



Full wwPDB NMR Structure Validation Report ⓘ

Mar 5, 2026 – 03:09 AM UTC

PDB ID : 1WF0 / pdb_00001wf0
Title : Solution structure of RRM domain in TAR DNA-binding protein-43
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Deposited on : 2004-05-25

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 ⓘ 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
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

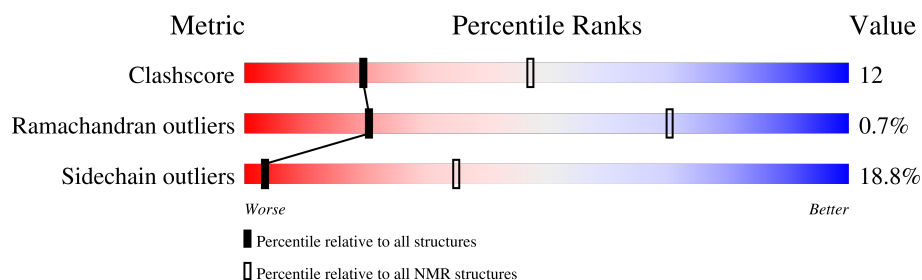
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment was not calculated.

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	88	

2 Ensemble composition and analysis

This entry contains 20 models. Model 7 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *lowest energy*.

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:7-A:73 (67)	0.32	7

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

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

The models can be grouped into 4 clusters and 7 single-model clusters were found.

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

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 1278 atoms, of which 618 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called TAR DNA-binding protein-43.

Mol	Chain	Residues	Atoms						Trace
1	A	88	Total	C	H	N	O	S	0
			1278	412	618	110	134	4	

There are 14 discrepancies between the modelled and reference sequences:

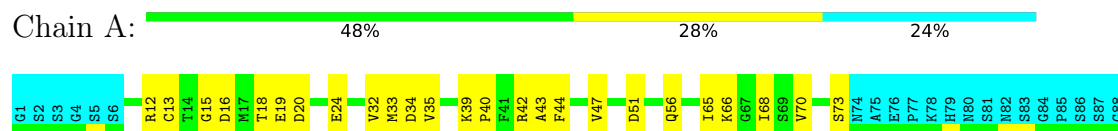
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	cloning artifact	UNP Q13148
A	2	SER	-	cloning artifact	UNP Q13148
A	3	SER	-	cloning artifact	UNP Q13148
A	4	GLY	-	cloning artifact	UNP Q13148
A	5	SER	-	cloning artifact	UNP Q13148
A	6	SER	-	cloning artifact	UNP Q13148
A	7	GLY	-	cloning artifact	UNP Q13148
A	15	GLY	GLU	SEE REMARK 999	UNP Q13148
A	83	SER	-	cloning artifact	UNP Q13148
A	84	GLY	-	cloning artifact	UNP Q13148
A	85	PRO	-	cloning artifact	UNP Q13148
A	86	SER	-	cloning artifact	UNP Q13148
A	87	SER	-	cloning artifact	UNP Q13148
A	88	GLY	-	cloning artifact	UNP Q13148

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: TAR DNA-binding protein-43

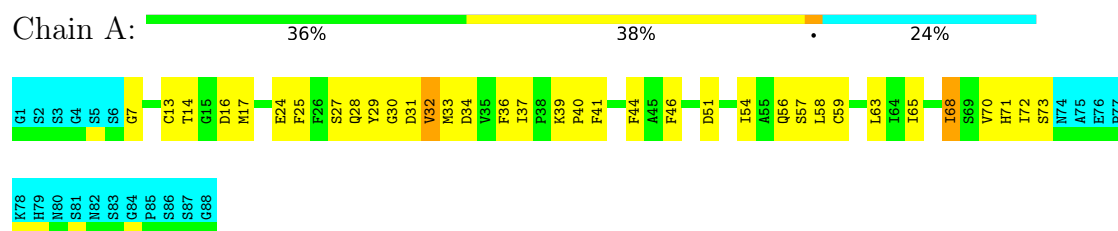


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

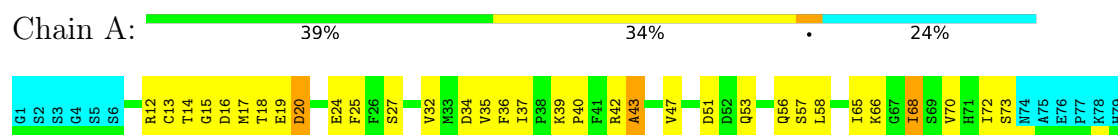
4.2.1 Score per residue for model 1

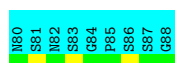
- Molecule 1: TAR DNA-binding protein-43



4.2.2 Score per residue for model 2

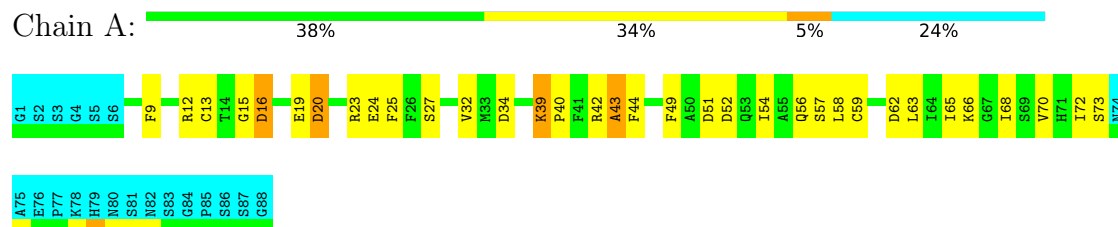
- Molecule 1: TAR DNA-binding protein-43





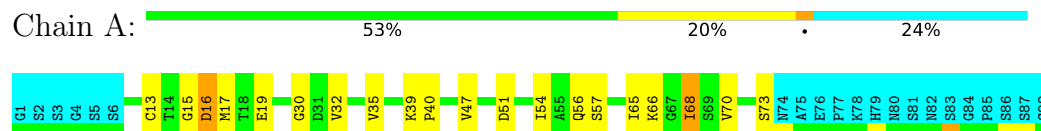
4.2.3 Score per residue for model 3

- Molecule 1: TAR DNA-binding protein-43



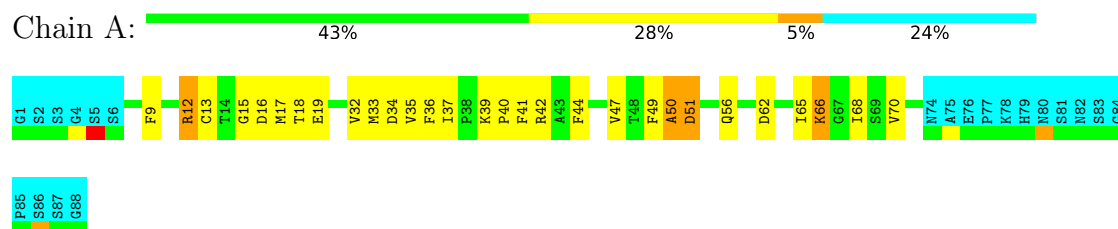
4.2.4 Score per residue for model 4

- Molecule 1: TAR DNA-binding protein-43



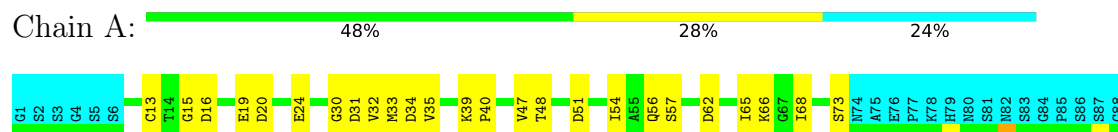
4.2.5 Score per residue for model 5

- Molecule 1: TAR DNA-binding protein-43



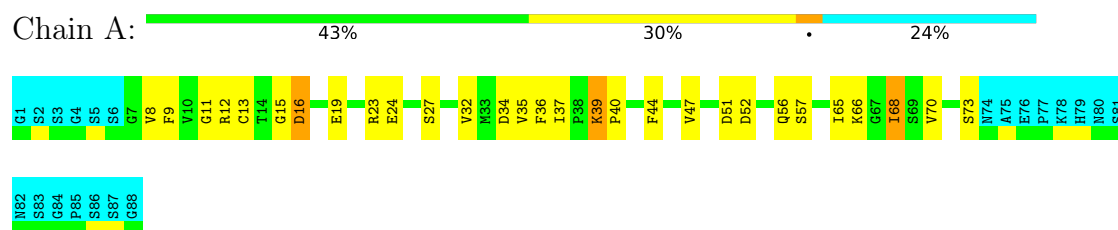
4.2.6 Score per residue for model 6

- Molecule 1: TAR DNA-binding protein-43



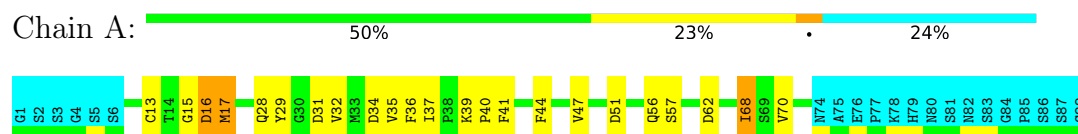
4.2.7 Score per residue for model 7 (medoid)

- Molecule 1: TAR DNA-binding protein-43



4.2.8 Score per residue for model 8

- Molecule 1: TAR DNA-binding protein-43



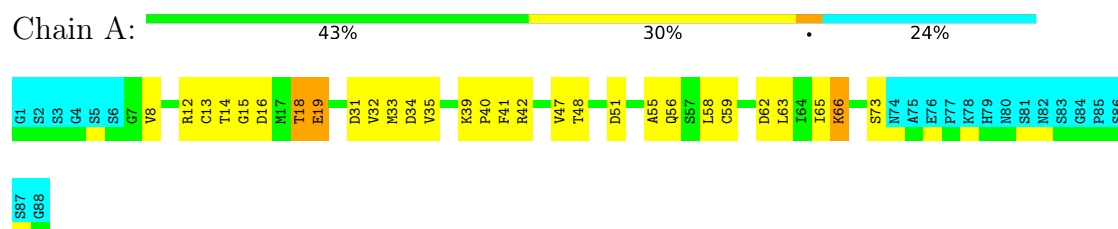
4.2.9 Score per residue for model 9

- Molecule 1: TAR DNA-binding protein-43



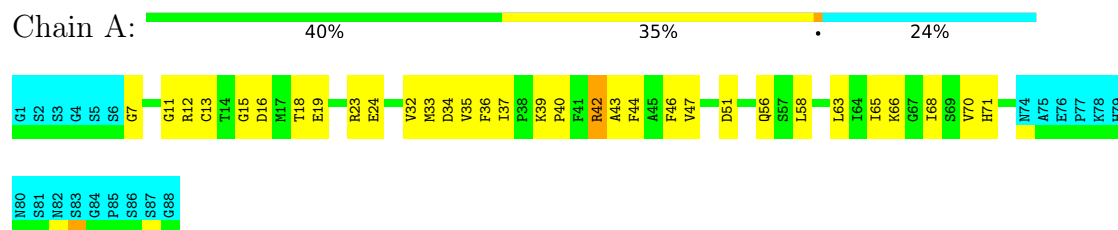
4.2.10 Score per residue for model 10

- Molecule 1: TAR DNA-binding protein-43



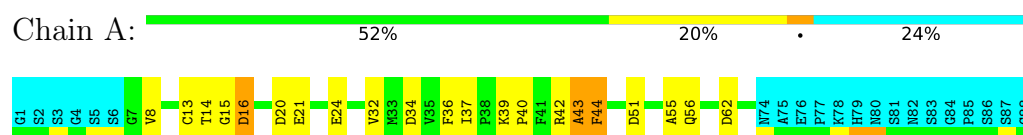
4.2.11 Score per residue for model 11

- Molecule 1: TAR DNA-binding protein-43



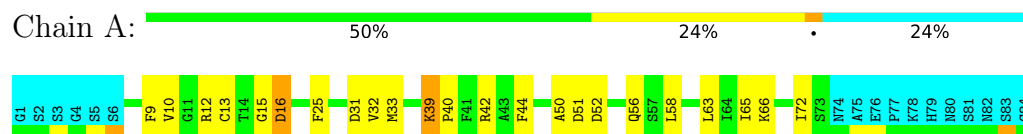
4.2.12 Score per residue for model 12

- Molecule 1: TAR DNA-binding protein-43



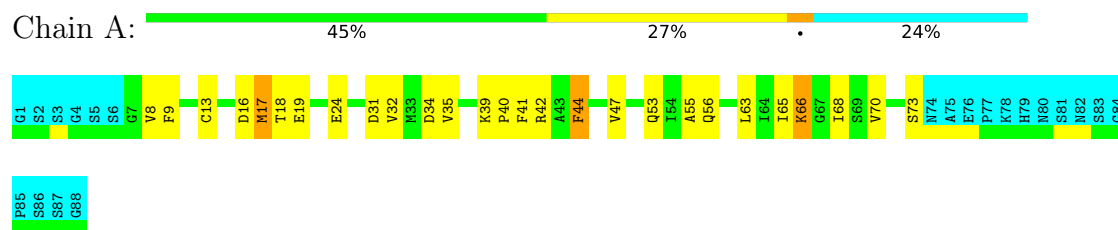
4.2.13 Score per residue for model 13

- Molecule 1: TAR DNA-binding protein-43



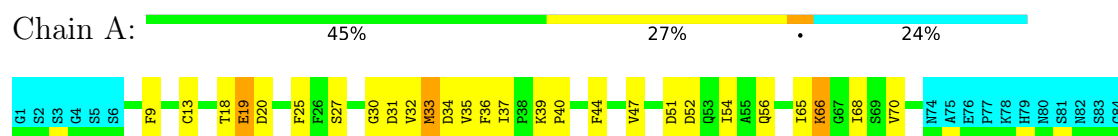
4.2.14 Score per residue for model 14

- Molecule 1: TAR DNA-binding protein-43



4.2.15 Score per residue for model 15

- Molecule 1: TAR DNA-binding protein-43



P85
S86
S87
G88

4.2.16 Score per residue for model 16

- Molecule 1: TAR DNA-binding protein-43

Chain A:  48% 25% • 24%

G1 S2 S3 S4 S5 S6 S7 V8 T14 T15 D16 M17 T18 E19 D20 E24 S27 D31 D34 V35 F36 I37 P38 K39 P40 F44 V47 D52 A55 L63 I64 I65 K66 H71 I72 S73 N74 A75 E76 E77 P77 K78 H79 N80 S81 N82 S83 S84 P85 S86

S87
G88

4.2.17 Score per residue for model 17

- Molecule 1: TAR DNA-binding protein-43

Chain A:  47% 28% • 24%

G1 S2 S3 S4 S5 S6 F9 R12 C13 G15 T14 G16 M17 D16 M18 E19 D20 V32 M33 D34 V35 K39 P40 F41 R42 A43 F44 V47 D51 Q56 D62 I65 K66 G67 I68 S73 N74 A75 E76 P77 K78 H79 N80 S81 N82 S83 G84 P85 S86 G88

4.2.18 Score per residue for model 18

- Molecule 1: TAR DNA-binding protein-43

Chain A:  52% 22% • 24%

G1 S2 S3 S4 S5 S6 C13 T14 R15 D16 M17 T18 E19 D20 E24 V32 M33 D34 V35 K39 P40 F41 R42 A43 F44 V47 D51 Q56 I68 S73 N74 A75 E76 P77 K78 H79 N80 S81 N82 S83 G84 P85 S86 G88

4.2.19 Score per residue for model 19

- Molecule 1: TAR DNA-binding protein-43

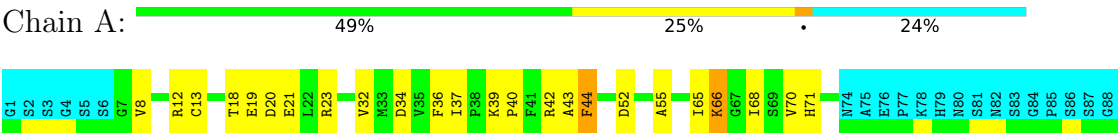
Chain A:  44% 28% • 24%

G1 S2 S3 S4 S5 S6 S7 R12 C13 T14 G15 D16 M17 T18 E19 E24 Y29 M33 D34 K39 P40 F41 R42 A43 F44 A45 F46 D51 Q56 S57 L58 L63 I64 I65 I68 S69 V70 S73 N74 A75 E76 P77 K78 H79 N80 S81 N82 S83 G84 P85

S86
S87
G88

4.2.20 Score per residue for model 20

● Molecule 1: TAR DNA-binding protein-43



5 Refinement protocol and experimental data overview ⓘ

The models were refined using the following method: *torsion angle dynamics*.

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

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

Software name	Classification	Version
CYANA	structure solution	1.0.8
CYANA	refinement	1.0.8

No chemical shift data was provided.

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	525	503	503	13±3
All	All	10500	10060	10060	257

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 12.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:68:ILE:CD1	1:A:70:VAL:HG13	0.72	2.15	19	11
1:A:33:MET:HE3	1:A:48:THR:HG22	0.71	1.61	10	2
1:A:35:VAL:HG22	1:A:47:VAL:HG13	0.71	1.61	7	11
1:A:35:VAL:HG13	1:A:47:VAL:HG22	0.70	1.61	15	6
1:A:58:LEU:HB3	1:A:72:ILE:HG21	0.69	1.65	2	4
1:A:44:PHE:C	1:A:44:PHE:CD1	0.67	2.73	20	12
1:A:68:ILE:HD11	1:A:70:VAL:HG13	0.65	1.68	19	3
1:A:65:ILE:HG22	1:A:66:LYS:HG3	0.64	1.69	7	9
1:A:30:GLY:HA3	1:A:54:ILE:HD13	0.62	1.70	6	4
1:A:68:ILE:C	1:A:68:ILE:HD12	0.62	2.20	17	1
1:A:33:MET:HE3	1:A:48:THR:CG2	0.58	2.27	10	2
1:A:32:VAL:O	1:A:32:VAL:HG13	0.58	1.99	18	13
1:A:35:VAL:HG22	1:A:47:VAL:HG22	0.57	1.75	18	1
1:A:10:VAL:O	1:A:10:VAL:HG12	0.57	1.98	13	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:17:MET:HE1	1:A:68:ILE:HD11	0.57	1.76	5	1
1:A:8:VAL:HG13	1:A:55:ALA:HB1	0.55	1.77	16	5
1:A:68:ILE:HD12	1:A:70:VAL:HG13	0.54	1.79	5	8
1:A:58:LEU:HD22	1:A:63:LEU:HD11	0.53	1.80	13	3
1:A:44:PHE:O	1:A:44:PHE:CD1	0.51	2.64	12	3
1:A:39:LYS:HA	1:A:40:PRO:C	0.51	2.31	14	20
1:A:12:ARG:O	1:A:70:VAL:HG12	0.51	2.06	5	1
1:A:68:ILE:CD1	1:A:70:VAL:CG1	0.50	2.89	15	4
1:A:68:ILE:HD11	1:A:70:VAL:CG1	0.50	2.36	1	2
1:A:42:ARG:O	1:A:43:ALA:C	0.49	2.56	11	9
1:A:36:PHE:CG	1:A:37:ILE:N	0.49	2.80	2	10
1:A:18:THR:O	1:A:19:GLU:C	0.49	2.55	10	10
1:A:28:GLN:HG3	1:A:29:TYR:CD1	0.49	2.43	1	2
1:A:20:ASP:OD1	1:A:21:GLU:N	0.48	2.46	12	1
1:A:16:ASP:OD1	1:A:16:ASP:C	0.48	2.56	13	1
1:A:25:PHE:CE2	1:A:65:ILE:HG12	0.48	2.43	15	3
1:A:65:ILE:O	1:A:66:LYS:CB	0.48	2.62	10	5
1:A:15:GLY:O	1:A:16:ASP:C	0.48	2.55	3	15
1:A:65:ILE:C	1:A:66:LYS:CG	0.47	2.86	16	6
1:A:32:VAL:O	1:A:33:MET:C	0.47	2.57	1	5
1:A:71:HIS:CD2	1:A:71:HIS:C	0.47	2.92	1	4
1:A:7:GLY:HA3	1:A:46:PHE:CZ	0.47	2.45	19	2
1:A:33:MET:HG2	1:A:50:ALA:HB2	0.47	1.86	13	2
1:A:19:GLU:O	1:A:23:ARG:CB	0.46	2.63	7	2
1:A:7:GLY:HA3	1:A:46:PHE:CE1	0.46	2.46	1	2
1:A:41:PHE:CD1	1:A:41:PHE:C	0.46	2.94	1	3
1:A:14:THR:O	1:A:15:GLY:C	0.46	2.58	10	3
1:A:44:PHE:CD1	1:A:44:PHE:O	0.46	2.68	13	2
1:A:12:ARG:O	1:A:68:ILE:HD13	0.46	2.11	20	1
1:A:41:PHE:O	1:A:41:PHE:CD1	0.46	2.68	8	2
1:A:68:ILE:CD1	1:A:70:VAL:HG12	0.45	2.41	1	1
1:A:18:THR:C	1:A:20:ASP:N	0.45	2.75	2	3
1:A:49:PHE:C	1:A:51:ASP:N	0.45	2.74	5	1
1:A:25:PHE:CZ	1:A:65:ILE:HG12	0.45	2.46	2	3
1:A:11:GLY:O	1:A:12:ARG:C	0.45	2.60	11	2
1:A:65:ILE:HG22	1:A:66:LYS:CG	0.45	2.42	14	1
1:A:62:ASP:O	1:A:62:ASP:CG	0.45	2.60	8	2
1:A:68:ILE:C	1:A:68:ILE:CD1	0.44	2.89	17	1
1:A:16:ASP:O	1:A:17:MET:C	0.44	2.59	14	2
1:A:25:PHE:C	1:A:25:PHE:CD1	0.44	2.96	15	1
1:A:37:ILE:HG21	1:A:41:PHE:CD1	0.44	2.48	5	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:42:ARG:C	1:A:44:PHE:N	0.44	2.76	17	1
1:A:42:ARG:O	1:A:44:PHE:N	0.43	2.50	17	1
1:A:41:PHE:CD2	1:A:44:PHE:O	0.43	2.72	1	1
1:A:20:ASP:OD1	1:A:23:ARG:NH2	0.43	2.52	3	1
1:A:37:ILE:CG2	1:A:41:PHE:CD1	0.42	3.02	5	1
1:A:19:GLU:HG2	1:A:35:VAL:HG12	0.42	1.91	2	1
1:A:64:ILE:HG23	1:A:68:ILE:O	0.42	2.13	19	1
1:A:52:ASP:OD1	1:A:52:ASP:C	0.42	2.62	16	1
1:A:18:THR:O	1:A:20:ASP:N	0.42	2.53	18	3
1:A:10:VAL:O	1:A:10:VAL:CG1	0.42	2.68	13	1
1:A:49:PHE:O	1:A:51:ASP:N	0.41	2.53	5	1
1:A:15:GLY:HA2	1:A:41:PHE:CZ	0.41	2.50	9	1
1:A:49:PHE:CD1	1:A:54:ILE:HG21	0.41	2.51	3	1
1:A:29:TYR:CD2	1:A:58:LEU:HD21	0.41	2.50	19	1
1:A:65:ILE:O	1:A:68:ILE:CG1	0.41	2.69	19	1
1:A:18:THR:O	1:A:21:GLU:N	0.41	2.54	20	1
1:A:25:PHE:CD2	1:A:65:ILE:HG23	0.41	2.51	2	1
1:A:58:LEU:O	1:A:59:CYS:C	0.41	2.63	10	1
1:A:17:MET:HE1	1:A:68:ILE:CD1	0.41	2.46	5	1
1:A:41:PHE:CE1	1:A:44:PHE:O	0.40	2.75	19	1

6.3 Torsion angles ⓘ

6.3.1 Protein backbone ⓘ

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	67/88 (76%)	59±2 (87±3%)	8±2 (12±3%)	0±1 (1±1%)	20	70
All	All	1340/1760 (76%)	1171 (87%)	159 (12%)	10 (1%)	20	70

All 4 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	43	ALA	5
1	A	17	MET	3

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Mol	Chain	Res	Type	Models (Total)
1	A	50	ALA	1
1	A	19	GLU	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	57/73 (78%)	46±3 (81±6%)	11±3 (19±6%)	3	35
All	All	1140/1460 (78%)	926 (81%)	214 (19%)	3	35

All 30 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	13	CYS	18
1	A	34	ASP	18
1	A	51	ASP	17
1	A	56	GLN	17
1	A	24	GLU	12
1	A	73	SER	12
1	A	16	ASP	9
1	A	31	ASP	9
1	A	68	ILE	9
1	A	66	LYS	9
1	A	57	SER	8
1	A	12	ARG	8
1	A	52	ASP	7
1	A	27	SER	6
1	A	20	ASP	6
1	A	19	GLU	6
1	A	62	ASP	6
1	A	42	ARG	6
1	A	32	VAL	5
1	A	63	LEU	5
1	A	17	MET	3
1	A	39	LYS	3
1	A	33	MET	3

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Mol	Chain	Res	Type	Models (Total)
1	A	44	PHE	3
1	A	14	THR	2
1	A	59	CYS	2
1	A	53	GLN	2
1	A	8	VAL	1
1	A	18	THR	1
1	A	23	ARG	1

6.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

6.5 Carbohydrates [i](#)

There are no 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

No chemical shift data were provided