



Full wwPDB NMR Structure Validation Report ⓘ

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PDB ID : 1QM1 / pdb_00001qm1
Title : Human prion protein fragment 90-230
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Deposited on : 1999-09-20

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

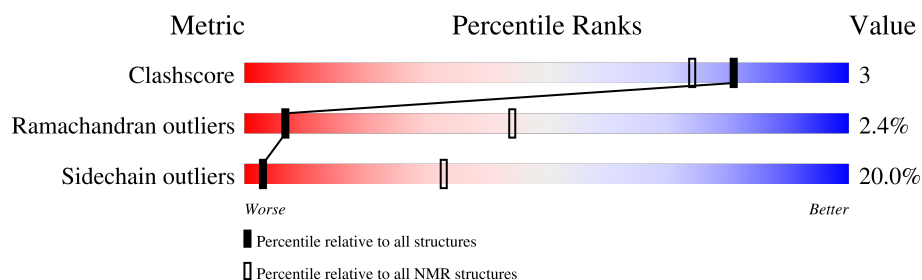
1 Overall quality at a glance

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	143	

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 19 as representative.

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:129-A:166, A:172-A:228 (95)	0.79	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	3, 4, 7, 10, 11, 12, 13, 15, 16, 19, 20
2	1, 2, 5, 6, 14, 17
3	8, 9, 18

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 1688 atoms, of which 811 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called PRION PROTEIN.

Mol	Chain	Residues	Atoms						Trace
1	A	104	Total	C	H	N	O	S	0
			1688	544	811	153	171	9	

There are 2 discrepancies between the modelled and reference sequences:

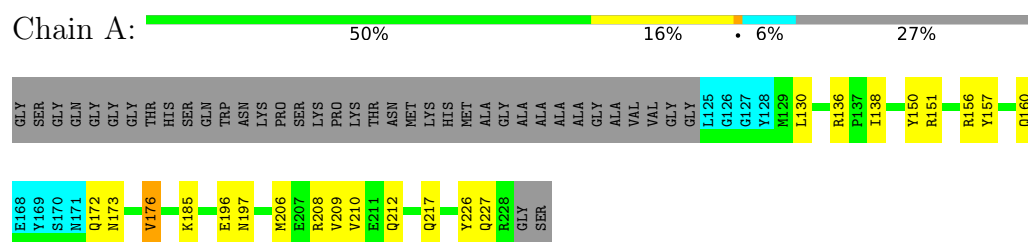
Chain	Residue	Modelled	Actual	Comment	Reference
A	88	GLY	-	cloning artifact	UNP P04156
A	89	SER	-	cloning artifact	UNP P04156

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: PRION PROTEIN

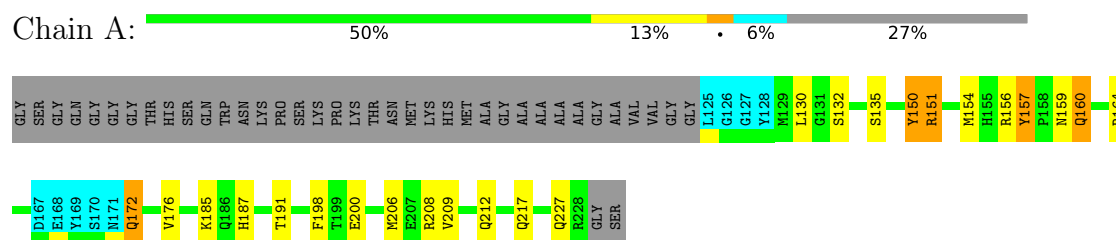


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

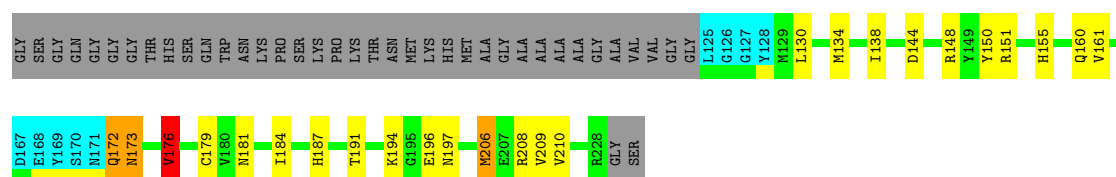
• Molecule 1: PRION PROTEIN



4.2.2 Score per residue for model 2

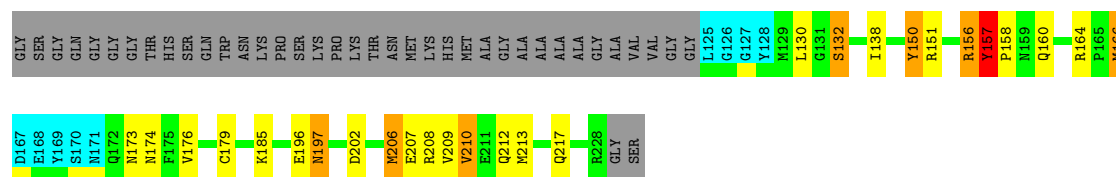
• Molecule 1: PRION PROTEIN





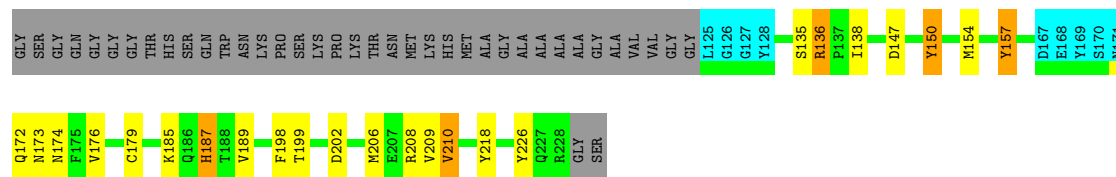
4.2.3 Score per residue for model 3

- Molecule 1: PRION PROTEIN



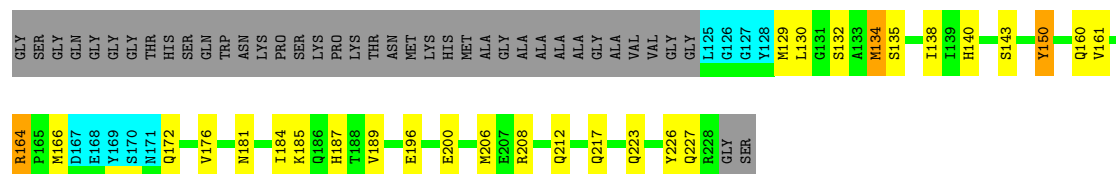
4.2.4 Score per residue for model 4

- Molecule 1: PRION PROTEIN



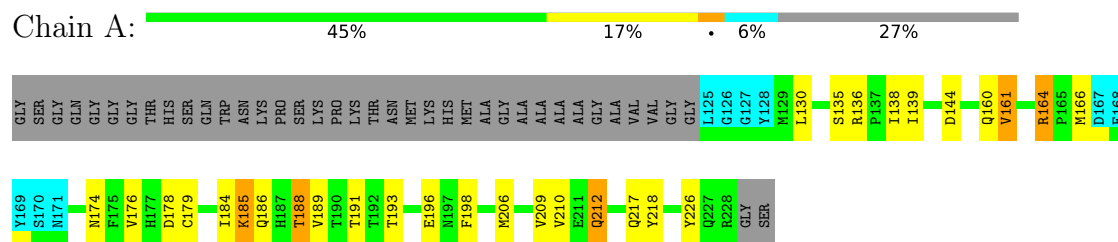
4.2.5 Score per residue for model 5

- Molecule 1: PRION PROTEIN



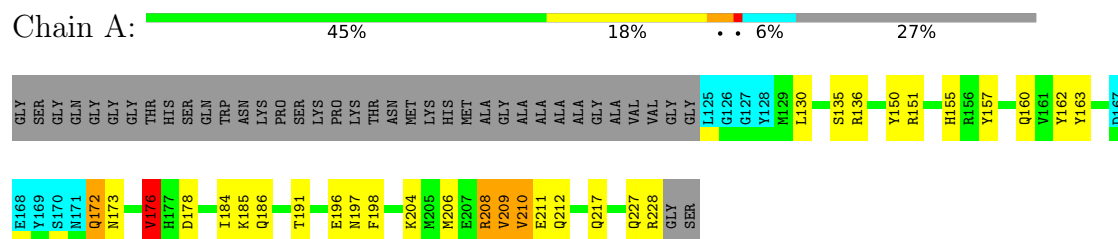
4.2.6 Score per residue for model 6

- Molecule 1: PRION PROTEIN



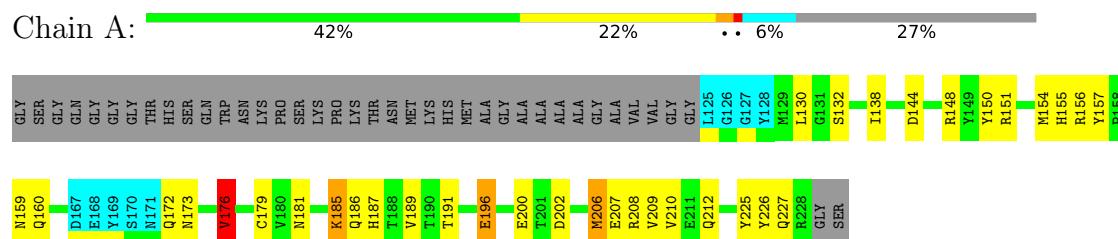
4.2.7 Score per residue for model 7

- Molecule 1: PRION PROTEIN



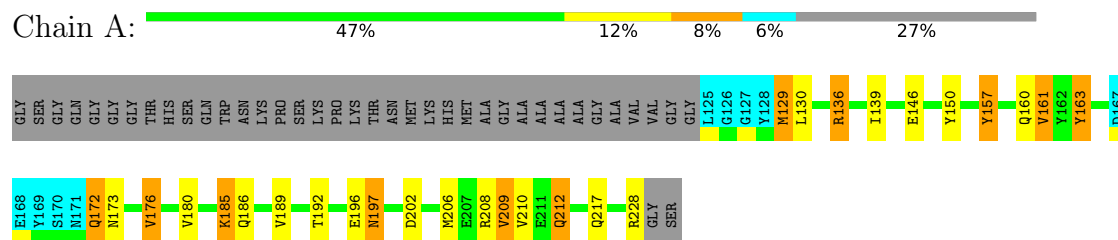
4.2.8 Score per residue for model 8

- Molecule 1: PRION PROTEIN



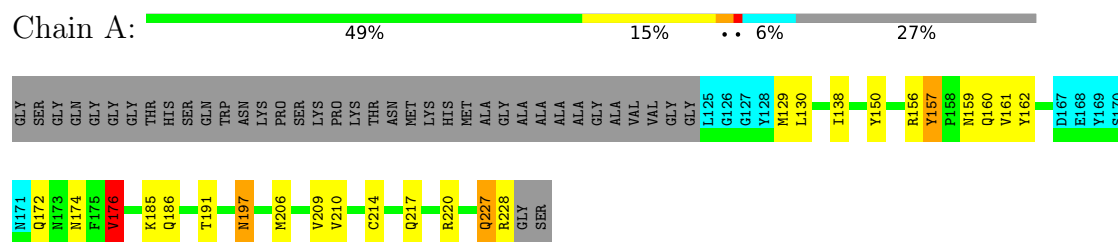
4.2.9 Score per residue for model 9

- Molecule 1: PRION PROTEIN



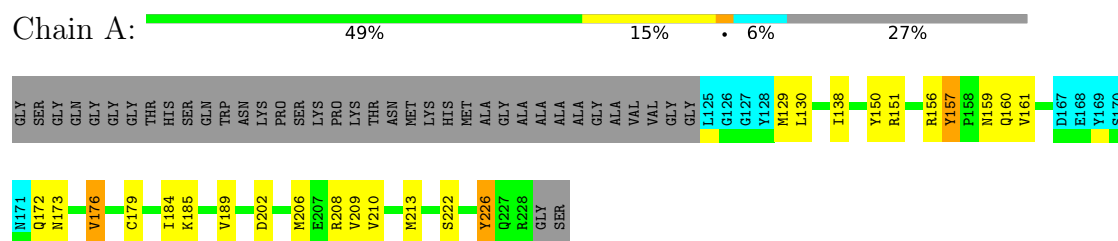
4.2.10 Score per residue for model 10

• Molecule 1: PRION PROTEIN



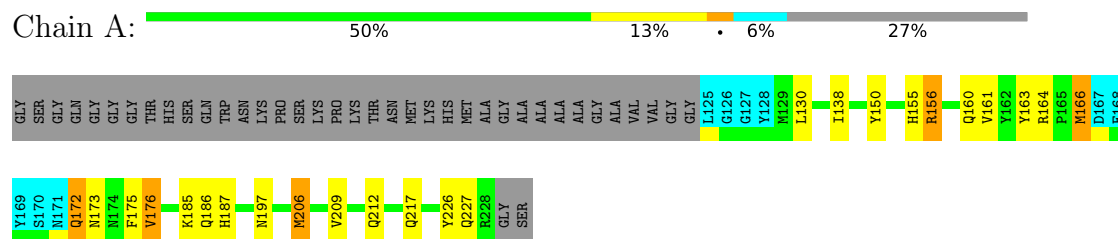
4.2.11 Score per residue for model 11 (medoid)

• Molecule 1: PRION PROTEIN



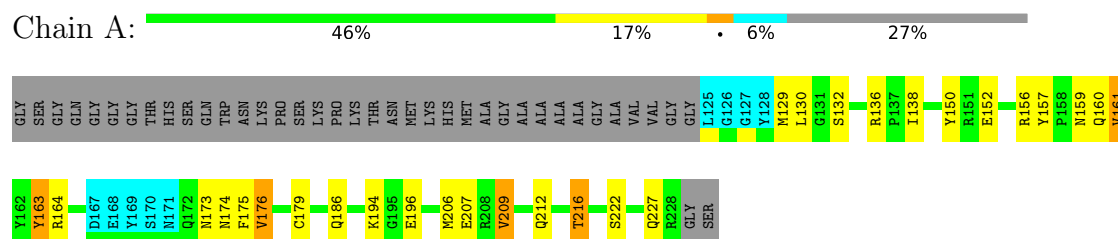
4.2.12 Score per residue for model 12

• Molecule 1: PRION PROTEIN



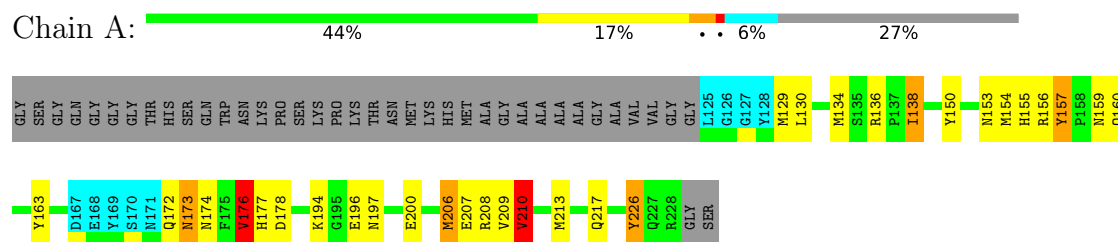
4.2.13 Score per residue for model 13

• Molecule 1: PRION PROTEIN



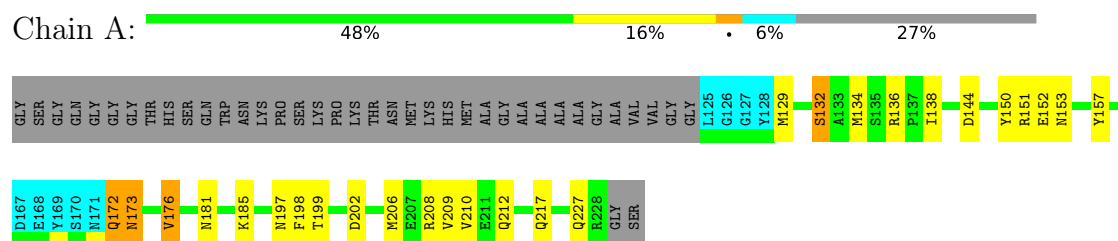
4.2.14 Score per residue for model 14

- Molecule 1: PRION PROTEIN



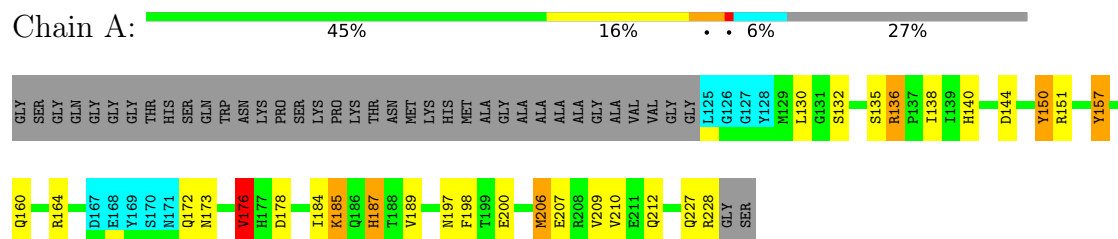
4.2.15 Score per residue for model 15

- Molecule 1: PRION PROTEIN



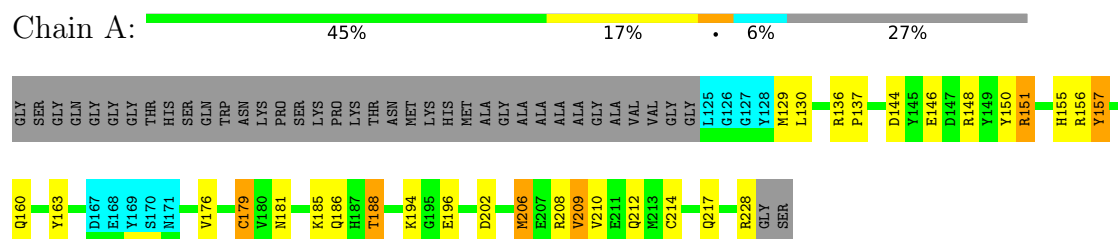
4.2.16 Score per residue for model 16

- Molecule 1: PRION PROTEIN



4.2.17 Score per residue for model 17

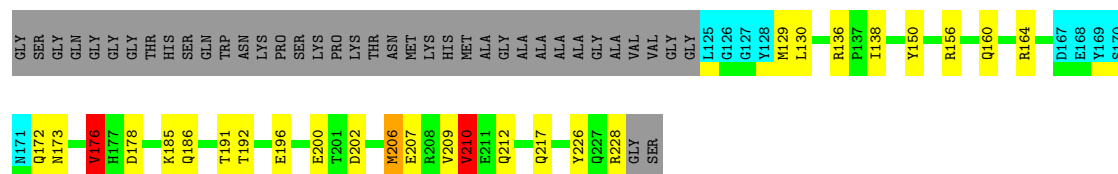
- Molecule 1: PRION PROTEIN



4.2.18 Score per residue for model 18

• Molecule 1: PRION PROTEIN

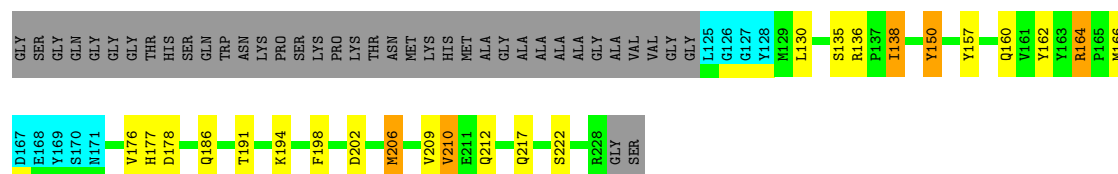
Chain A: 48% 17% 6% 27%



4.2.19 Score per residue for model 19

• Molecule 1: PRION PROTEIN

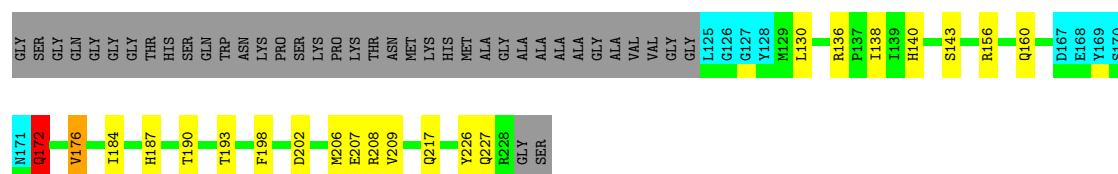
Chain A: 50% 13% 6% 27%



4.2.20 Score per residue for model 20

• Molecule 1: PRION PROTEIN

Chain A: 51% 14% 6% 27%



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: *LEAST RESTRAINT VIOLATION*.

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

Software name	Classification	Version
OPALp	refinement	
DYANA	structure solution	

No chemical shift data was provided.

6 Model quality i

6.1 Standard geometry i

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	0.73±0.01	0±0/824 (0.0± 0.0%)	1.53±0.05	5±2/1111 (0.4± 0.2%)
All	All	0.73	0/16480 (0.0%)	1.53	91/22220 (0.4%)

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	2.2±1.5
All	All	0	45

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	227	GLN	CA-C-N	7.56	135.31	121.70	15	2
1	A	227	GLN	C-N-CA	7.56	135.31	121.70	15	2
1	A	197	ASN	CA-CB-CG	7.53	120.13	112.60	3	3
1	A	164	ARG	CD-NE-CZ	7.17	134.43	124.40	5	1
1	A	188	THR	CA-CB-CG2	6.74	121.95	110.50	17	2
1	A	140	HIS	CB-CG-CD2	-6.66	122.54	131.20	5	3
1	A	176	VAL	CA-CB-CG2	6.36	121.21	110.40	20	2
1	A	156	ARG	CA-C-O	-6.18	116.25	119.77	10	1
1	A	198	PHE	CA-CB-CG	6.17	119.97	113.80	16	2
1	A	132	SER	N-CA-C	6.07	118.38	110.43	3	1
1	A	179	CYS	CA-C-N	6.04	128.18	120.56	6	8
1	A	179	CYS	C-N-CA	6.04	128.18	120.56	6	8
1	A	156	ARG	CB-CG-CD	5.83	124.70	111.30	12	1
1	A	146	GLU	CB-CG-CD	5.71	122.31	112.60	17	1
1	A	187	HIS	CA-C-N	5.67	128.19	120.54	2	3

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	187	HIS	C-N-CA	5.67	128.19	120.54	2	3
1	A	197	ASN	CA-C-N	5.66	132.36	121.54	15	1
1	A	197	ASN	C-N-CA	5.66	132.36	121.54	15	1
1	A	217	GLN	CA-C-N	5.55	128.00	120.44	10	1
1	A	217	GLN	C-N-CA	5.55	128.00	120.44	10	1
1	A	209	VAL	CA-CB-CG1	5.55	119.83	110.40	7	1
1	A	178	ASP	CA-C-N	5.54	128.03	120.54	19	2
1	A	178	ASP	C-N-CA	5.54	128.03	120.54	19	2
1	A	136	ARG	CA-C-N	5.52	125.61	119.87	16	3
1	A	136	ARG	C-N-CA	5.52	125.61	119.87	16	3
1	A	129	MET	CB-CA-C	5.49	120.86	109.38	9	1
1	A	187	HIS	CB-CG-CD2	-5.43	124.15	131.20	5	1
1	A	216	THR	OG1-CB-CG2	-5.35	98.60	109.30	13	1
1	A	173	ASN	CA-C-N	5.31	127.39	120.28	9	1
1	A	173	ASN	C-N-CA	5.31	127.39	120.28	9	1
1	A	209	VAL	CB-CA-C	5.30	119.30	112.14	1	2
1	A	177	HIS	CA-C-N	5.28	127.61	120.44	14	2
1	A	177	HIS	C-N-CA	5.28	127.61	120.44	14	2
1	A	191	THR	CB-CA-C	5.25	117.85	109.02	10	1
1	A	176	VAL	CG1-CB-CG2	-5.24	99.26	110.80	8	6
1	A	146	GLU	CA-C-N	5.24	127.56	120.38	9	1
1	A	146	GLU	C-N-CA	5.24	127.56	120.38	9	1
1	A	210	VAL	CA-CB-CG2	5.22	119.28	110.40	19	4
1	A	172	GLN	CA-C-N	5.18	127.48	120.38	7	1
1	A	172	GLN	C-N-CA	5.18	127.48	120.38	7	1
1	A	155	HIS	CB-CG-CD2	-5.16	124.49	131.20	14	2
1	A	187	HIS	CA-CB-CG	-5.11	108.69	113.80	12	1
1	A	206	MET	CA-CB-CG	5.05	124.19	114.10	12	1
1	A	210	VAL	CA-C-O	-5.02	115.34	120.71	14	1
1	A	192	THR	CA-CB-OG1	5.02	117.13	109.60	9	1
1	A	200	GLU	N-CA-CB	-5.00	102.55	110.06	18	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	150	TYR	Sidechain	6
1	A	151	ARG	Sidechain	5
1	A	136	ARG	Sidechain	5
1	A	226	TYR	Sidechain	4

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Mol	Chain	Res	Type	Group	Models (Total)
1	A	163	TYR	Sidechain	4
1	A	208	ARG	Sidechain	3
1	A	164	ARG	Sidechain	3
1	A	148	ARG	Sidechain	2
1	A	198	PHE	Sidechain	2
1	A	218	TYR	Sidechain	2
1	A	228	ARG	Sidechain	2
1	A	157	TYR	Sidechain	2
1	A	156	ARG	Sidechain	2
1	A	162	TYR	Sidechain	1
1	A	225	TYR	Sidechain	1
1	A	220	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	806	755	758	4±2
All	All	16120	15100	15160	82

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 3.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:130:LEU:HD11	1:A:160:GLN:HB3	0.93	1.41	18	18
1:A:134:MET:HE1	1:A:217:GLN:HG2	0.63	1.69	5	2
1:A:166:MET:HE1	1:A:222:SER:HA	0.59	1.73	19	1
1:A:185:LYS:O	1:A:189:VAL:HG23	0.58	1.98	11	7
1:A:173:ASN:HA	1:A:176:VAL:HG23	0.57	1.75	14	10
1:A:159:ASN:HA	1:A:213:MET:HE1	0.55	1.78	11	1
1:A:158:PRO:O	1:A:213:MET:HE1	0.54	2.01	3	1
1:A:134:MET:HE1	1:A:213:MET:O	0.54	2.01	14	1
1:A:191:THR:HG22	1:A:196:GLU:HB3	0.52	1.82	6	3
1:A:206:MET:O	1:A:210:VAL:HG23	0.51	2.05	19	8
1:A:184:ILE:CG1	1:A:210:VAL:HG21	0.49	2.37	11	5

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:130:LEU:HD12	1:A:161:VAL:O	0.48	2.08	13	5
1:A:176:VAL:HG12	1:A:214:CYS:HB2	0.48	1.86	10	1
1:A:136:ARG:HH12	1:A:209:VAL:CG2	0.48	2.22	9	1
1:A:191:THR:HG21	1:A:198:PHE:CE2	0.47	2.45	1	2
1:A:172:GLN:CD	1:A:172:GLN:H	0.47	2.18	10	2
1:A:191:THR:HG21	1:A:198:PHE:CZ	0.46	2.46	7	2
1:A:130:LEU:HD13	1:A:162:TYR:CD1	0.45	2.47	19	1
1:A:176:VAL:O	1:A:180:VAL:HG23	0.44	2.11	9	1
1:A:130:LEU:HD13	1:A:162:TYR:CE1	0.44	2.47	10	1
1:A:166:MET:HE1	1:A:222:SER:CA	0.43	2.43	19	1
1:A:156:ARG:CG	1:A:157:TYR:H	0.43	2.27	3	1
1:A:139:ILE:HD11	1:A:212:GLN:HG3	0.42	1.90	6	2
1:A:136:ARG:HH12	1:A:209:VAL:HG21	0.41	1.75	9	1
1:A:138:ILE:HD11	1:A:154:MET:HE1	0.41	1.93	14	1
1:A:184:ILE:HD11	1:A:206:MET:C	0.40	2.41	5	1
1:A:137:PRO:HG2	1:A:209:VAL:HG23	0.40	1.93	17	1
1:A:150:TYR:CD1	1:A:157:TYR:CD2	0.40	3.09	11	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	94/143 (66%)	85±2 (90±2%)	7±2 (7±2%)	2±1 (2±1%)	7	44
All	All	1880/2860 (66%)	1695 (90%)	140 (7%)	45 (2%)	7	44

All 10 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	138	ILE	16
1	A	172	GLN	10
1	A	157	TYR	8
1	A	166	MET	4
1	A	196	GLU	2

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Mol	Chain	Res	Type	Models (Total)
1	A	159	ASN	1
1	A	132	SER	1
1	A	198	PHE	1
1	A	135	SER	1
1	A	136	ARG	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	90/120 (75%)	72±4 (80±4%)	18±4 (20±4%)	3	33
All	All	1800/2400 (75%)	1440 (80%)	360 (20%)	3	33

All 63 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	176	VAL	20
1	A	206	MET	19
1	A	209	VAL	18
1	A	150	TYR	17
1	A	212	GLN	14
1	A	157	TYR	12
1	A	185	LYS	12
1	A	208	ARG	11
1	A	217	GLN	11
1	A	172	GLN	10
1	A	202	ASP	10
1	A	186	GLN	10
1	A	227	GLN	9
1	A	129	MET	9
1	A	156	ARG	8
1	A	164	ARG	8
1	A	197	ASN	8
1	A	210	VAL	8
1	A	132	SER	7
1	A	196	GLU	7

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Mol	Chain	Res	Type	Models (Total)
1	A	207	GLU	7
1	A	226	TYR	7
1	A	135	SER	6
1	A	151	ARG	6
1	A	144	ASP	6
1	A	174	ASN	6
1	A	161	VAL	6
1	A	187	HIS	5
1	A	200	GLU	5
1	A	173	ASN	5
1	A	181	ASN	5
1	A	194	LYS	5
1	A	136	ARG	5
1	A	159	ASN	4
1	A	155	HIS	4
1	A	178	ASP	4
1	A	163	TYR	4
1	A	228	ARG	4
1	A	154	MET	3
1	A	134	MET	2
1	A	166	MET	2
1	A	199	THR	2
1	A	143	SER	2
1	A	188	THR	2
1	A	193	THR	2
1	A	191	THR	2
1	A	222	SER	2
1	A	175	PHE	2
1	A	152	GLU	2
1	A	153	ASN	2
1	A	160	GLN	1
1	A	147	ASP	1
1	A	223	GLN	1
1	A	204	LYS	1
1	A	211	GLU	1
1	A	148	ARG	1
1	A	216	THR	1
1	A	179	CYS	1
1	A	214	CYS	1
1	A	192	THR	1
1	A	138	ILE	1
1	A	184	ILE	1

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Mol	Chain	Res	Type	Models (Total)
1	A	190	THR	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