



Full wwPDB NMR Structure Validation Report ⓘ

Mar 5, 2026 – 06:36 PM UTC

PDB ID : 1Q9F / pdb_00001q9f
Title : NMR STRUCTURE OF THE OUTER MEMBRANE PROTEIN OMPX IN
DHPC MICELLES
Authors : Fernandez, C.; Hilty, C.; Wider, G.; Guntert, P.; Wuthrich, K.
Deposited on : 2003-08-25

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

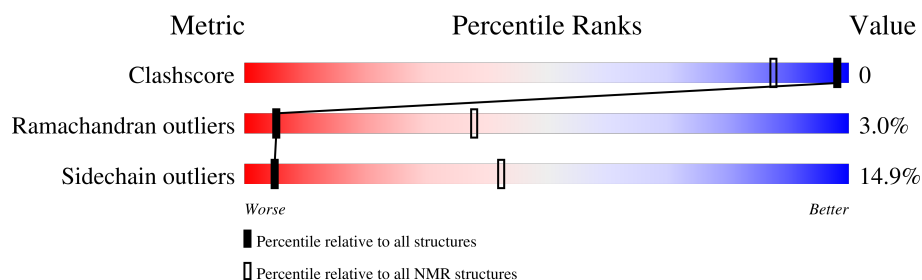
1 Overall quality at a glance

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	148	

2 Ensemble composition and analysis

This entry contains 20 models. Model 5 is the overall representative, medoid model (most similar to other models).

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:1-A:50, A:57-A:89, A:103-A:148 (129)	1.56	5

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 2 single-model clusters were found.

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

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 2223 atoms, of which 1066 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Outer membrane protein X.

Mol	Chain	Residues	Atoms						Trace
1	A	148	Total	C	H	N	O	S	0
			2223	731	1066	190	233	3	

There is a discrepancy between the modelled and reference sequences:

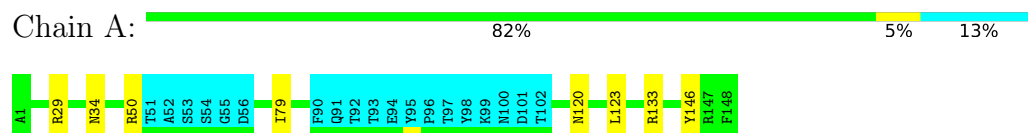
Chain	Residue	Modelled	Actual	Comment	Reference
A	100	ASN	HIS	engineered mutation	UNP P36546

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: Outer membrane protein X

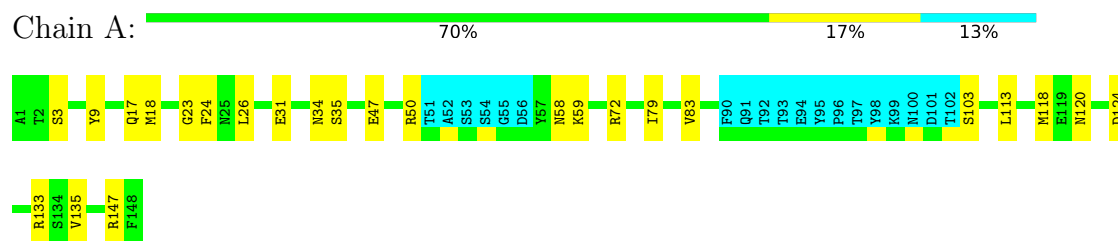


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

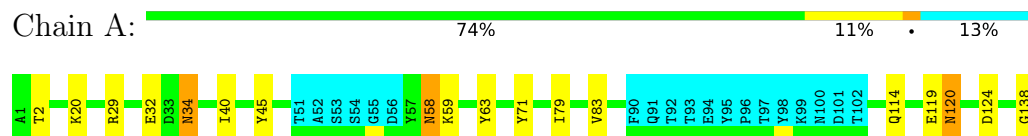
4.2.1 Score per residue for model 1

- Molecule 1: Outer membrane protein X



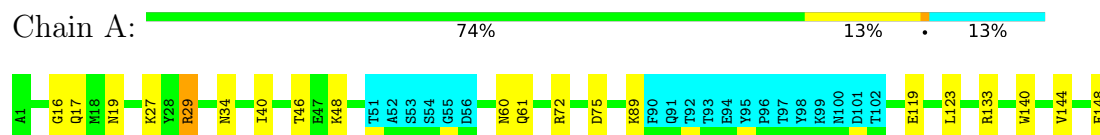
4.2.2 Score per residue for model 2

- Molecule 1: Outer membrane protein X



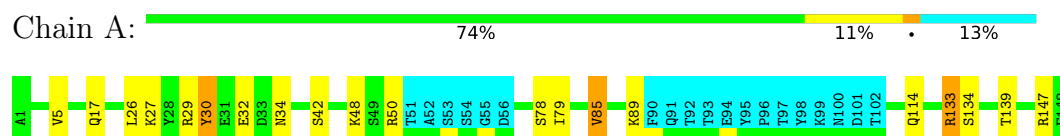
4.2.3 Score per residue for model 3

- Molecule 1: Outer membrane protein X



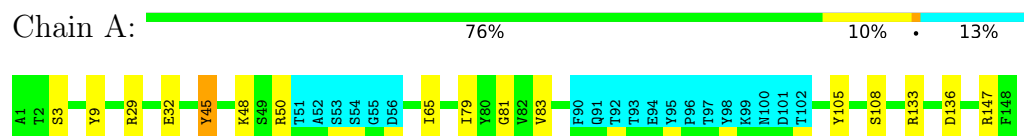
4.2.4 Score per residue for model 4

- Molecule 1: Outer membrane protein X



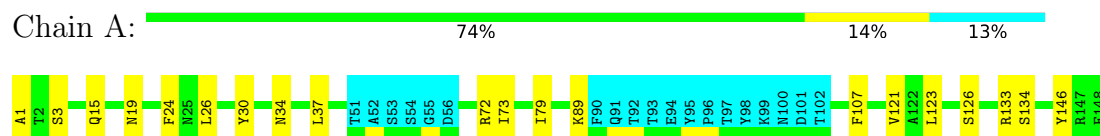
4.2.5 Score per residue for model 5 (medoid)

- Molecule 1: Outer membrane protein X



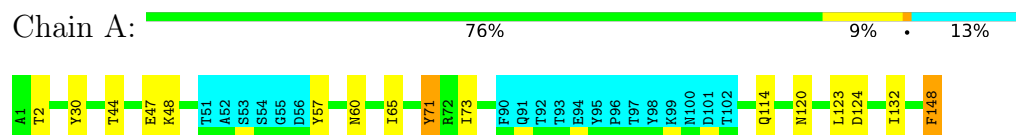
4.2.6 Score per residue for model 6

- Molecule 1: Outer membrane protein X



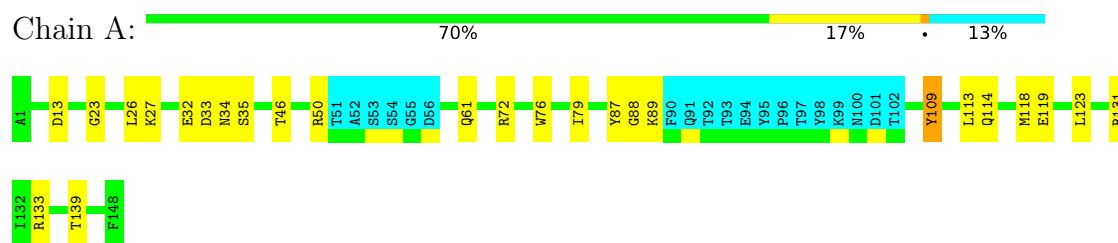
4.2.7 Score per residue for model 7

- Molecule 1: Outer membrane protein X



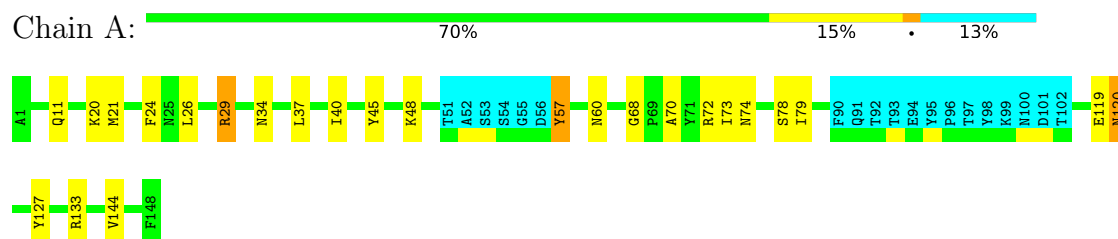
4.2.8 Score per residue for model 8

- Molecule 1: Outer membrane protein X



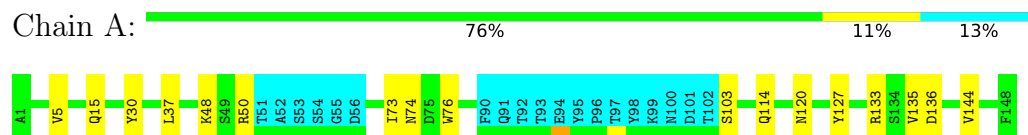
4.2.9 Score per residue for model 9

- Molecule 1: Outer membrane protein X



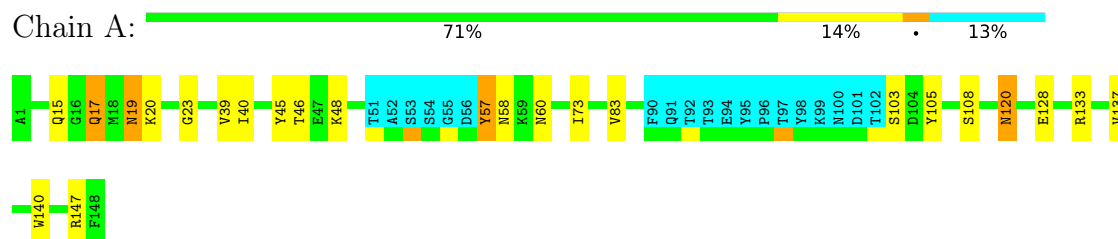
4.2.10 Score per residue for model 10

- Molecule 1: Outer membrane protein X



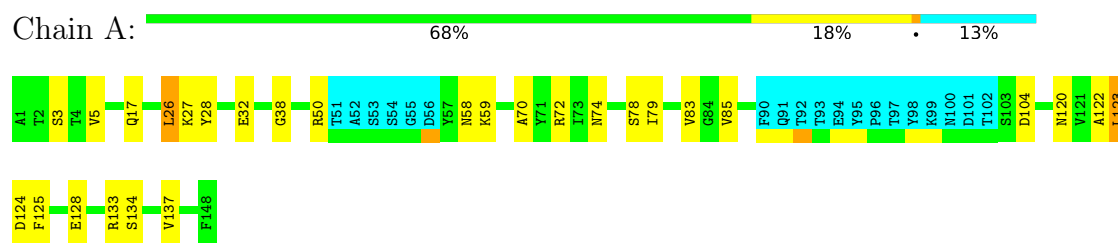
4.2.11 Score per residue for model 11

- Molecule 1: Outer membrane protein X



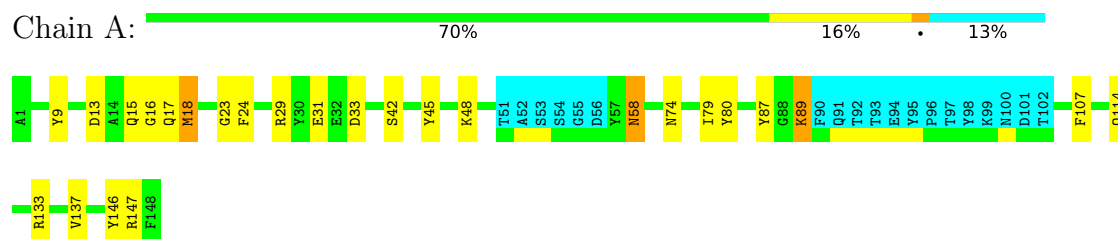
4.2.12 Score per residue for model 12

- Molecule 1: Outer membrane protein X



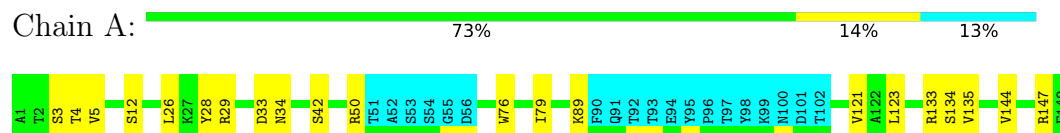
4.2.13 Score per residue for model 13

- Molecule 1: Outer membrane protein X



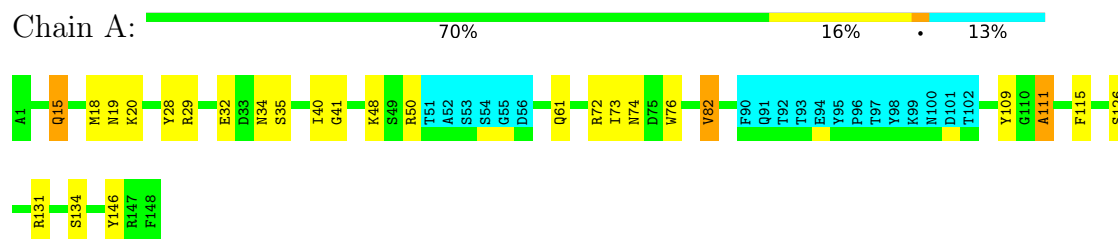
4.2.14 Score per residue for model 14

- Molecule 1: Outer membrane protein X



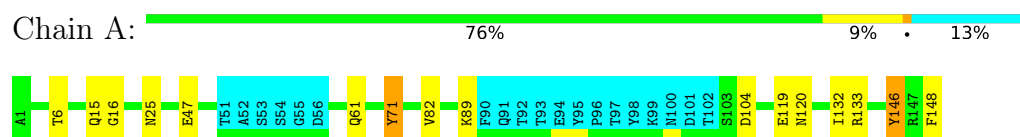
4.2.15 Score per residue for model 15

- Molecule 1: Outer membrane protein X



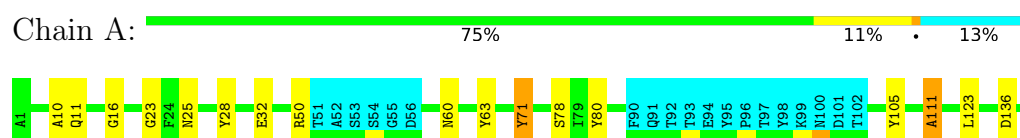
4.2.16 Score per residue for model 16

- Molecule 1: Outer membrane protein X



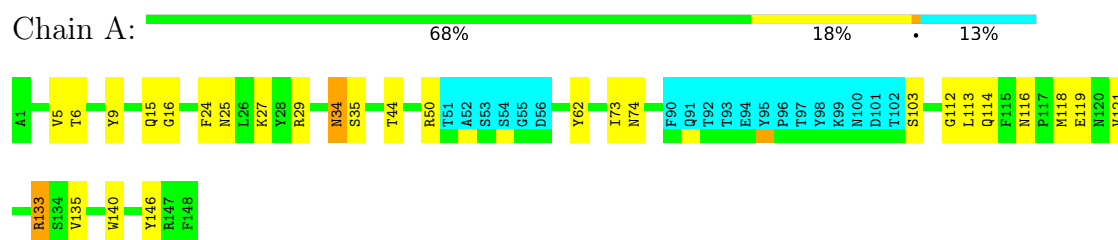
4.2.17 Score per residue for model 17

- Molecule 1: Outer membrane protein X



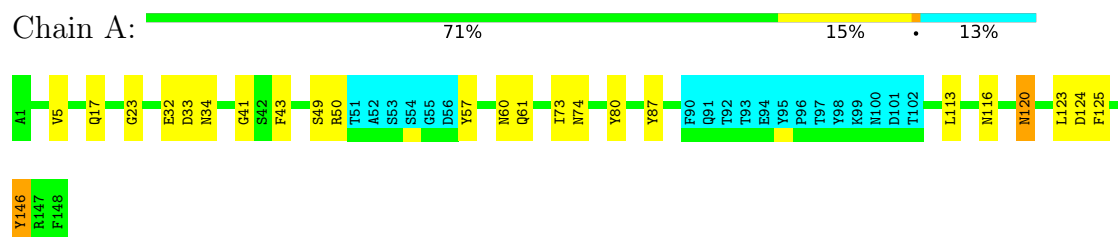
4.2.18 Score per residue for model 18

- Molecule 1: Outer membrane protein X



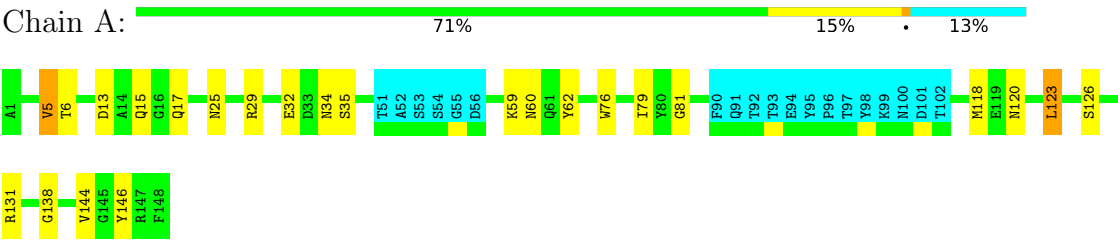
4.2.19 Score per residue for model 19

- Molecule 1: Outer membrane protein X



4.2.20 Score per residue for model 20

- Molecule 1: Outer membrane protein X



5 Refinement protocol and experimental data overview

The models were refined using the following method: *TORSION ANGLE DYNAMICS (CANDID)*.

Of the 400 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
OPALp	refinement	2.6
CYANA	structure solution	1.0
TALOS	structure solution	

No chemical shift data was provided.

6 Model quality

6.1 Standard geometry

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	0.62±0.01	0±0/1034 (0.0± 0.0%)	1.29±0.04	1±2/1398 (0.1± 0.1%)
All	All	0.62	0/20680 (0.0%)	1.29	25/27960 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	Chirality	Planarity
1	A	0.0±0.0	2.9±1.5
All	All	0	58

There are no bond-length outliers.

All unique angle outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	148	PHE	CA-CB-CG	10.12	123.92	113.80	7	3
1	A	137	VAL	CA-C-N	7.01	128.12	121.46	12	2
1	A	137	VAL	C-N-CA	7.01	128.12	121.46	12	2
1	A	118	MET	CA-C-N	6.42	131.40	121.19	20	2
1	A	118	MET	C-N-CA	6.42	131.40	121.19	20	2
1	A	119	GLU	CA-C-N	5.69	132.41	121.54	9	1
1	A	119	GLU	C-N-CA	5.69	132.41	121.54	9	1
1	A	105	TYR	CA-C-N	5.65	125.49	121.65	11	1
1	A	105	TYR	C-N-CA	5.65	125.49	121.65	11	1
1	A	19	ASN	CA-CB-CG	5.40	118.00	112.60	11	1
1	A	50	ARG	CA-C-N	5.33	128.79	121.33	18	1
1	A	50	ARG	C-N-CA	5.33	128.79	121.33	18	1
1	A	125	PHE	CA-CB-CG	5.28	119.08	113.80	12	1
1	A	136	ASP	CA-CB-CG	-5.26	107.34	112.60	10	1
1	A	17	GLN	CA-C-N	5.14	128.08	120.17	12	1

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	17	GLN	C-N-CA	5.14	128.08	120.17	12	1
1	A	132	ILE	CB-CA-C	5.13	118.96	113.22	16	1
1	A	85	VAL	CA-C-N	5.08	125.95	121.58	4	1
1	A	85	VAL	C-N-CA	5.08	125.95	121.58	4	1

There are no chirality outliers.

All unique planar outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Group	Models (Total)
1	A	29	ARG	Sidechain	6
1	A	133	ARG	Sidechain	4
1	A	146	TYR	Sidechain	4
1	A	40	ILE	Peptide	3
1	A	72	ARG	Sidechain	3
1	A	50	ARG	Sidechain	3
1	A	57	TYR	Sidechain,Peptide	3
1	A	71	TYR	Sidechain	3
1	A	138	GLY	Peptide	2
1	A	30	TYR	Sidechain	2
1	A	45	TYR	Sidechain	2
1	A	127	TYR	Sidechain	2
1	A	28	TYR	Sidechain	2
1	A	41	GLY	Peptide	2
1	A	62	TYR	Sidechain	2
1	A	1	ALA	Peptide	1
1	A	46	THR	Peptide	1
1	A	87	TYR	Peptide	1
1	A	109	TYR	Sidechain	1
1	A	68	GLY	Peptide	1
1	A	80	TYR	Sidechain	1
1	A	147	ARG	Sidechain	1
1	A	20	LYS	Peptide	1
1	A	74	ASN	Peptide	1
1	A	134	SER	Peptide	1
1	A	25	ASN	Peptide	1
1	A	105	TYR	Sidechain	1
1	A	121	VAL	Peptide	1
1	A	125	PHE	Peptide	1
1	A	131	ARG	Sidechain	1

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	1008	938	940	1±1
All	All	20160	18760	18800	15

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:79:ILE:HG12	1:A:113:LEU:HD13	0.56	1.75	8	1
1:A:10:ALA:HB2	1:A:25:ASN:HD21	0.51	1.65	17	1
1:A:40:ILE:HD11	1:A:70:ALA:HB2	0.50	1.81	9	1
1:A:123:LEU:HD13	1:A:144:VAL:HG12	0.49	1.84	20	1
1:A:122:ALA:C	1:A:123:LEU:HD23	0.48	2.34	12	1
1:A:26:LEU:HD13	1:A:27:LYS:H	0.48	1.69	12	1
1:A:80:TYR:HA	1:A:111:ALA:HB3	0.45	1.88	17	1
1:A:82:VAL:HG22	1:A:111:ALA:HB2	0.43	1.90	15	1
1:A:112:GLY:C	1:A:113:LEU:HD22	0.43	2.38	18	1
1:A:120:ASN:HA	1:A:146:TYR:CD2	0.42	2.49	19	1
1:A:5:VAL:HG11	1:A:146:TYR:CD1	0.42	2.49	18	1
1:A:38:GLY:HA3	1:A:70:ALA:HB3	0.41	1.92	12	1
1:A:5:VAL:CG2	1:A:146:TYR:HB2	0.41	2.46	20	1
1:A:26:LEU:HD13	1:A:27:LYS:N	0.40	2.31	12	1
1:A:120:ASN:C	1:A:120:ASN:ND2	0.40	2.80	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	127/148 (86%)	108±4 (85±3%)	16±3 (12±3%)	4±2 (3±1%)	5	38
All	All	2540/2960 (86%)	2151 (85%)	314 (12%)	75 (3%)	5	38

All 21 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	133	ARG	8
1	A	23	GLY	6
1	A	15	GLN	6
1	A	73	ILE	6
1	A	120	ASN	5
1	A	16	GLY	5
1	A	60	ASN	5
1	A	17	GLN	4
1	A	58	ASN	4
1	A	119	GLU	4
1	A	74	ASN	4
1	A	34	ASN	3
1	A	89	LYS	3
1	A	76	TRP	3
1	A	81	GLY	2
1	A	111	ALA	2
1	A	103	SER	1
1	A	75	ASP	1
1	A	88	GLY	1
1	A	118	MET	1
1	A	18	MET	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	101/118 (86%)	86±3 (85±3%)	15±3 (15±3%)	5	42
All	All	2020/2360 (86%)	1720 (85%)	300 (15%)	5	42

All 90 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	34	ASN	11
1	A	79	ILE	10
1	A	32	GLU	9
1	A	48	LYS	9
1	A	123	LEU	9
1	A	120	ASN	8
1	A	26	LEU	7
1	A	50	ARG	7
1	A	114	GLN	7
1	A	29	ARG	6
1	A	5	VAL	6
1	A	3	SER	5
1	A	24	PHE	5
1	A	35	SER	5
1	A	83	VAL	5
1	A	124	ASP	5
1	A	147	ARG	5
1	A	61	GLN	5
1	A	89	LYS	5
1	A	9	TYR	4
1	A	59	LYS	4
1	A	72	ARG	4
1	A	135	VAL	4
1	A	45	TYR	4
1	A	71	TYR	4
1	A	17	GLN	4
1	A	19	ASN	4
1	A	27	LYS	4
1	A	140	TRP	4
1	A	144	VAL	4
1	A	78	SER	4
1	A	133	ARG	4
1	A	134	SER	4
1	A	33	ASP	4
1	A	18	MET	3
1	A	47	GLU	3
1	A	20	LYS	3
1	A	58	ASN	3
1	A	146	TYR	3
1	A	30	TYR	3
1	A	42	SER	3
1	A	37	LEU	3
1	A	126	SER	3

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Mol	Chain	Res	Type	Models (Total)
1	A	13	ASP	3
1	A	57	TYR	3
1	A	15	GLN	3
1	A	103	SER	3
1	A	6	THR	3
1	A	31	GLU	2
1	A	113	LEU	2
1	A	2	THR	2
1	A	63	TYR	2
1	A	46	THR	2
1	A	85	VAL	2
1	A	139	THR	2
1	A	65	ILE	2
1	A	108	SER	2
1	A	136	ASP	2
1	A	107	PHE	2
1	A	121	VAL	2
1	A	44	THR	2
1	A	109	TYR	2
1	A	131	ARG	2
1	A	11	GLN	2
1	A	60	ASN	2
1	A	128	GLU	2
1	A	28	TYR	2
1	A	104	ASP	2
1	A	87	TYR	2
1	A	76	TRP	2
1	A	73	ILE	2
1	A	82	VAL	2
1	A	25	ASN	2
1	A	74	ASN	2
1	A	116	ASN	2
1	A	118	MET	1
1	A	40	ILE	1
1	A	119	GLU	1
1	A	105	TYR	1
1	A	132	ILE	1
1	A	148	PHE	1
1	A	21	MET	1
1	A	39	VAL	1
1	A	137	VAL	1
1	A	4	THR	1

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Mol	Chain	Res	Type	Models (Total)
1	A	12	SER	1
1	A	115	PHE	1
1	A	43	PHE	1
1	A	49	SER	1
1	A	80	TYR	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