



Full wwPDB NMR Structure Validation Report ⓘ

May 28, 2020 – 10:10 pm BST

PDB ID : 2JQA
Title : Solution structure of apo-DR1885 from *Deinococcus radiodurans*
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Deposited on : 2007-05-30

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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

Cyrange : Kirchner and Güntert (2011)
NmrClust : Kelley et al. (1996)
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
ShiftChecker : 2.11
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

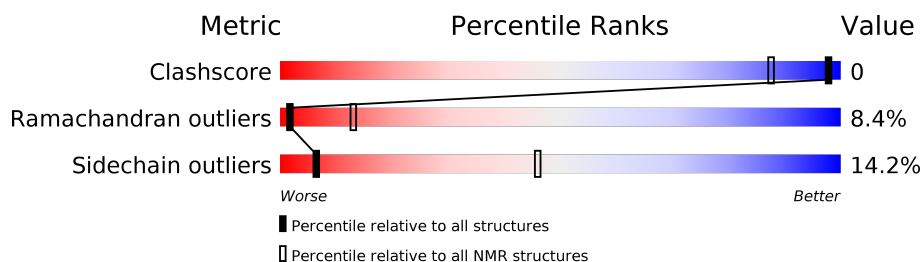
1 Overall quality at a glance

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	158937	12864
Ramachandran outliers	154571	11451
Sidechain outliers	154315	11428

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	149	 68% 12% 19%

2 Ensemble composition and analysis

This entry contains 20 models. Model 15 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:28-A:147 (120)	1.03	15

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 6 single-model clusters were found.

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

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 2215 atoms, of which 1137 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Hypothetical protein.

Mol	Chain	Residues	Atoms						Trace
1	A	149	Total	C	H	N	O	S	0
			2215	673	1137	195	200	10	

There are 5 discrepancies between the modelled and reference sequences:

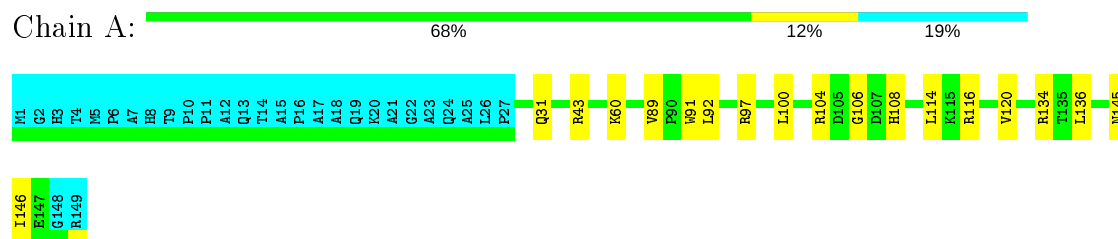
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	CLONING ARTIFACT	UNP Q9RT80
A	146	ILE	-	CLONING ARTIFACT	UNP Q9RT80
A	147	GLU	-	CLONING ARTIFACT	UNP Q9RT80
A	148	GLY	-	CLONING ARTIFACT	UNP Q9RT80
A	149	ARG	-	CLONING ARTIFACT	UNP Q9RT80

4 Residue-property plots

4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA and DNA 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: Hypothetical protein

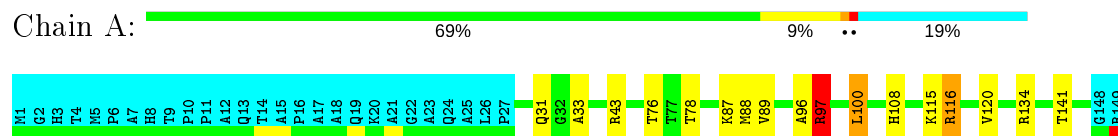


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

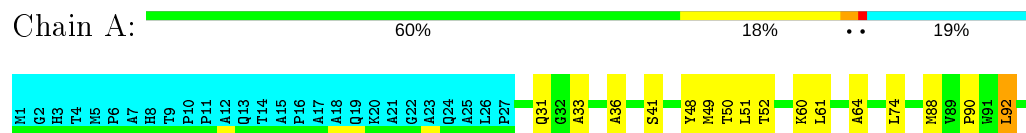
4.2.1 Score per residue for model 1

- Molecule 1: Hypothetical protein



4.2.2 Score per residue for model 2

- Molecule 1: Hypothetical protein





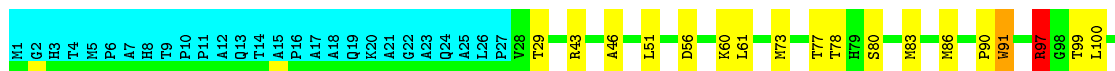
4.2.3 Score per residue for model 3

- Molecule 1: Hypothetical protein



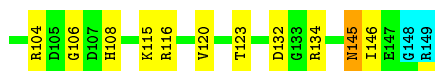
4.2.4 Score per residue for model 4

- Molecule 1: Hypothetical protein



4.2.5 Score per residue for model 5

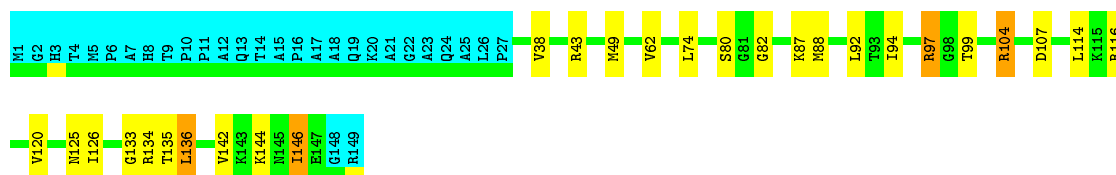
- Molecule 1: Hypothetical protein



4.2.6 Score per residue for model 6

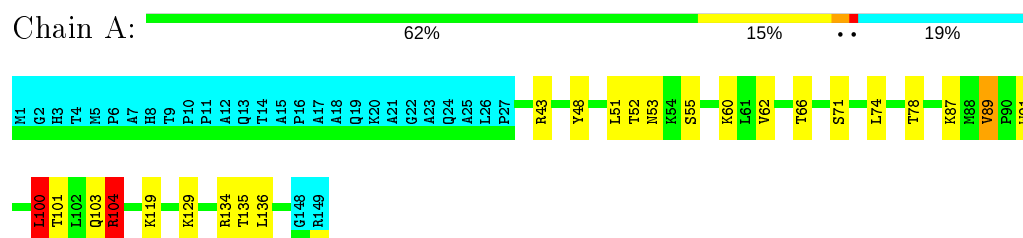
- Molecule 1: Hypothetical protein





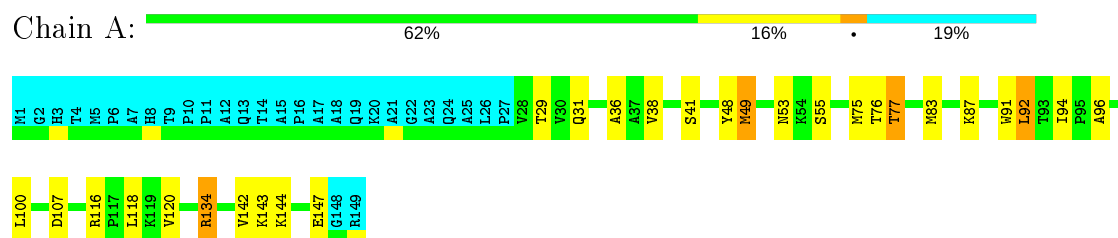
4.2.7 Score per residue for model 7

- Molecule 1: Hypothetical protein



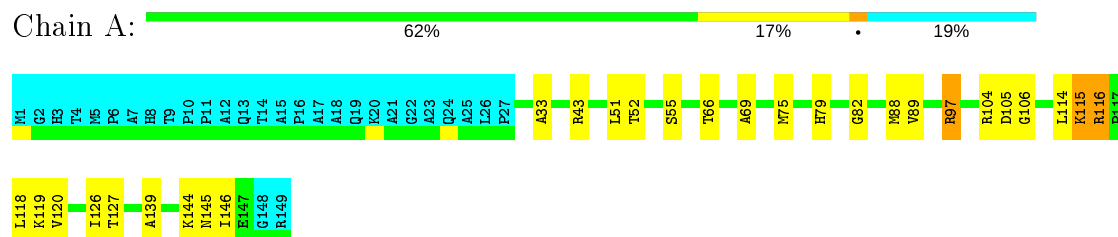
4.2.8 Score per residue for model 8

- Molecule 1: Hypothetical protein



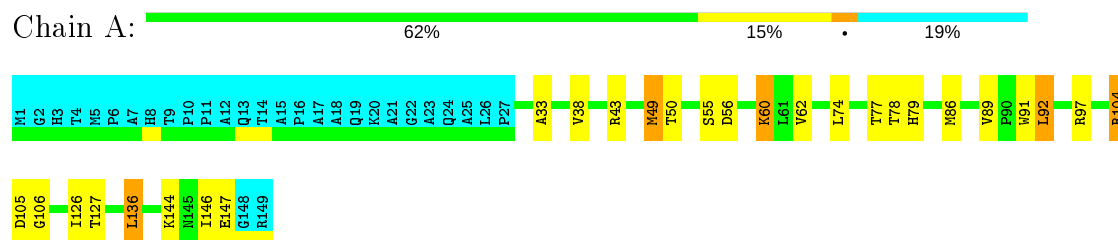
4.2.9 Score per residue for model 9

- Molecule 1: Hypothetical protein



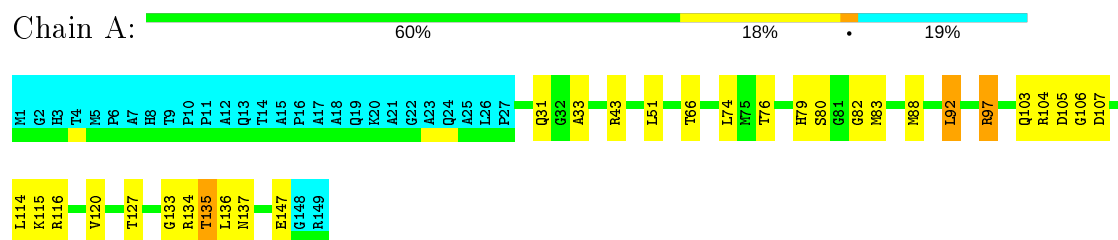
4.2.10 Score per residue for model 10

- Molecule 1: Hypothetical protein



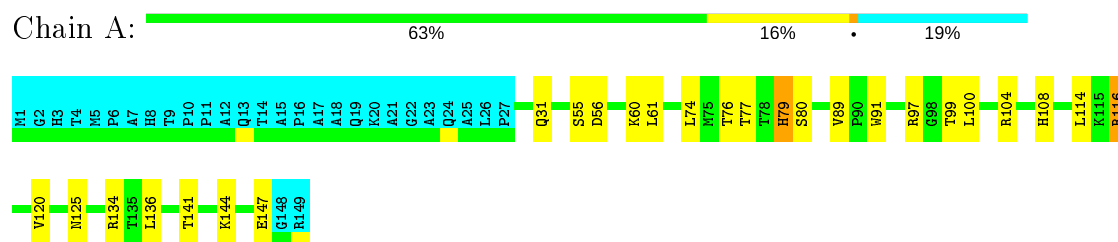
4.2.11 Score per residue for model 11

- Molecule 1: Hypothetical protein



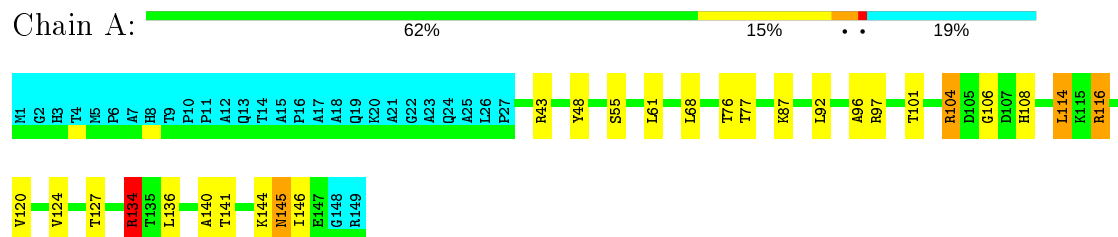
4.2.12 Score per residue for model 12

- Molecule 1: Hypothetical protein



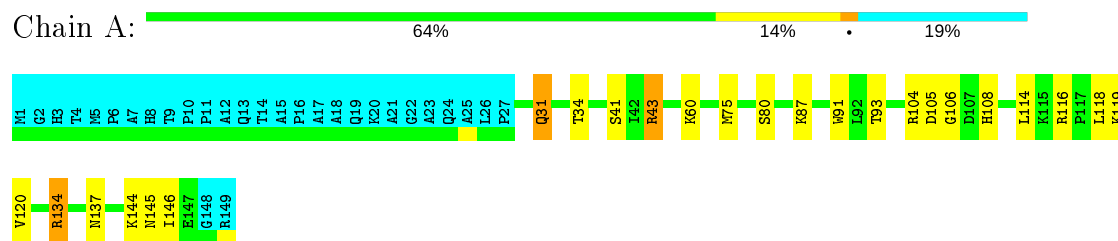
4.2.13 Score per residue for model 13

- Molecule 1: Hypothetical protein



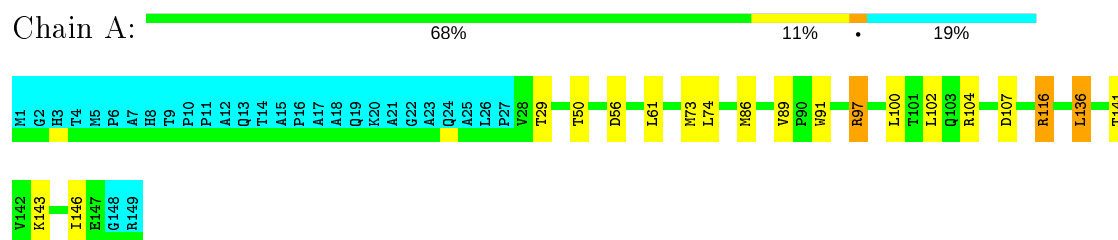
4.2.14 Score per residue for model 14

- Molecule 1: Hypothetical protein



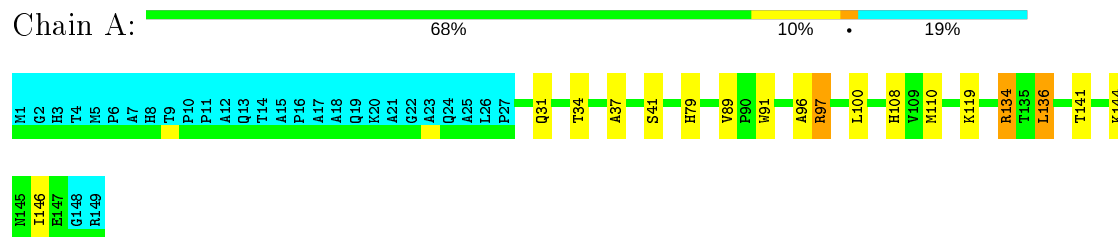
4.2.15 Score per residue for model 15 (medoid)

- Molecule 1: Hypothetical protein



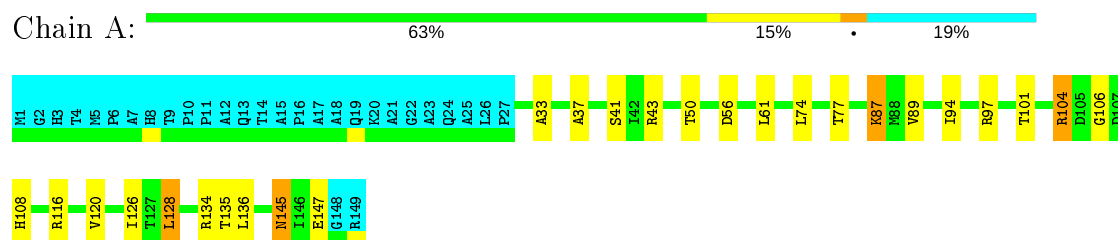
4.2.16 Score per residue for model 16

- Molecule 1: Hypothetical protein



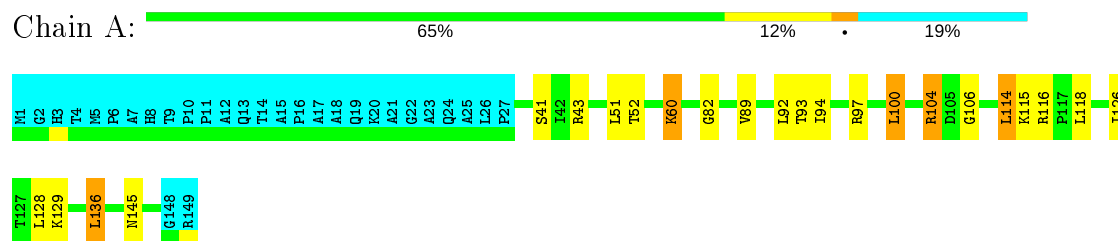
4.2.17 Score per residue for model 17

- Molecule 1: Hypothetical protein



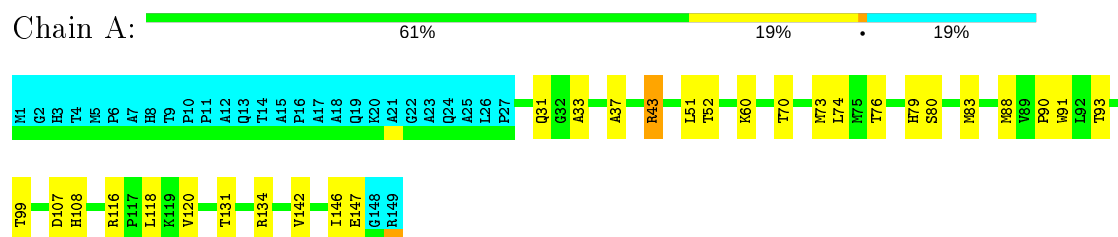
4.2.18 Score per residue for model 18

- Molecule 1: Hypothetical protein



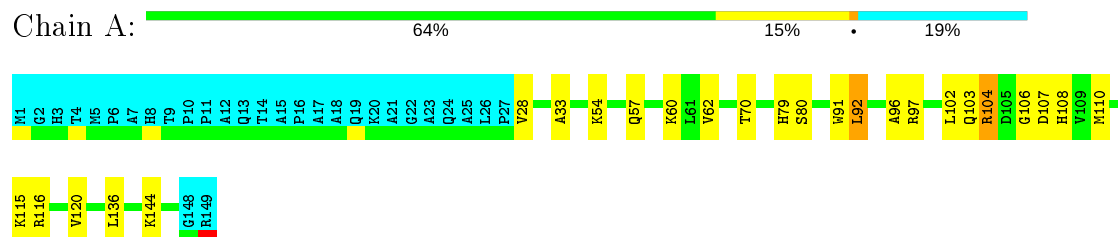
4.2.19 Score per residue for model 19

- Molecule 1: Hypothetical protein



4.2.20 Score per residue for model 20

- Molecule 1: Hypothetical protein



5 Refinement protocol and experimental data overview [i](#)

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

Of the 300 calculated structures, 20 were deposited, based on the following criterion: *target function*.

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

Software name	Classification	Version
AMBER	refinement	8
DYANA	structure solution	

No chemical shift data was provided. No validations of the models with respect to experimental NMR restraints is performed at this time.

COVALENT-GEOMETRY INFOmissingINFO

5.1 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	878	937	937	1±1
All	All	17560	18740	18740	14

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 0.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:100:LEU:HD12	1:A:100:LEU:H	0.70	1.46	18	1
1:A:118:LEU:HB3	1:A:142:VAL:HG21	0.55	1.78	8	1
1:A:64:ALA:HB1	1:A:126:ILE:HD11	0.52	1.82	2	1
1:A:94:ILE:HG22	1:A:100:LEU:H	0.49	1.68	7	1
1:A:114:LEU:HD23	1:A:115:LYS:H	0.48	1.68	18	1
1:A:92:LEU:HA	1:A:100:LEU:HD21	0.47	1.85	8	1
1:A:91:TRP:CD1	1:A:100:LEU:HD12	0.46	2.46	4	1
1:A:37:ALA:HB2	1:A:142:VAL:CG1	0.46	2.40	19	1
1:A:69:ALA:HB2	1:A:115:LYS:HE3	0.45	1.88	9	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:61:LEU:HD21	1:A:128:LEU:HB2	0.45	1.87	17	1
1:A:126:ILE:HD13	1:A:127:THR:N	0.44	2.28	2	1
1:A:100:LEU:CD2	1:A:102:LEU:HD11	0.43	2.44	15	1
1:A:36:ALA:HB2	1:A:48:TYR:CE1	0.42	2.50	2	1
1:A:46:ALA:HB1	1:A:108:HIS:CE1	0.40	2.52	4	1

5.2 Torsion angles ⓘ

5.2.1 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	120/149 (81%)	89±4 (74±4%)	21±5 (17±4%)	10±3 (8±2%)	2	13
All	All	2400/2980 (81%)	1781 (74%)	417 (17%)	202 (8%)	2	13

All 50 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	120	VAL	15
1	A	146	ILE	11
1	A	106	GLY	11
1	A	89	VAL	10
1	A	33	ALA	10
1	A	136	LEU	9
1	A	145	ASN	8
1	A	97	ARG	8
1	A	55	SER	6
1	A	80	SER	6
1	A	96	ALA	6
1	A	31	GLN	5
1	A	104	ARG	5
1	A	88	MET	5
1	A	92	LEU	5
1	A	91	TRP	4
1	A	99	THR	4

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Mol	Chain	Res	Type	Models (Total)
1	A	62	VAL	4
1	A	147	GLU	4
1	A	41	SER	4
1	A	115	LYS	4
1	A	144	LYS	4
1	A	56	ASP	4
1	A	107	ASP	4
1	A	90	PRO	4
1	A	37	ALA	3
1	A	78	THR	3
1	A	82	GLY	3
1	A	79	HIS	3
1	A	60	LYS	3
1	A	134	ARG	2
1	A	77	THR	2
1	A	87	LYS	2
1	A	114	LEU	2
1	A	93	THR	2
1	A	133	GLY	2
1	A	135	THR	2
1	A	76	THR	1
1	A	28	VAL	1
1	A	119	LYS	1
1	A	95	PRO	1
1	A	94	ILE	1
1	A	137	ASN	1
1	A	124	VAL	1
1	A	36	ALA	1
1	A	49	MET	1
1	A	121	GLY	1
1	A	101	THR	1
1	A	116	ARG	1
1	A	139	ALA	1

5.2.2 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	97/115 (84%)	83±3 (86±3%)	14±3 (14±3%)	6	46
All	All	1940/2300 (84%)	1664 (86%)	276 (14%)	6	46

All 73 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	92	LEU	11
1	A	134	ARG	10
1	A	108	HIS	10
1	A	74	LEU	10
1	A	136	LEU	9
1	A	51	LEU	9
1	A	126	ILE	8
1	A	60	LYS	8
1	A	91	TRP	7
1	A	114	LEU	7
1	A	104	ARG	7
1	A	87	LYS	7
1	A	105	ASP	6
1	A	77	THR	6
1	A	144	LYS	6
1	A	52	THR	6
1	A	141	THR	6
1	A	97	ARG	6
1	A	100	LEU	6
1	A	31	GLN	5
1	A	145	ASN	5
1	A	76	THR	5
1	A	61	LEU	5
1	A	73	MET	4
1	A	127	THR	4
1	A	75	MET	4
1	A	94	ILE	4
1	A	43	ARG	4
1	A	50	THR	4
1	A	118	LEU	4
1	A	79	HIS	4
1	A	49	MET	4
1	A	103	GLN	4
1	A	83	MET	4
1	A	86	MET	3
1	A	119	LYS	3

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Mol	Chain	Res	Type	Models (Total)
1	A	38	VAL	3
1	A	66	THR	3
1	A	107	ASP	3
1	A	29	THR	3
1	A	48	TYR	3
1	A	135	THR	3
1	A	116	ARG	3
1	A	56	ASP	2
1	A	110	MET	2
1	A	41	SER	2
1	A	125	ASN	2
1	A	70	THR	2
1	A	80	SER	2
1	A	34	THR	2
1	A	128	LEU	2
1	A	53	ASN	2
1	A	101	THR	2
1	A	44	ASP	1
1	A	146	ILE	1
1	A	143	LYS	1
1	A	78	THR	1
1	A	147	GLU	1
1	A	102	LEU	1
1	A	59	ILE	1
1	A	55	SER	1
1	A	99	THR	1
1	A	120	VAL	1
1	A	54	LYS	1
1	A	89	VAL	1
1	A	88	MET	1
1	A	57	GLN	1
1	A	129	LYS	1
1	A	93	THR	1
1	A	132	ASP	1
1	A	123	THR	1
1	A	137	ASN	1
1	A	131	THR	1

5.2.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.4 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.5 Ligand geometry [i](#)

There are no ligands in this entry.

5.6 Other polymers [i](#)

There are no such molecules in this entry.

5.7 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Chemical shift validation

No chemical shift data were provided