



wwPDB NMR Structure Validation Summary Report ⓘ

Mar 10, 2026 – 03:42 AM UTC

PDB ID : 2LV3 / pdb_00002lv3
BMRB ID : 17636
Title : Structure-functional characterization of Grx domain of Mus musculus TGR
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Deposited on : 2012-06-28

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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) : 2.49

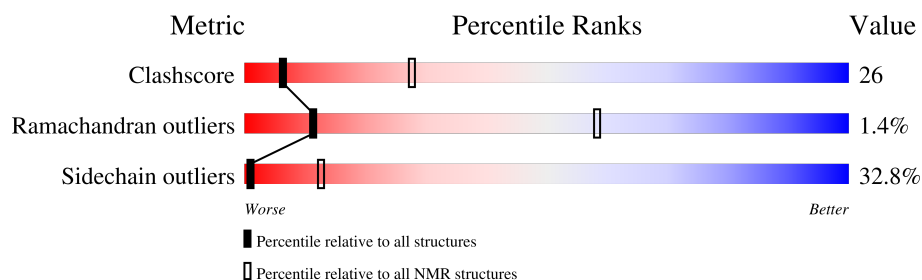
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 87%.

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	118	39% 32% 9% 6% 14%

2 Ensemble composition and analysis

This entry contains 20 models. Model 11 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *fewest violations*.

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:27-A:121 (95)	0.43	11

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. No single-model clusters were found.

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

3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 1638 atoms, of which 821 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Thioredoxin reductase 3.

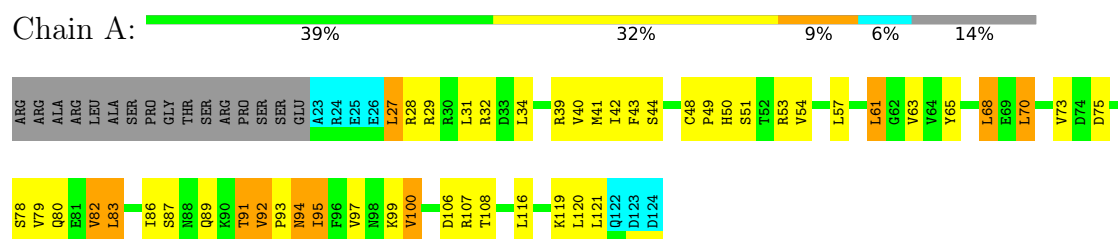
Mol	Chain	Residues	Atoms						Trace
1	A	102	Total	C	H	N	O	S	0
			1638	508	821	150	156	3	

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.

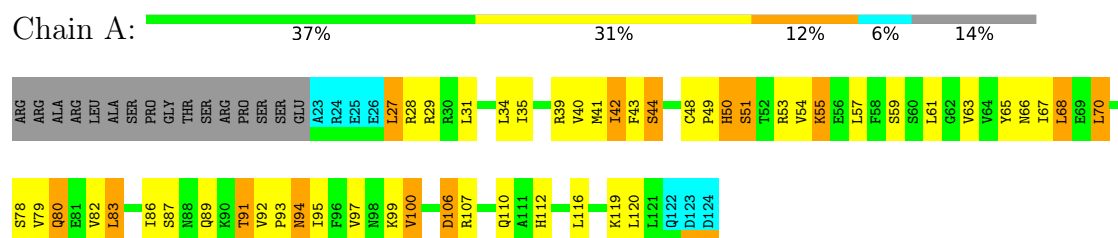
- Molecule 1: Thioredoxin reductase 3



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

The representative model is number 11. Colouring as in section 4.1 above.

- Molecule 1: Thioredoxin reductase 3



5 Refinement protocol and experimental data overview

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

Of the 20 calculated structures, 20 were deposited, based on the following criterion: *all calculated structures submitted*.

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

Software name	Classification	Version
CYANA 2.1	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	1400
Number of shifts mapped to atoms	1248
Number of unparsed shifts	0
Number of shifts with mapping errors	152
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	87%

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	758	775	775	39±4
All	All	15160	15500	15500	783

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 26.

5 of 251 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:102:VAL:HG11	1:A:108:THR:HG23	0.99	1.35	15	4
1:A:31:LEU:HD13	1:A:83:LEU:HD23	0.92	1.41	10	1
1:A:83:LEU:HD22	1:A:86:ILE:HD12	0.87	1.44	16	9
1:A:70:LEU:HD12	1:A:92:VAL:HG11	0.87	1.47	16	1
1:A:83:LEU:HD12	1:A:86:ILE:HD12	0.85	1.48	19	2

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	95/118 (81%)	88±1 (92±1%)	6±1 (6±2%)	1±1 (1±1%)	11	58
All	All	1900/2360 (81%)	1753 (92%)	121 (6%)	26 (1%)	11	58

All 3 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	106	ASP	14
1	A	73	VAL	11
1	A	105	CYS	1

6.3.2 Protein sidechains ⓘ

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	87/106 (82%)	58±4 (67±5%)	29±4 (33±5%)	1	13
All	All	1740/2120 (82%)	1169 (67%)	571 (33%)	1	13

5 of 64 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	44	SER	20
1	A	87	SER	20
1	A	89	GLN	20
1	A	94	ASN	20
1	A	95	ILE	20

6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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 87% for the well-defined parts and 87% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *assigned_chem_shift_list_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	1400
Number of shifts mapped to atoms	1248
Number of unparsed shifts	0
Number of shifts with mapping errors	152
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

The following assigned chemical shifts were not mapped to the molecules present in the coordinate file.

- No matching atom found in the structure. First 5 (of 152) occurrences are reported below.

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	7	ARG	H	8.165	0.020	1
1	A	7	ARG	HA	4.224	0.020	1
1	A	7	ARG	HB2	1.79	0.020	2
1	A	7	ARG	HB3	1.697	0.020	2
1	A	7	ARG	HG2	1.54	0.020	1
1	A	7	ARG	HG3	1.54	0.020	1
1	A	7	ARG	CA	56.136	0.3	1
1	A	7	ARG	CB	30.583	0.3	1
1	A	7	ARG	CG	27.289	0.3	1
1	A	7	ARG	N	121.462	0.3	1
1	A	8	ARG	H	8.412	0.020	1
1	A	8	ARG	HA	4.232	0.020	1
1	A	8	ARG	HB2	1.72	0.020	1
1	A	8	ARG	HB3	1.72	0.020	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	8	ARG	CA	56.208	0.3	1
1	A	8	ARG	CB	30.583	0.3	1
1	A	8	ARG	N	123.153	0.3	1
1	A	9	ALA	H	8.284	0.020	1
1	A	9	ALA	HA	4.202	0.020	1
1	A	9	ALA	HB1	1.286	0.020	1
1	A	9	ALA	HB2	1.286	0.020	1
1	A	9	ALA	HB3	1.286	0.020	1
1	A	9	ALA	CA	52.403	0.3	1
1	A	9	ALA	CB	18.943	0.3	1
1	A	9	ALA	N	126.117	0.3	1
1	A	10	ARG	H	8.285	0.020	1
1	A	10	ARG	HA	4.216	0.020	1
1	A	10	ARG	HB2	1.699	0.020	1
1	A	10	ARG	HB3	1.699	0.020	1
1	A	10	ARG	HD2	3.105	0.020	1
1	A	10	ARG	HD3	3.105	0.020	1
1	A	10	ARG	CA	55.998	0.3	1
1	A	10	ARG	CB	30.681	0.3	1
1	A	10	ARG	CD	43.227	0.3	1
1	A	10	ARG	N	121.268	0.3	1
1	A	11	LEU	H	8.305	0.020	1
1	A	11	LEU	HA	4.265	0.020	1
1	A	11	LEU	HB2	1.516	0.020	1
1	A	11	LEU	HB3	1.516	0.020	1
1	A	11	LEU	HD11	0.843	0.020	2
1	A	11	LEU	HD12	0.843	0.020	2
1	A	11	LEU	HD13	0.843	0.020	2
1	A	11	LEU	HD21	0.778	0.020	2
1	A	11	LEU	HD22	0.778	0.020	2
1	A	11	LEU	HD23	0.778	0.020	2
1	A	11	LEU	HG	1.556	0.020	1
1	A	11	LEU	CA	54.96	0.3	1
1	A	11	LEU	CB	42.448	0.3	1
1	A	11	LEU	CD1	24.649	0.3	1
1	A	11	LEU	CD2	23.484	0.3	1
1	A	11	LEU	CG	27.16	0.3	1
1	A	11	LEU	N	124.359	0.3	1
1	A	12	ALA	H	8.274	0.020	1
1	A	12	ALA	HA	4.241	0.020	1
1	A	12	ALA	HB1	1.282	0.020	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	12	ALA	HB2	1.282	0.020	1
1	A	12	ALA	HB3	1.282	0.020	1
1	A	12	ALA	CA	52.248	0.3	1
1	A	12	ALA	CB	19.312	0.3	1
1	A	12	ALA	N	125.64	0.3	1
1	A	13	SER	H	8.278	0.020	1
1	A	13	SER	HA	4.635	0.020	1
1	A	13	SER	HB2	3.66	0.020	1
1	A	13	SER	HB3	3.66	0.020	1
1	A	13	SER	CA	56.34	0.3	1
1	A	13	SER	CB	63.214	0.3	1
1	A	13	SER	N	117.457	0.3	1
1	A	14	PRO	HA	4.367	0.020	1
1	A	14	PRO	HB2	2.231	0.020	2
1	A	14	PRO	HB3	1.89	0.020	2
1	A	14	PRO	HD2	3.74	0.020	2
1	A	14	PRO	HD3	3.662	0.020	2
1	A	14	PRO	HG2	1.94	0.020	1
1	A	14	PRO	HG3	1.94	0.020	1
1	A	14	PRO	C	177.125	0.3	1
1	A	14	PRO	CA	63.544	0.3	1
1	A	14	PRO	CB	32.131	0.3	1
1	A	14	PRO	CD	50.794	0.3	1
1	A	14	PRO	CG	27.439	0.3	1
1	A	15	GLY	H	8.455	0.020	1
1	A	15	GLY	HA2	3.915	0.020	1
1	A	15	GLY	HA3	3.915	0.020	1
1	A	15	GLY	C	174.413	0.3	1
1	A	15	GLY	CA	45.276	0.3	1
1	A	15	GLY	N	109.946	0.3	1
1	A	16	THR	H	7.98	0.020	1
1	A	16	THR	HA	4.313	0.020	1
1	A	16	THR	HB	4.177	0.020	1
1	A	16	THR	HG21	1.106	0.020	1
1	A	16	THR	HG22	1.106	0.020	1
1	A	16	THR	HG23	1.106	0.020	1
1	A	16	THR	CA	61.621	0.3	1
1	A	16	THR	CB	69.819	0.3	1
1	A	16	THR	CG2	21.482	0.3	1
1	A	16	THR	N	113.735	0.3	1
1	A	17	SER	H	8.349	0.020	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	17	SER	HA	4.388	0.020	1
1	A	17	SER	HB2	3.766	0.020	1
1	A	17	SER	HB3	3.766	0.020	1
1	A	17	SER	CA	58.272	0.3	1
1	A	17	SER	CB	63.741	0.3	1
1	A	17	SER	N	119.262	0.3	1
1	A	18	ARG	H	8.342	0.020	1
1	A	18	ARG	HA	4.561	0.020	1
1	A	18	ARG	HB2	1.748	0.020	2
1	A	18	ARG	HB3	1.638	0.020	2
1	A	18	ARG	HD2	3.11	0.020	1
1	A	18	ARG	HD3	3.11	0.020	1
1	A	18	ARG	HG2	1.586	0.020	1
1	A	18	ARG	HG3	1.586	0.020	1
1	A	18	ARG	C	174.009	0.3	1
1	A	18	ARG	CA	53.878	0.3	1
1	A	18	ARG	CB	30.005	0.3	1
1	A	18	ARG	CD	43.209	0.3	1
1	A	18	ARG	CG	26.539	0.3	1
1	A	18	ARG	N	124.559	0.3	1
1	A	19	PRO	HA	4.366	0.020	1
1	A	19	PRO	HB2	2.225	0.020	2
1	A	19	PRO	HB3	1.831	0.020	2
1	A	19	PRO	HD2	3.74	0.020	1
1	A	19	PRO	HD3	3.74	0.020	1
1	A	19	PRO	HG2	1.953	0.020	1
1	A	19	PRO	HG3	1.953	0.020	1
1	A	19	PRO	CA	63.306	0.3	1
1	A	19	PRO	CB	31.782	0.3	1
1	A	19	PRO	CD	50.809	0.3	1
1	A	19	PRO	CG	27.143	0.3	1
1	A	20	SER	H	8.564	0.020	1
1	A	20	SER	HA	4.344	0.020	1
1	A	20	SER	HB2	3.961	0.020	2
1	A	20	SER	HB3	3.851	0.020	2
1	A	20	SER	CA	58.503	0.3	1
1	A	20	SER	CB	63.538	0.3	1
1	A	20	SER	N	118.012	0.3	1
1	A	21	SER	H	8.41	0.020	1
1	A	21	SER	HA	4.259	0.020	1
1	A	21	SER	HB2	3.872	0.020	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	21	SER	HB3	3.872	0.020	1
1	A	21	SER	CA	59.909	0.3	1
1	A	21	SER	CB	63.144	0.3	1
1	A	21	SER	N	123.738	0.3	1
1	A	22	GLU	H	8.447	0.020	1
1	A	22	GLU	HA	4.078	0.020	1
1	A	22	GLU	HB2	1.956	0.020	1
1	A	22	GLU	HB3	1.956	0.020	1
1	A	22	GLU	HG2	2.232	0.020	1
1	A	22	GLU	HG3	2.232	0.020	1
1	A	22	GLU	C	178.352	0.3	1
1	A	22	GLU	CA	58.731	0.3	1
1	A	22	GLU	CB	29.267	0.3	1
1	A	22	GLU	CG	36.644	0.3	1
1	A	22	GLU	N	123.738	0.3	1

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
$^{13}\text{C}_\alpha$	116	-0.42 ± 0.22	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	109	0.32 ± 0.18	None needed (< 0.5 ppm)
$^{13}\text{C}'$	83	-0.31 ± 0.09	None needed (< 0.5 ppm)
^{15}N	112	-0.71 ± 0.36	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 87%, i.e. 1174 atoms were assigned a chemical shift out of a possible 1349. 0 out of 23 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	448/477 (94%)	191/194 (98%)	166/190 (87%)	91/93 (98%)
Sidechain	666/793 (84%)	451/514 (88%)	203/241 (84%)	12/38 (32%)
Aromatic	60/79 (76%)	30/40 (75%)	30/36 (83%)	0/3 (0%)
Overall	1174/1349 (87%)	672/748 (90%)	399/467 (85%)	103/134 (77%)

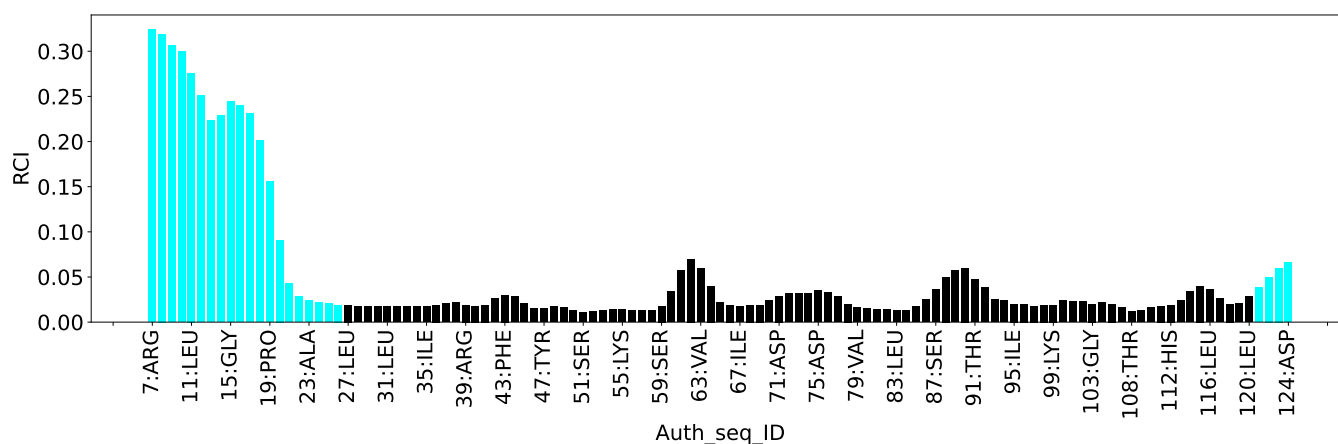
7.1.4 Statistically unusual chemical shifts [i](#)

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	0
Intra-residue ($ i-j =0$)	0
Sequential ($ i-j =1$)	0
Medium range ($ i-j >1$ and $ i-j <5$)	0
Long range ($ i-j \geq 5$)	0
Inter-chain	0
Hydrogen bond restraints	0
Disulfide bond restraints	0
Total dihedral-angle restraints	175
Number of unmapped restraints	0
Number of restraints per residue	0
Number of long range restraints per residue 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. There are no distance restraints

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)	21.6	9.65

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Bins (°)	Average number of violations per model	Max (°)
10.0-20.0 (Medium)	1.2	19.98
>20.0 (Large)	0.5	23.37

9 Distance violation analysis ⓘ

No distance restraints data found

10 Dihedral-angle violation analysis [i](#)

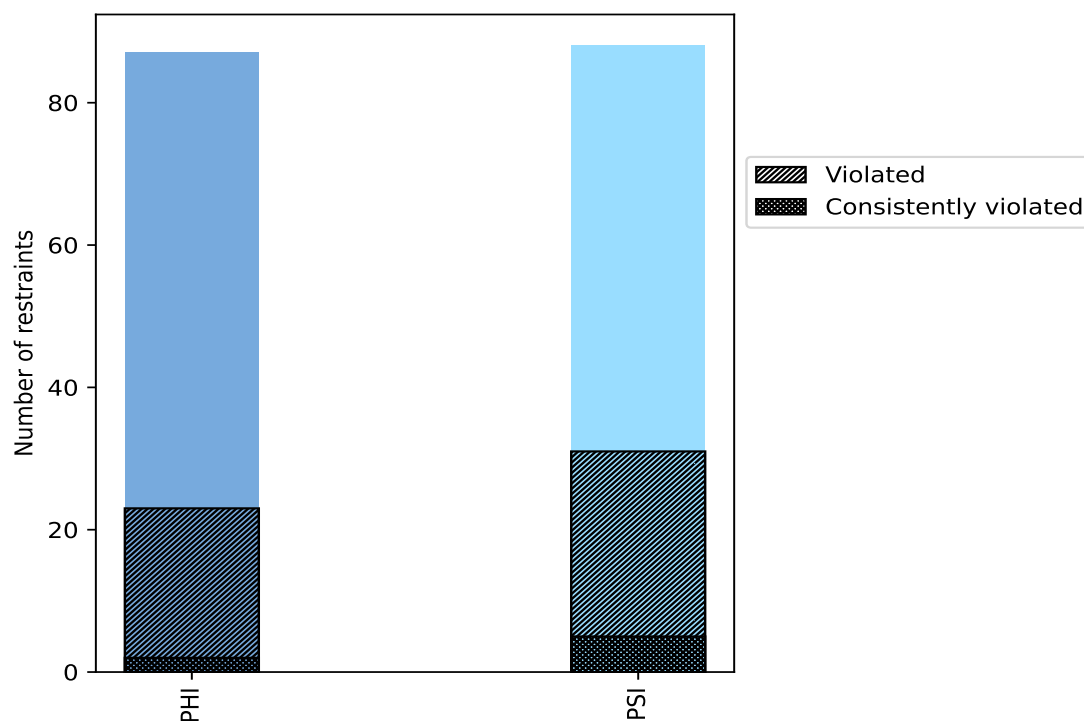
10.1 Summary of dihedral-angle violations [i](#)

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	87	49.7	23	26.4	13.1	2	2.3	1.1
PSI	88	50.3	31	35.2	17.7	5	5.7	2.9
Total	175	100.0	54	30.9	30.9	7	4.0	4.0

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](#)



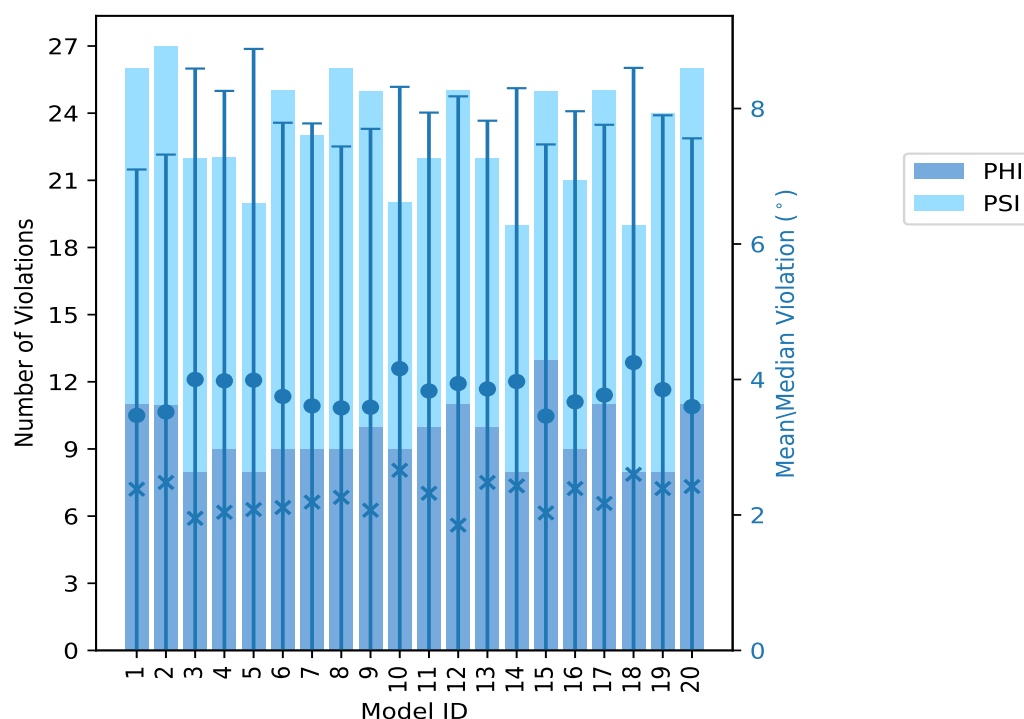
Violated and consistently violated restraints are shown using different hatch patterns in their respective categories

10.2 Dihedral-angle violation statistics for each model

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	11	15	26	3.47	19.41	3.63	2.38
2	11	16	27	3.52	19.62	3.8	2.48
3	8	14	22	4.0	20.21	4.59	1.95
4	9	13	22	3.98	20.28	4.28	2.04
5	8	12	20	3.99	23.37	4.89	2.08
6	9	16	25	3.75	19.52	4.04	2.11
7	9	14	23	3.61	19.98	4.17	2.19
8	9	17	26	3.58	19.24	3.86	2.26
9	10	15	25	3.59	20.14	4.11	2.07
10	9	11	20	4.16	20.27	4.16	2.66
11	10	12	22	3.83	19.6	4.11	2.32
12	11	14	25	3.94	20.7	4.24	1.85
13	10	12	22	3.86	19.1	3.96	2.48
14	8	11	19	3.97	20.1	4.33	2.43
15	13	12	25	3.46	19.92	4.01	2.03
16	9	12	21	3.67	20.12	4.29	2.39
17	11	14	25	3.77	19.72	3.99	2.17
18	8	11	19	4.25	18.79	4.35	2.6
19	8	16	24	3.85	19.82	4.05	2.39
20	11	15	26	3.6	20.51	3.96	2.42

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

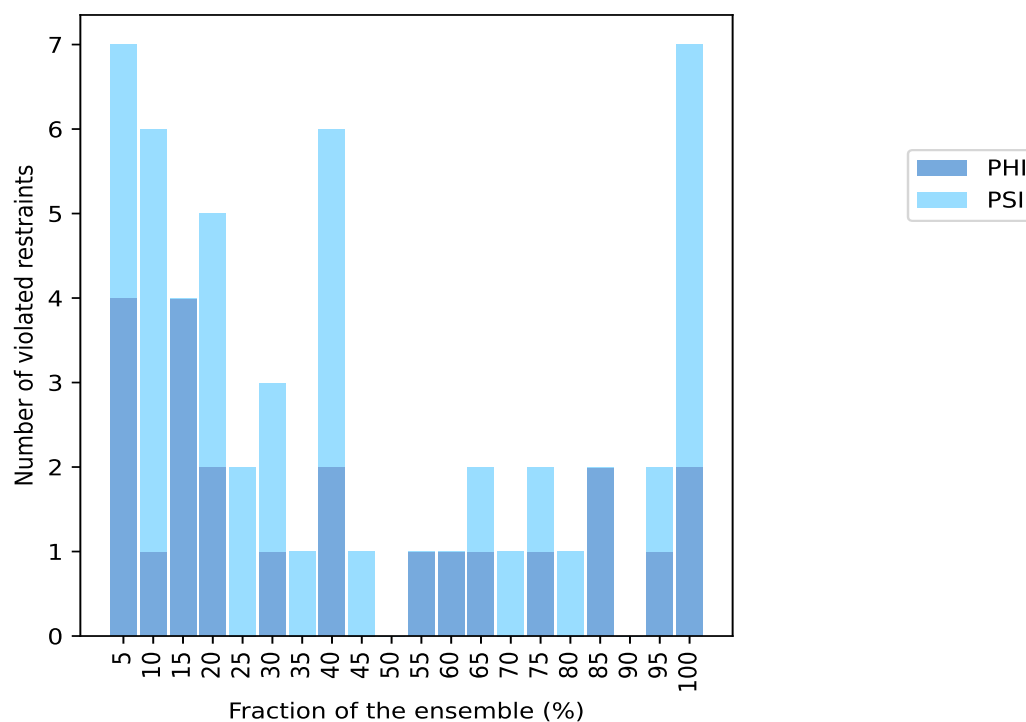
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Number of violated restraints			Fraction of the ensemble	
PHI	PSI	Total	Count ¹	%
1	0	1	12	60.0
1	1	2	13	65.0
0	1	1	14	70.0
1	1	2	15	75.0
0	1	1	16	80.0
2	0	2	17	85.0
0	0	0	18	90.0
1	1	2	19	95.0
2	5	7	20	100.0

¹ Number of models with violations

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

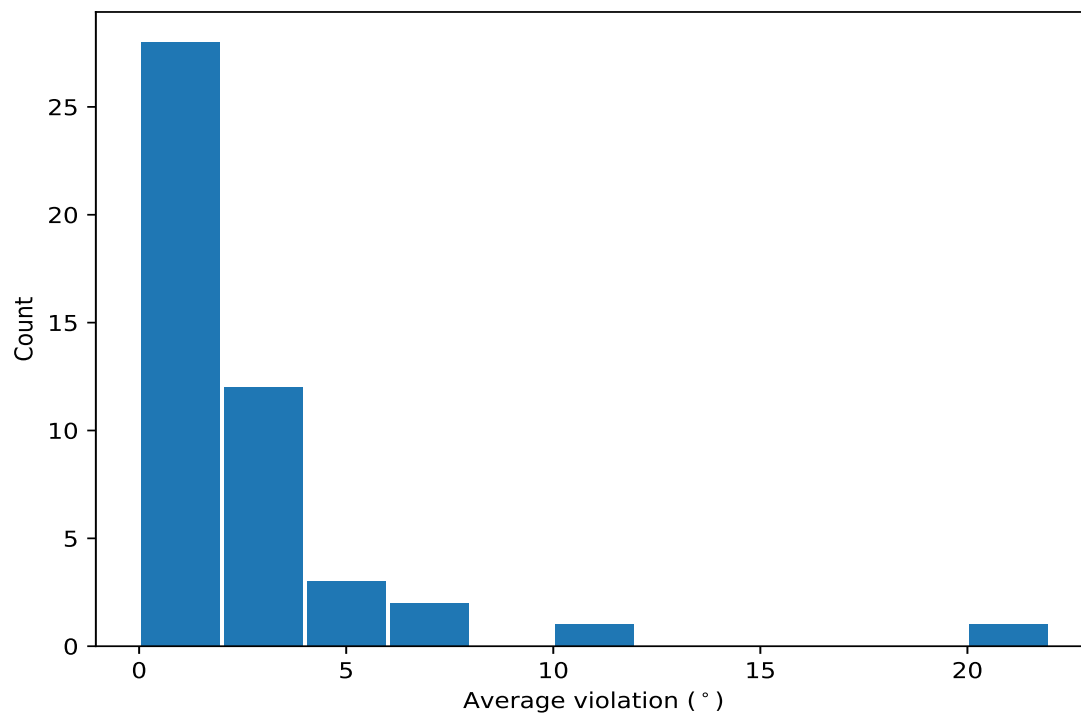


10.4 Most violated dihedral-angle restraints in the ensemble ⓘ

10.4.1 Histogram : Distribution of mean dihedral-angle violations ⓘ

The following histogram shows the distribution of the average value of the violation. The average is calculated for each restraint that is violated in more than one model over all the violated models

in the ensemble



10.4.2 Table: Most violated dihedral-angle restraints [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.

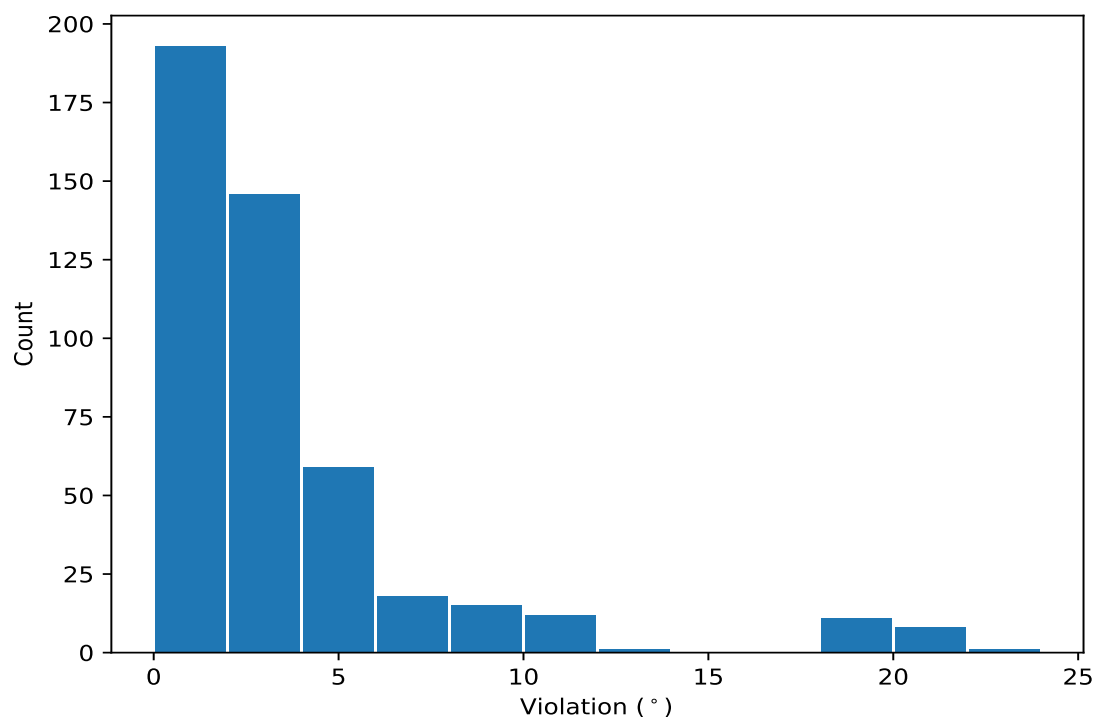
Key	Atom-1	Atom-2	Atom-3	Atom-4	Models ¹	Mean	SD ²	Median
(1,125)	1:92:A:VAL:N	1:92:A:VAL:CA	1:92:A:VAL:C	1:93:A:PRO:N	20	20.02	0.9	19.95
(1,123)	1:91:A:THR:N	1:91:A:THR:CA	1:91:A:THR:C	1:92:A:VAL:N	20	10.14	1.12	10.4
(1,49)	1:49:A:PRO:N	1:49:A:PRO:CA	1:49:A:PRO:C	1:50:A:HIS:N	20	6.24	0.98	6.12
(1,81)	1:67:A:ILE:N	1:67:A:ILE:CA	1:67:A:ILE:C	1:68:A:LEU:N	20	6.09	1.98	5.5
(1,131)	1:95:A:ILE:N	1:95:A:ILE:CA	1:95:A:ILE:C	1:96:A:PHE:N	20	5.17	1.42	5.05
(1,82)	1:67:A:ILE:C	1:68:A:LEU:N	1:68:A:LEU:CA	1:68:A:LEU:C	20	4.1	1.75	3.61
(1,80)	1:66:A:ASN:C	1:67:A:ILE:N	1:67:A:ILE:CA	1:67:A:ILE:C	20	3.19	1.32	3.0
(1,127)	1:93:A:PRO:N	1:93:A:PRO:CA	1:93:A:PRO:C	1:94:A:ASN:N	19	2.56	0.97	2.47
(1,164)	1:116:A:LEU:C	1:117:A:LEU:N	1:117:A:LEU:CA	1:117:A:LEU:C	19	2.07	0.66	1.96
(1,44)	1:46:A:SER:C	1:47:A:TYR:N	1:47:A:TYR:CA	1:47:A:TYR:C	17	2.64	0.84	2.46

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

10.5 All violated dihedral-angle restraints [i](#)

10.5.1 Histogram : Distribution of violations [i](#)

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



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

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

Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,125)	1:92:A:VAL:N	1:92:A:VAL:CA	1:92:A:VAL:C	1:93:A:PRO:N	5	23.37
(1,125)	1:92:A:VAL:N	1:92:A:VAL:CA	1:92:A:VAL:C	1:93:A:PRO:N	12	20.7
(1,125)	1:92:A:VAL:N	1:92:A:VAL:CA	1:92:A:VAL:C	1:93:A:PRO:N	20	20.51
(1,125)	1:92:A:VAL:N	1:92:A:VAL:CA	1:92:A:VAL:C	1:93:A:PRO:N	4	20.28
(1,125)	1:92:A:VAL:N	1:92:A:VAL:CA	1:92:A:VAL:C	1:93:A:PRO:N	10	20.27
(1,125)	1:92:A:VAL:N	1:92:A:VAL:CA	1:92:A:VAL:C	1:93:A:PRO:N	3	20.21
(1,125)	1:92:A:VAL:N	1:92:A:VAL:CA	1:92:A:VAL:C	1:93:A:PRO:N	9	20.14
(1,125)	1:92:A:VAL:N	1:92:A:VAL:CA	1:92:A:VAL:C	1:93:A:PRO:N	16	20.12
(1,125)	1:92:A:VAL:N	1:92:A:VAL:CA	1:92:A:VAL:C	1:93:A:PRO:N	14	20.1
(1,125)	1:92:A:VAL:N	1:92:A:VAL:CA	1:92:A:VAL:C	1:93:A:PRO:N	7	19.98