, A:7-A:10, A:12-A:21, B:22-B:43 (40)	0.14	4

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

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

The models can be grouped into 3 clusters and 3 single-model clusters were found.

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

3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 827 atoms, of which 404 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Insulin A chain.

Mol	Chain	Residues	Atoms							Trace
1	A	21	Total	C	H	N	O	S	Se	0
			305	97	146	24	34	2	2	

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	6	SEC	CYS	engineered mutation	UNP P01308
A	11	SEC	CYS	engineered mutation	UNP P01308
A	21	GLY	ASN	conflict	UNP P01308

- Molecule 2 is a protein called Insulin A chain.

Mol	Chain	Residues	Atoms							Trace
2	B	32	Total	C	H	N	O	S		0
			522	170	258	48	44	2		

4 Residue-property plots

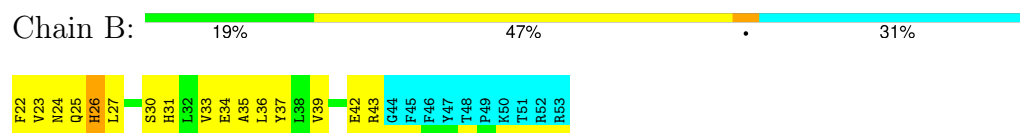
4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outliers are shown as green connectors. Residues which are classified as ill-defined in the NMR ensemble, are shown in cyan with an underline colour-coded according to the previous scheme. Residues which were present in the experimental sample, but not modelled in the final structure are shown in grey.

- Molecule 1: Insulin A chain



- Molecule 2: Insulin A chain



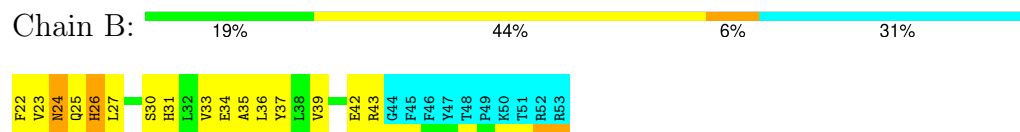
4.2 Residue scores for the representative (medoid) model from the NMR ensemble

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

- Molecule 1: Insulin A chain



- Molecule 2: Insulin A chain



5 Refinement protocol and experimental data overview

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

Of the 100 calculated structures, 20 were deposited, based on the following criterion: *structures with the least restraint violations*.

The following table shows the software used for structure solution, optimisation and refinement.

Software name	Classification	Version
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	602
Number of shifts mapped to atoms	602
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	52%

6 Model quality [i](#)

6.1 Standard geometry [i](#)

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

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	Bond lengths		Bond angles	
		RMSZ	#Z>5	RMSZ	#Z>5
1	A	1.41±0.01	0±0/142 (0.0± 0.0%)	1.17±0.02	0±0/187 (0.0± 0.0%)
2	B	1.47±0.01	0±0/177 (0.0± 0.0%)	1.41±0.01	1±0/240 (0.4± 0.0%)
All	All	1.44	0/6380 (0.0%)	1.31	20/8540 (0.2%)

There are no bond-length outliers.

All unique angle outliers are listed below.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
2	B	26	HIS	CA-CB-CG	-8.85	104.95	113.80	18	20

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	143	133	133	15±2
2	B	173	168	165	18±2
All	All	6320	6020	5960	566

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 46.

5 of 72 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:35:ALA:O	2:B:39:VAL:HG23	0.78	1.78	9	20
1:A:2:ILE:HD12	1:A:19:TYR:CG	0.72	2.19	1	20
1:A:9:SER:C	2:B:26:HIS:NE2	0.66	2.54	3	20
1:A:5:GLN:H	1:A:5:GLN:NE2	0.65	1.90	7	2
1:A:2:ILE:HG23	1:A:3:VAL:N	0.63	2.09	16	20

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	17/21 (81%)	15±1 (90±6%)	1±1 (7±4%)	0±0 (3±3%)	5	39
2	B	21/32 (66%)	16±1 (78±4%)	4±1 (21±5%)	0±0 (1±2%)	15	65
All	All	760/1060 (72%)	635 (84%)	111 (15%)	14 (2%)	9	52

All 2 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	3	VAL	10
2	B	43	ARG	4

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	17/17 (100%)	14±0 (81±2%)	3±0 (19±2%)	3	35
2	B	19/28 (68%)	17±1 (88±3%)	2±1 (12±3%)	7	49
All	All	720/900 (80%)	610 (85%)	110 (15%)	5	41

5 of 9 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	8	THR	20
1	A	9	SER	20
1	A	10	ILE	20
2	B	27	LEU	20
2	B	25	GLN	19

6.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

6.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.6 Ligand geometry [i](#)

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 52% for the well-defined parts and 52% 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	602
Number of shifts mapped to atoms	602
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

- Can not parse the chemical shift value. First 5 (of 226) occurrences are reported below.

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	2	ILE	HG12	0.876	0.003	.
1	A	2	ILE	HG13	0.994	0.004	.
1	A	3	VAL	HG11	0.927	0.003	.
1	A	3	VAL	HG12	0.927	0.003	.
1	A	3	VAL	HG13	0.927	0.003	.
1	A	3	VAL	HG21	0.993	0.002	.
1	A	3	VAL	HG22	0.993	0.002	.
1	A	3	VAL	HG23	0.993	0.002	.
1	A	3	VAL	CG1	21.218	0.000	.
1	A	3	VAL	CG2	22.274	0.000	.
1	A	4	GLU	HB2	2.183	0.002	.
1	A	4	GLU	HG2	2.519	0.008	.
1	A	5	GLN	HB2	2.145	0.003	.
1	A	5	GLN	HB3	2.099	0.003	.
1	A	5	GLN	HE21	7.662	0.001	.
1	A	5	GLN	HE22	6.979	0.001	.
1	A	5	GLN	HG2	2.555	0.003	.

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	5	GLN	HG3	2.449	0.004	.
1	A	7	CYS	HB2	3.883	0.003	.
1	A	7	CYS	HB3	3.417	0.003	.
1	A	9	SER	HB2	3.889	0.003	.
1	A	9	SER	HB3	4.060	0.003	.
1	A	10	ILE	HG12	0.301	0.006	.
1	A	10	ILE	HG13	1.014	0.004	.
1	A	12	SER	HB2	4.323	0.005	.
1	A	12	SER	HB3	4.019	0.004	.
1	A	13	LEU	HD11	0.808	0.002	.
1	A	13	LEU	HD12	0.808	0.002	.
1	A	13	LEU	HD13	0.808	0.002	.
1	A	13	LEU	HD21	0.761	0.003	.
1	A	13	LEU	HD22	0.761	0.003	.
1	A	13	LEU	HD23	0.761	0.003	.
1	A	13	LEU	CD1	23.907	0.000	.
1	A	13	LEU	CD2	24.595	0.000	.
1	A	14	TYR	HB2	3.007	0.003	.
1	A	14	TYR	HB3	2.935	0.002	.
1	A	14	TYR	HD1	7.085	0.002	.
1	A	14	TYR	HD2	7.084	0.002	.
1	A	14	TYR	HE1	6.858	0.003	.
1	A	14	TYR	HE2	6.859	0.002	.
1	A	14	TYR	CD1	132.779	0.000	.
1	A	14	TYR	CD2	132.779	0.000	.
1	A	14	TYR	CE1	118.313	0.000	.
1	A	14	TYR	CE2	118.313	0.000	.
1	A	15	GLN	HB2	2.454	0.003	.
1	A	15	GLN	HB3	1.987	0.005	.
1	A	15	GLN	HE21	7.021	0.002	.
1	A	15	GLN	HE22	7.554	0.001	.
1	A	15	GLN	HG2	2.400	0.004	.
1	A	15	GLN	HG3	2.452	0.005	.
1	A	16	LEU	HB2	1.820	0.005	.
1	A	16	LEU	HB3	1.967	0.003	.
1	A	16	LEU	HD11	0.898	0.000	.
1	A	16	LEU	HD12	0.898	0.000	.
1	A	16	LEU	HD13	0.898	0.000	.
1	A	16	LEU	HD21	0.808	0.002	.
1	A	16	LEU	HD22	0.808	0.002	.
1	A	16	LEU	HD23	0.808	0.002	.

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	16	LEU	CD1	25.674	0.000	.
1	A	16	LEU	CD2	26.091	0.000	.
1	A	17	GLU	HB2	2.138	0.004	.
1	A	17	GLU	HG2	2.623	0.003	.
1	A	18	ASN	HB2	2.643	0.003	.
1	A	18	ASN	HB3	2.520	0.005	.
1	A	18	ASN	HD21	6.603	0.001	.
1	A	18	ASN	HD22	7.204	0.001	.
1	A	19	TYR	HB2	2.997	0.003	.
1	A	19	TYR	HB3	3.492	0.003	.
1	A	19	TYR	HD1	7.413	0.002	.
1	A	19	TYR	HD2	7.414	0.002	.
1	A	19	TYR	HE1	6.759	0.003	.
1	A	19	TYR	HE2	6.759	0.003	.
1	A	19	TYR	CD1	133.896	0.000	.
1	A	19	TYR	CD2	133.891	0.000	.
1	A	19	TYR	CE1	117.702	0.000	.
1	A	19	TYR	CE2	117.701	0.000	.
1	A	20	CYS	HB2	2.877	0.003	.
1	A	20	CYS	HB3	3.192	0.004	.
1	A	21	GLY	HA2	4.020	0.002	.
1	B	22	PHE	HD1	7.243	0.001	.
1	B	22	PHE	HD2	7.243	0.002	.
1	B	22	PHE	HE1	7.391	0.002	.
1	B	22	PHE	HE2	7.391	0.002	.
1	B	22	PHE	CD1	132.109	0.000	.
1	B	22	PHE	CD2	132.109	0.000	.
1	B	22	PHE	CE1	131.754	0.000	.
1	B	22	PHE	CE2	131.754	0.000	.
1	B	23	VAL	HG11	0.886	0.003	.
1	B	23	VAL	HG12	0.886	0.003	.
1	B	23	VAL	HG13	0.886	0.003	.
1	B	23	VAL	HG21	0.867	0.008	.
1	B	23	VAL	HG22	0.867	0.008	.
1	B	23	VAL	HG23	0.867	0.008	.
1	B	23	VAL	CG1	20.414	0.000	.
1	B	23	VAL	CG2	20.823	0.000	.
1	B	24	ASN	HD21	7.576	0.001	.
1	B	24	ASN	HD22	6.926	0.001	.
1	B	25	GLN	HB2	1.933	0.003	.
1	B	25	GLN	HB3	2.122	0.008	.

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	B	25	GLN	HE21	7.406	0.002	.
1	B	25	GLN	HE22	6.842	0.001	.
1	B	25	GLN	HG2	2.293	0.002	.
1	B	25	GLN	HG3	2.142	0.004	.
1	B	26	HIS	HB2	3.285	0.003	.
1	B	26	HIS	HB3	3.595	0.002	.
1	B	27	LEU	HB2	1.811	0.004	.
1	B	27	LEU	HB3	0.867	0.004	.
1	B	27	LEU	HD11	0.898	0.002	.
1	B	27	LEU	HD12	0.898	0.002	.
1	B	27	LEU	HD13	0.898	0.002	.
1	B	27	LEU	HD21	0.724	0.002	.
1	B	27	LEU	HD22	0.724	0.002	.
1	B	27	LEU	HD23	0.724	0.002	.
1	B	27	LEU	CD1	26.046	0.000	.
1	B	27	LEU	CD2	23.554	0.000	.
1	B	28	CYS	HB2	2.941	0.002	.
1	B	28	CYS	HB3	3.248	0.001	.
1	B	29	GLY	HA2	4.020	0.002	.
1	B	31	HIS	HB2	3.335	0.002	.
1	B	31	HIS	HB3	3.639	0.003	.
1	B	32	LEU	HB2	1.204	0.004	.
1	B	32	LEU	HB3	1.958	0.004	.
1	B	32	LEU	HD11	0.753	0.003	.
1	B	32	LEU	HD12	0.753	0.003	.
1	B	32	LEU	HD13	0.753	0.003	.
1	B	32	LEU	HD21	0.803	0.007	.
1	B	32	LEU	HD22	0.803	0.007	.
1	B	32	LEU	HD23	0.803	0.007	.
1	B	32	LEU	CD1	22.100	0.000	.
1	B	32	LEU	CD2	25.045	0.000	.
1	B	33	VAL	HG11	0.975	0.003	.
1	B	33	VAL	HG12	0.975	0.003	.
1	B	33	VAL	HG13	0.975	0.003	.
1	B	33	VAL	HG21	0.992	0.002	.
1	B	33	VAL	HG22	0.992	0.002	.
1	B	33	VAL	HG23	0.992	0.002	.
1	B	33	VAL	CG1	21.312	0.000	.
1	B	33	VAL	CG2	22.544	0.000	.
1	B	34	GLU	HB2	2.201	0.004	.
1	B	36	LEU	HB2	1.327	0.003	.

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	B	36	LEU	HB3	0.865	0.003	.
1	B	36	LEU	HD11	0.491	0.003	.
1	B	36	LEU	HD12	0.491	0.003	.
1	B	36	LEU	HD13	0.491	0.003	.
1	B	36	LEU	HD21	0.679	0.002	.
1	B	36	LEU	HD22	0.679	0.002	.
1	B	36	LEU	HD23	0.679	0.002	.
1	B	36	LEU	CD1	25.599	0.000	.
1	B	36	LEU	CD2	24.081	0.000	.
1	B	37	TYR	HD1	7.169	0.003	.
1	B	37	TYR	HD2	7.168	0.003	.
1	B	37	TYR	HE1	6.810	0.002	.
1	B	37	TYR	HE2	6.811	0.003	.
1	B	37	TYR	CD1	132.909	0.000	.
1	B	37	TYR	CD2	132.909	0.000	.
1	B	37	TYR	CE1	118.080	0.000	.
1	B	37	TYR	CE2	118.080	0.000	.
1	B	38	LEU	HB2	1.708	0.003	.
1	B	38	LEU	HB3	1.938	0.004	.
1	B	38	LEU	HD11	0.969	0.002	.
1	B	38	LEU	HD12	0.969	0.002	.
1	B	38	LEU	HD13	0.969	0.002	.
1	B	38	LEU	HD21	0.947	0.002	.
1	B	38	LEU	HD22	0.947	0.002	.
1	B	38	LEU	HD23	0.947	0.002	.
1	B	38	LEU	CD1	24.755	0.000	.
1	B	38	LEU	CD2	23.469	0.000	.
1	B	39	VAL	HG11	0.917	0.002	.
1	B	39	VAL	HG12	0.917	0.002	.
1	B	39	VAL	HG13	0.917	0.002	.
1	B	39	VAL	HG21	1.048	0.002	.
1	B	39	VAL	HG22	1.048	0.002	.
1	B	39	VAL	HG23	1.048	0.002	.
1	B	39	VAL	CG1	21.307	0.000	.
1	B	39	VAL	CG2	22.347	0.000	.
1	B	40	CYS	HB2	2.931	0.002	.
1	B	40	CYS	HB3	3.334	0.004	.
1	B	41	GLY	HA2	3.959	0.003	.
1	B	42	GLU	HB2	2.237	0.002	.
1	B	43	ARG	HG2	1.748	0.002	.
1	B	43	ARG	HG3	1.825	0.003	.

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	B	44	GLY	HA2	3.989	0.004	.
1	B	45	PHE	HB2	2.896	0.003	.
1	B	45	PHE	HB3	3.166	0.003	.
1	B	45	PHE	HD1	6.890	0.007	.
1	B	45	PHE	HD2	6.891	0.004	.
1	B	45	PHE	HE1	7.078	0.003	.
1	B	45	PHE	HE2	7.079	0.006	.
1	B	45	PHE	CD1	132.262	0.000	.
1	B	45	PHE	CD2	132.262	0.000	.
1	B	45	PHE	CE1	130.966	0.000	.
1	B	45	PHE	CE2	130.966	0.000	.
1	B	46	PHE	HB2	3.037	0.004	.
1	B	46	PHE	HB3	3.193	0.002	.
1	B	46	PHE	HD1	7.216	0.002	.
1	B	46	PHE	HD2	7.216	0.001	.
1	B	46	PHE	HE1	7.305	0.001	.
1	B	46	PHE	HE2	7.305	0.000	.
1	B	46	PHE	CD1	131.925	0.000	.
1	B	46	PHE	CD2	131.925	0.000	.
1	B	46	PHE	CE1	131.228	0.000	.
1	B	46	PHE	CE2	131.228	0.000	.
1	B	47	TYR	HD1	7.064	0.003	.
1	B	47	TYR	HD2	7.063	0.003	.
1	B	47	TYR	HE1	6.767	0.004	.
1	B	47	TYR	HE2	6.767	0.002	.
1	B	47	TYR	CD1	132.816	0.037	.
1	B	47	TYR	CD2	132.849	0.000	.
1	B	47	TYR	CE1	117.979	0.000	.
1	B	47	TYR	CE2	117.979	0.000	.
1	B	49	PRO	HB2	1.913	0.005	.
1	B	49	PRO	HB3	2.210	0.003	.
1	B	49	PRO	HG2	1.918	0.004	.
1	B	49	PRO	HG3	2.011	0.002	.
1	B	50	LYS	HB2	1.768	0.004	.
1	B	50	LYS	HB3	1.854	0.004	.
1	B	50	LYS	HG2	1.429	0.004	.
1	B	50	LYS	HG3	1.475	0.005	.
1	B	52	ARG	HB2	1.783	0.001	.
1	B	52	ARG	HB3	1.902	0.002	.
1	B	52	ARG	HG2	1.770	0.003	.
1	B	52	ARG	HG3	1.663	0.003	.

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	B	53	ARG	HB2	1.778	0.003	.
1	B	53	ARG	HB3	1.941	0.001	.
1	B	53	ARG	HG2	1.775	0.001	.
1	B	53	ARG	HG3	1.650	0.003	.

7.1.2 Chemical shift referencing [i](#)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	51	0.21 ± 0.16	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	46	0.55 ± 0.15	Should be applied
$^{13}\text{C}'$	0	—	None (insufficient data)
^{15}N	46	0.51 ± 0.50	None needed (imprecise)

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 52%, i.e. 278 atoms were assigned a chemical shift out of a possible 537. 0 out of 10 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	153/203 (75%)	76/83 (92%)	40/80 (50%)	37/40 (92%)
Sidechain	115/283 (41%)	50/186 (27%)	59/89 (66%)	6/8 (75%)
Aromatic	10/51 (20%)	5/25 (20%)	5/24 (21%)	0/2 (0%)
Overall	278/537 (52%)	131/294 (45%)	104/193 (54%)	43/50 (86%)

7.1.4 Statistically unusual chemical shifts [i](#)

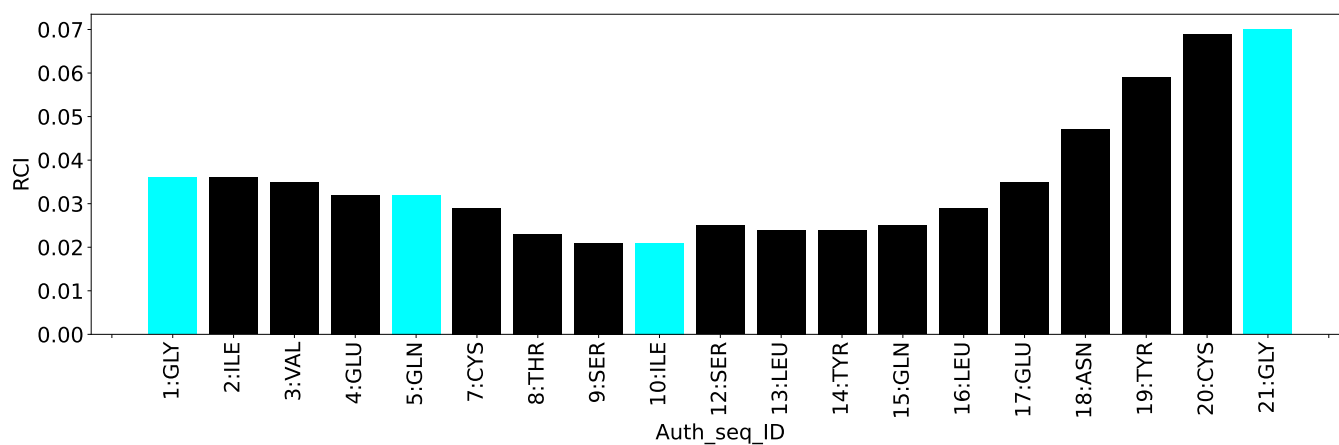
There are no statistically unusual chemical shifts.

7.1.5 Random Coil Index (RCI) plots [i](#)

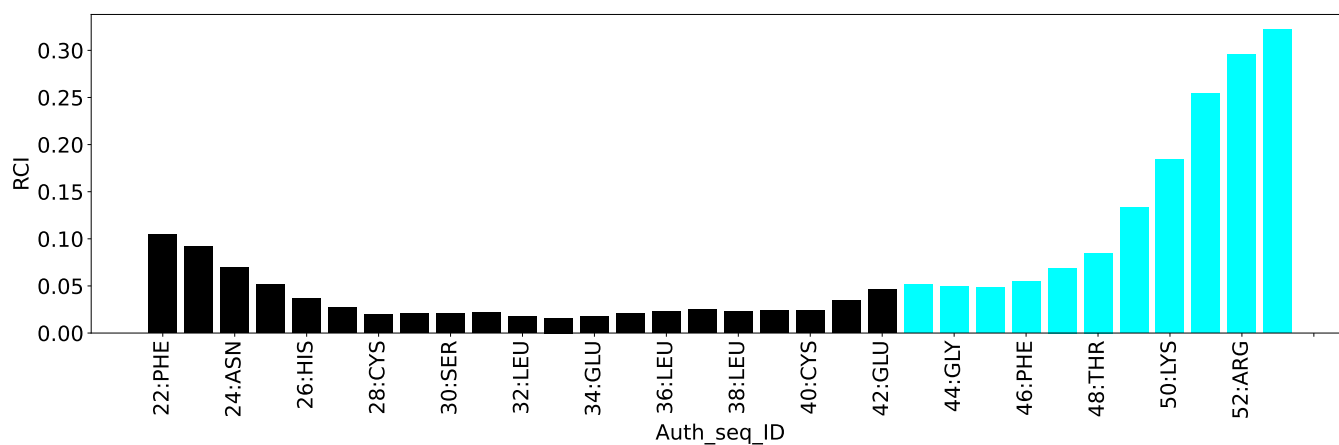
The image below reports *random coil index* values for the protein chains in the structure. The height of each bar gives a probability of a given residue to be disordered, as predicted from the available chemical shifts and the amino acid sequence. A value above 0.2 is an indication of significant predicted 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:



Random coil index (RCI) for chain B:



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	1296
Intra-residue ($ i-j =0$)	431
Sequential ($ i-j =1$)	301
Medium range ($ i-j >1$ and $ i-j <5$)	275
Long range ($ i-j \geq 5$)	111
Inter-chain	178
Hydrogen bond restraints	0
Disulfide bond restraints	0
Total dihedral-angle restraints	0
Number of unmapped restraints	0
Number of restraints per residue	24.5
Number of long range restraints per residue ¹	2.1

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

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)	37.6	0.2
0.2-0.5 (Medium)	19.5	0.5
>0.5 (Large)	4.9	2.91

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

Dihedral-angle violations less than 1° are not included in the calculation. There are no dihedral-angle violations

9 Distance violation analysis ⓘ

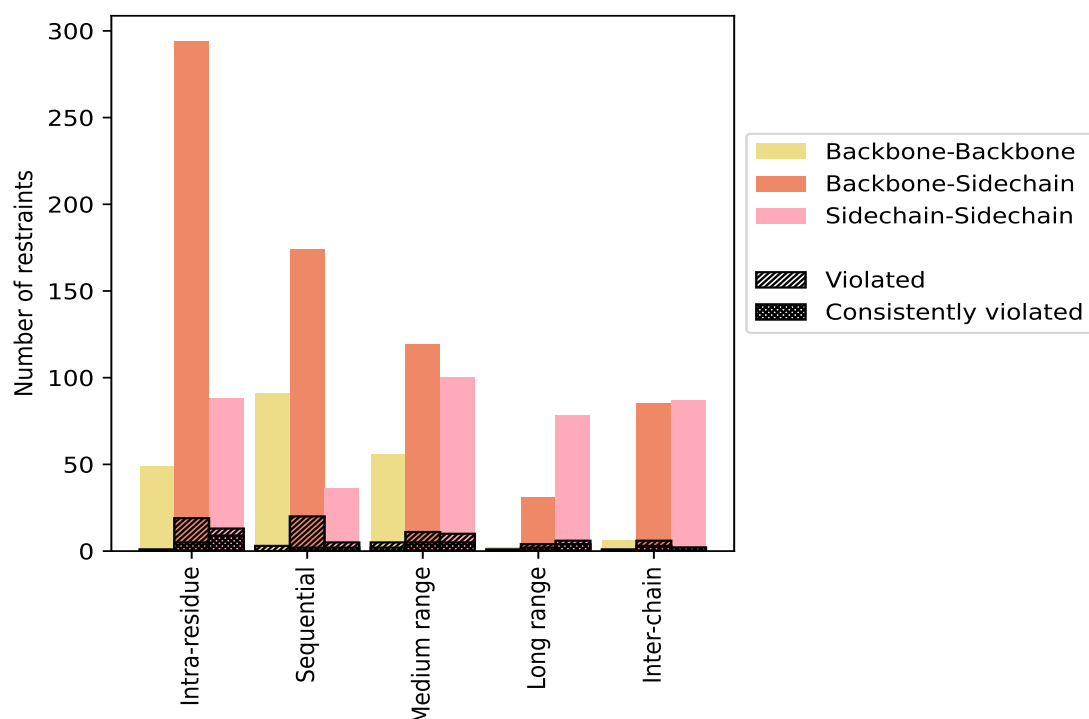
9.1 Summary of distance violations ⓘ

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.

Restrains type	Count	% ¹	Violated ³			Consistently Violated ⁴		
			Count	% ²	% ¹	Count	% ²	% ¹
Intra-residue ($i-j =0$)	431	33.3	33	7.7	2.5	14	3.2	1.1
Backbone-Backbone	49	3.8	1	2.0	0.1	0	0.0	0.0
Backbone-Sidechain	294	22.7	19	6.5	1.5	5	1.7	0.4
Sidechain-Sidechain	88	6.8	13	14.8	1.0	9	10.2	0.7
Sequential ($i-j =1$)	301	23.2	28	9.3	2.2	4	1.3	0.3
Backbone-Backbone	91	7.0	3	3.3	0.2	0	0.0	0.0
Backbone-Sidechain	174	13.4	20	11.5	1.5	2	1.1	0.2
Sidechain-Sidechain	36	2.8	5	13.9	0.4	2	5.6	0.2
Medium range ($i-j >1$ & $i-j <5$)	275	21.2	26	9.5	2.0	12	4.4	0.9
Backbone-Backbone	56	4.3	5	8.9	0.4	2	3.6	0.2
Backbone-Sidechain	119	9.2	11	9.2	0.8	5	4.2	0.4
Sidechain-Sidechain	100	7.7	10	10.0	0.8	5	5.0	0.4
Long range ($i-j \geq 5$)	111	8.6	11	9.9	0.8	6	5.4	0.5
Backbone-Backbone	2	0.2	1	50.0	0.1	0	0.0	0.0
Backbone-Sidechain	31	2.4	4	12.9	0.3	2	6.5	0.2
Sidechain-Sidechain	78	6.0	6	7.7	0.5	4	5.1	0.3
Inter-chain	178	13.7	9	5.1	0.7	5	2.8	0.4
Backbone-Backbone	6	0.5	1	16.7	0.1	0	0.0	0.0
Backbone-Sidechain	85	6.6	6	7.1	0.5	3	3.5	0.2
Sidechain-Sidechain	87	6.7	2	2.3	0.2	2	2.3	0.2
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	1296	100.0	107	8.3	8.3	41	3.2	3.2
Backbone-Backbone	204	15.7	11	5.4	0.8	2	1.0	0.2
Backbone-Sidechain	703	54.2	60	8.5	4.6	17	2.4	1.3
Sidechain-Sidechain	389	30.0	36	9.3	2.8	22	5.7	1.7

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 [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	20	13	13	10	7	63	0.29	2.25	0.37	0.19
2	19	14	17	10	6	66	0.28	2.91	0.41	0.18
3	17	12	14	10	6	59	0.31	2.5	0.42	0.2
4	20	13	13	9	7	62	0.27	1.38	0.25	0.2
5	19	13	15	10	6	63	0.29	2.81	0.4	0.18
6	22	14	14	8	7	65	0.24	1.59	0.21	0.19
7	18	16	16	10	7	67	0.26	1.28	0.24	0.19
8	20	15	14	8	7	64	0.23	1.39	0.19	0.19
9	22	13	15	9	6	65	0.28	2.75	0.38	0.19
10	19	14	16	10	6	65	0.28	2.88	0.41	0.17

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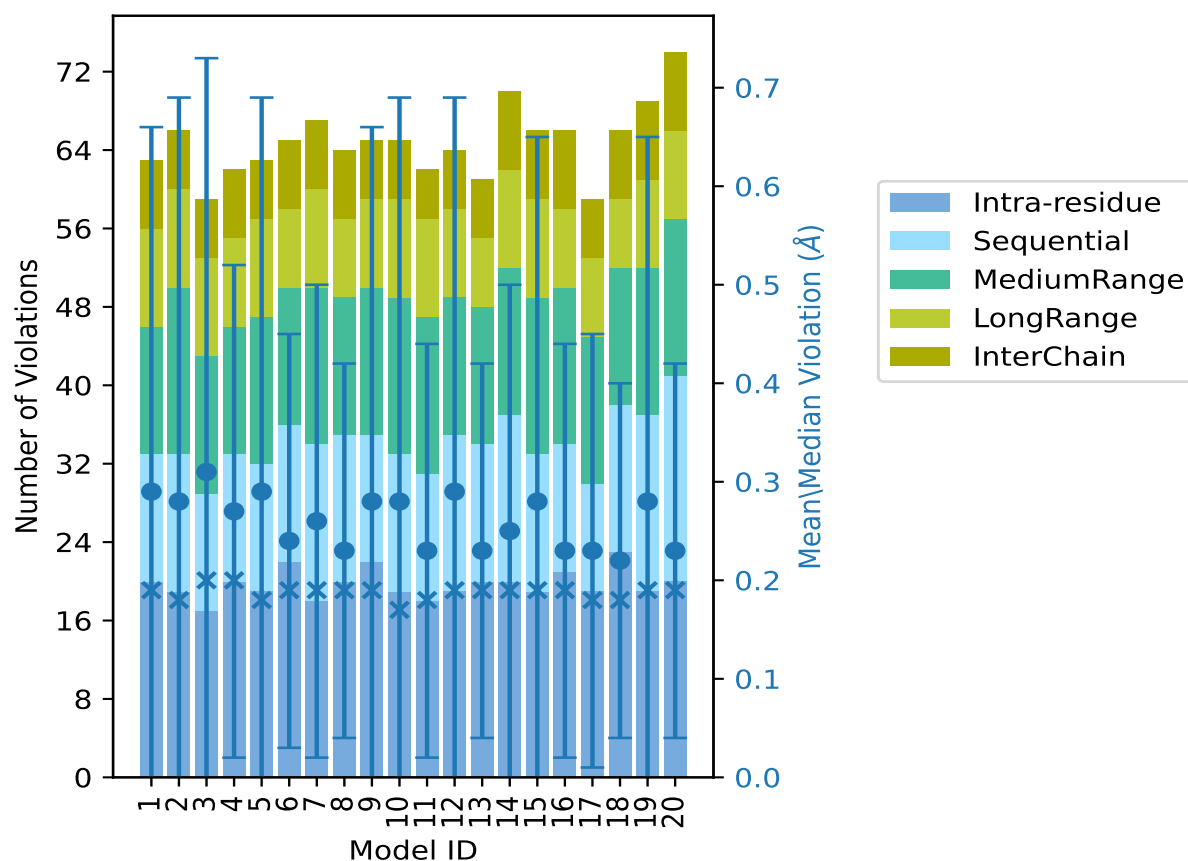
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Model ID	Number of violations						Mean (Å)	Max (Å)	SD ⁶ (Å)	Median (Å)
	IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total				
11	18	13	16	10	5	62	0.23	1.62	0.21	0.18
12	19	16	14	9	6	64	0.29	2.82	0.4	0.19
13	20	14	14	7	6	61	0.23	1.4	0.19	0.19
14	20	17	15	10	8	70	0.25	1.62	0.25	0.19
15	19	14	16	10	7	66	0.28	2.35	0.37	0.19
16	21	13	16	8	8	66	0.23	1.6	0.21	0.19
17	19	11	15	8	6	59	0.23	1.64	0.22	0.18
18	23	15	14	7	7	66	0.22	1.42	0.18	0.18
19	19	18	15	9	8	69	0.28	2.37	0.37	0.19
20	20	21	16	9	8	74	0.23	1.37	0.19	0.19

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 ⓘ



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 ⓘ

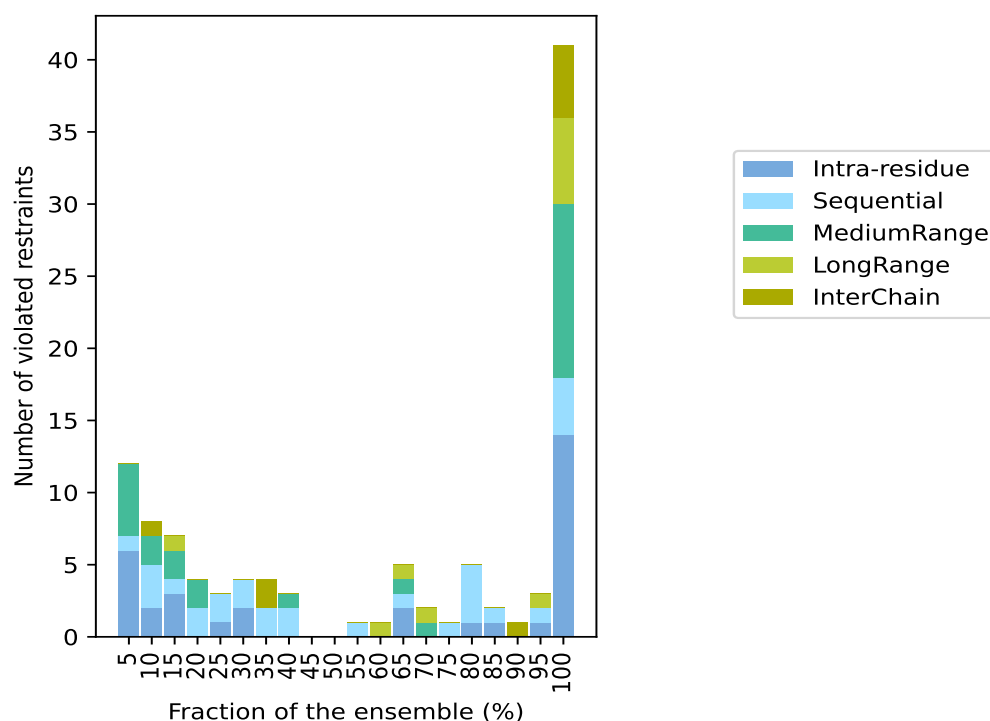
Violation analysis may find that some restraints are violated in few models and some are violated in most of models. The following table provides this information as number of violated restraints for a given fraction of the ensemble. In total, 1189(IR:398, SQ:273, MR:249, LR:100, IC:169) restraints are 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	%
6	1	5	0	0	12	1	5.0
2	3	2	0	1	8	2	10.0
3	1	2	1	0	7	3	15.0
0	2	2	0	0	4	4	20.0
1	2	0	0	0	3	5	25.0
2	2	0	0	0	4	6	30.0
0	2	0	0	2	4	7	35.0
0	2	1	0	0	3	8	40.0
0	0	0	0	0	0	9	45.0
0	0	0	0	0	0	10	50.0
0	1	0	0	0	1	11	55.0
0	0	0	1	0	1	12	60.0
2	1	1	1	0	5	13	65.0
0	0	1	1	0	2	14	70.0
0	1	0	0	0	1	15	75.0
1	4	0	0	0	5	16	80.0
1	1	0	0	0	2	17	85.0
0	0	0	0	1	1	18	90.0
1	1	0	1	0	3	19	95.0
14	4	12	6	5	41	20	100.0

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

⁵Inter-chain restraints, ⁶ Number of models with violations

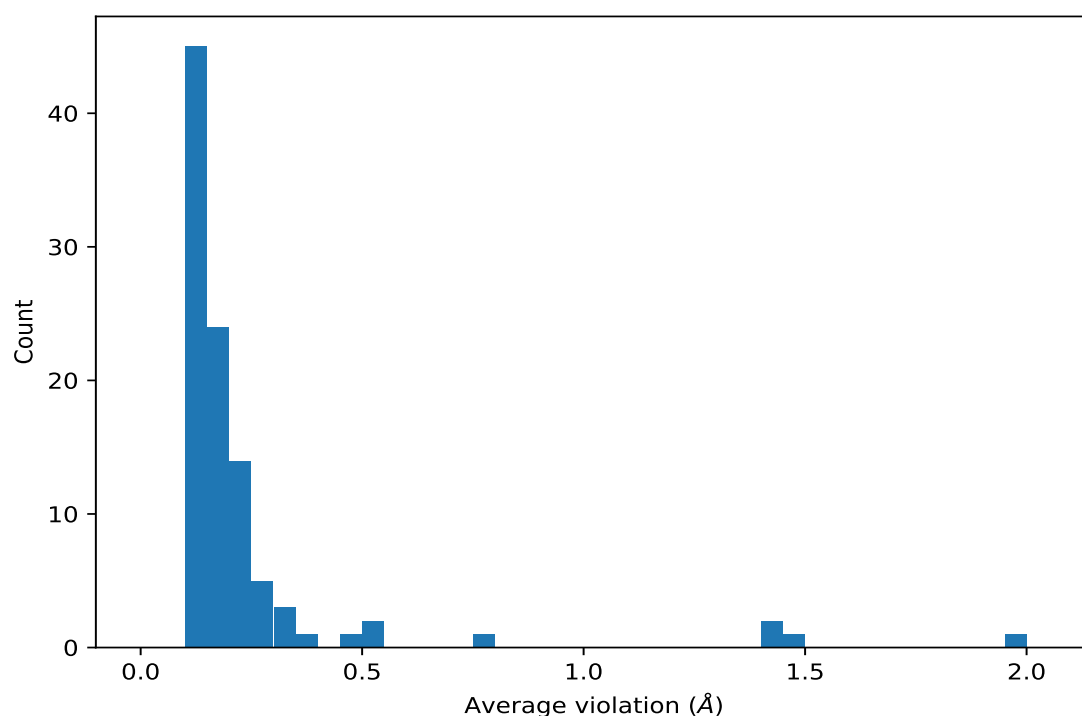
9.3.1 Bar graph : Distance violation statistics for the ensemble [i](#)



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 violations for the 10 worst performing restraints, sorted by number of violated models and the mean violation value. The Key (restraint list ID, restraint ID) is the unique identifier for a given restraint. Rows with same key represent combinatorial or ambiguous restraints and are counted as a single restraint.

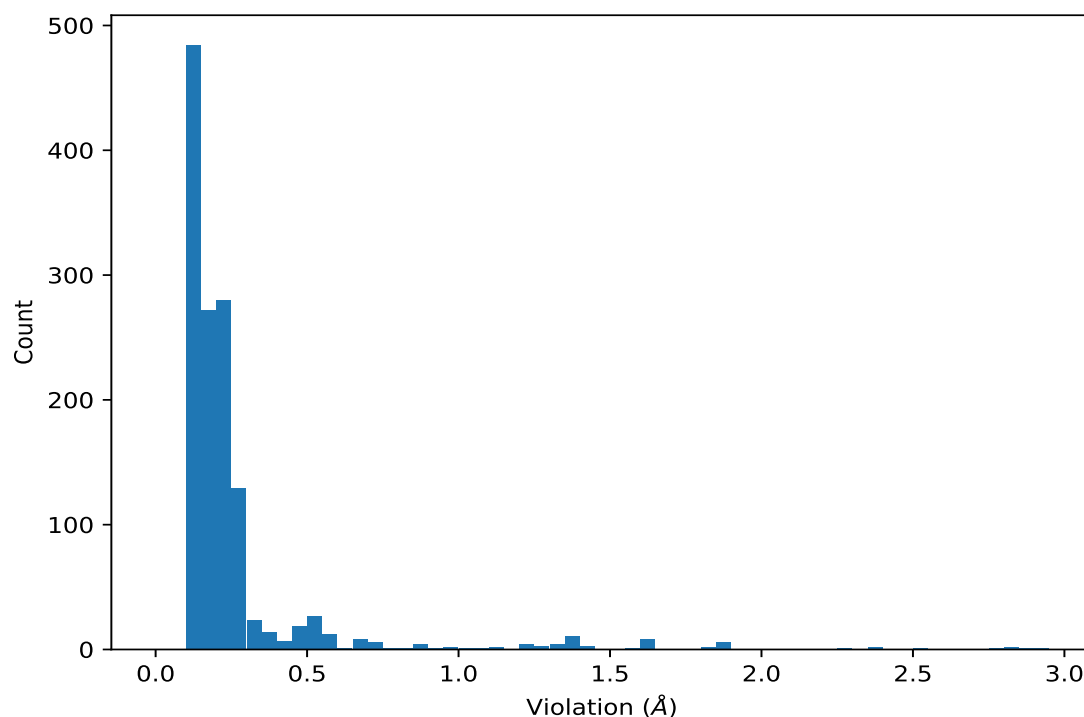
Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,650)	2:23:B:VAL:HA	2:25:B:GLN:H	20	1.49	0.12	1.42
(1,830)	2:31:B:HIS:HE1	2:34:B:GLU:HB3	20	0.75	0.09	0.72
(1,1006)	2:36:B:LEU:HB2	2:45:B:PHE:HB3	20	0.54	0.03	0.53
(1,300)	1:11:A:SEC:HB3	1:15:A:GLN:HB3	20	0.52	0.04	0.51
(1,503)	1:16:A:LEU:HB3	2:39:B:VAL:HA	20	0.48	0.02	0.48
(1,1062)	2:37:B:TYR:HE1	2:45:B:PHE:HD2	20	0.36	0.05	0.36
(1,1196)	2:46:B:PHE:HB3	2:46:B:PHE:HE1	20	0.32	0.04	0.3
(1,1171)	2:45:B:PHE:HB3	2:45:B:PHE:HE1	20	0.3	0.01	0.3
(1,230)	1:9:A:SER:HB2	2:26:B:HIS:HE1	20	0.3	0.01	0.3
(1,1168)	2:45:B:PHE:HA	2:45:B:PHE:HE1	20	0.26	0.02	0.27

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 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)
(1,142)	1:5:A:GLN:HG3	1:11:A:SEC:HA	2	2.91
(1,142)	1:5:A:GLN:HG3	1:11:A:SEC:HA	10	2.88
(1,142)	1:5:A:GLN:HG3	1:11:A:SEC:HA	12	2.82
(1,142)	1:5:A:GLN:HG3	1:11:A:SEC:HA	5	2.81
(1,142)	1:5:A:GLN:HG3	1:11:A:SEC:HA	9	2.75
(1,142)	1:5:A:GLN:HG3	1:11:A:SEC:HA	3	2.5
(1,142)	1:5:A:GLN:HG3	1:11:A:SEC:HA	19	2.37
(1,142)	1:5:A:GLN:HG3	1:11:A:SEC:HA	15	2.35
(1,142)	1:5:A:GLN:HG3	1:11:A:SEC:HA	1	2.25
(1,143)	1:5:A:GLN:HG2	1:11:A:SEC:HB2	3	1.9

10 Dihedral-angle violation analysis ⓘ

No dihedral-angle restraints found