



Full wwPDB NMR Structure Validation Report ⓘ

Mar 10, 2026 – 01:17 PM UTC

PDB ID : 1XYQ / pdb_00001xyq
Title : NMR structure of the pig prion protein
Authors : Lysek, D.A.; Schorn, C.; Herrmann, T.; Wuthrich, K.
Deposited on : 2004-11-10

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

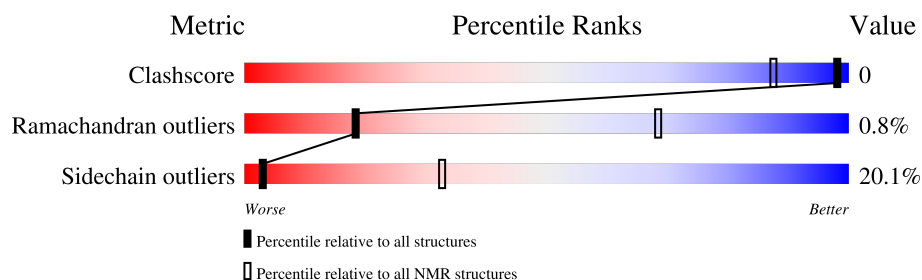
1 Overall quality at a glance

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	111	72% 14% 14%

2 Ensemble composition and analysis ⓘ

This entry contains 20 models. Model 19 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:127-A:167, A:171-A:225 (96)	0.66	19

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 and 5 single-model clusters were found.

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

3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 1763 atoms, of which 854 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Major prion protein.

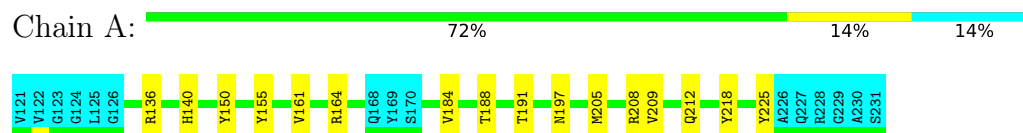
Mol	Chain	Residues	Atoms							Trace
1	A	111	Total	C	H	N	O	S		0
			1763	568	854	156	178	7		

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: Major prion protein

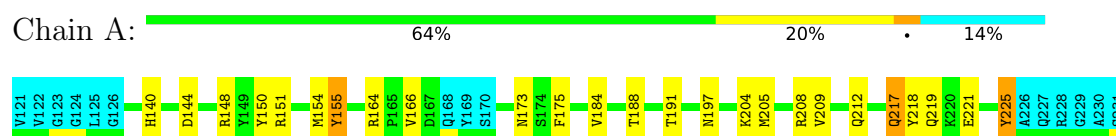


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

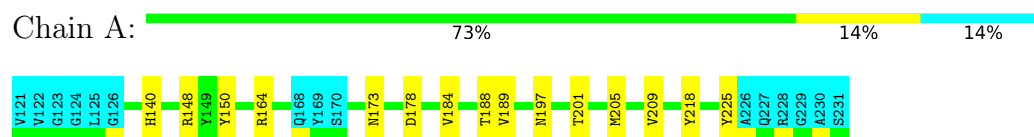
4.2.1 Score per residue for model 1

- Molecule 1: Major prion protein



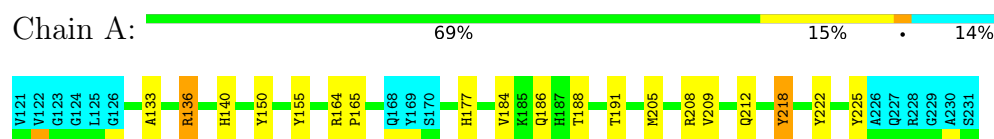
4.2.2 Score per residue for model 2

- Molecule 1: Major prion protein



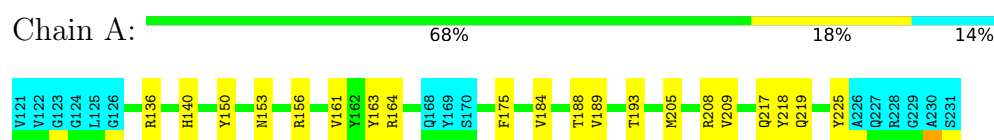
4.2.3 Score per residue for model 3

- Molecule 1: Major prion protein



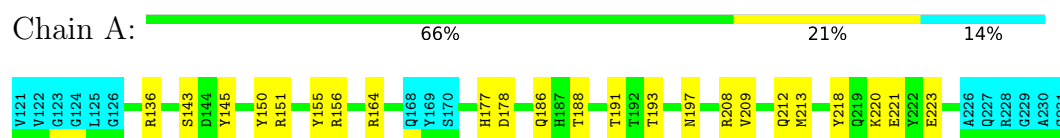
4.2.4 Score per residue for model 4

- Molecule 1: Major prion protein



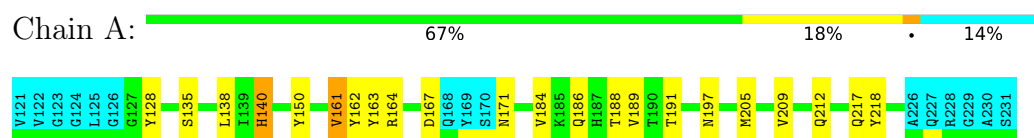
4.2.5 Score per residue for model 5

- Molecule 1: Major prion protein



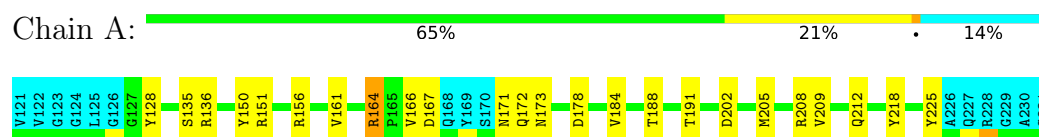
4.2.6 Score per residue for model 6

- Molecule 1: Major prion protein



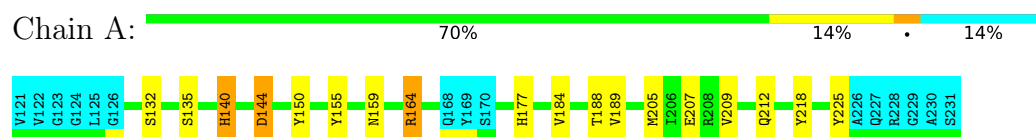
4.2.7 Score per residue for model 7

- Molecule 1: Major prion protein



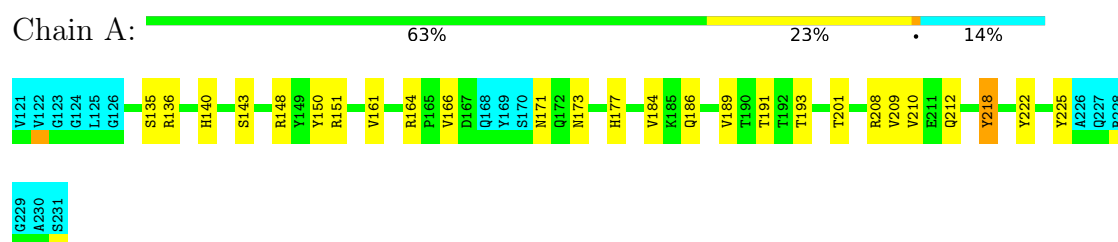
4.2.8 Score per residue for model 8

- Molecule 1: Major prion protein



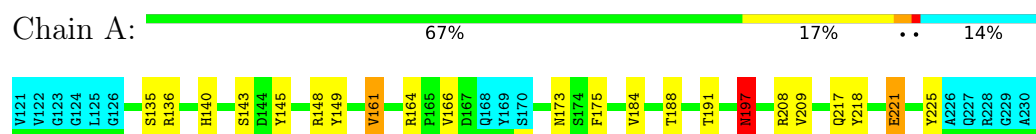
4.2.9 Score per residue for model 9

- Molecule 1: Major prion protein



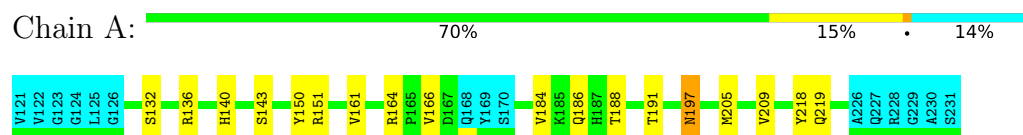
4.2.10 Score per residue for model 10

- Molecule 1: Major prion protein



4.2.11 Score per residue for model 11

- Molecule 1: Major prion protein



4.2.12 Score per residue for model 12

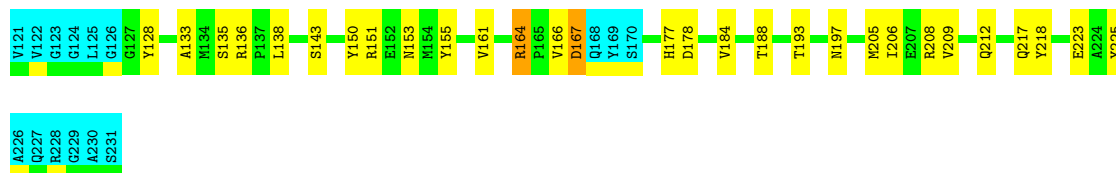
- Molecule 1: Major prion protein





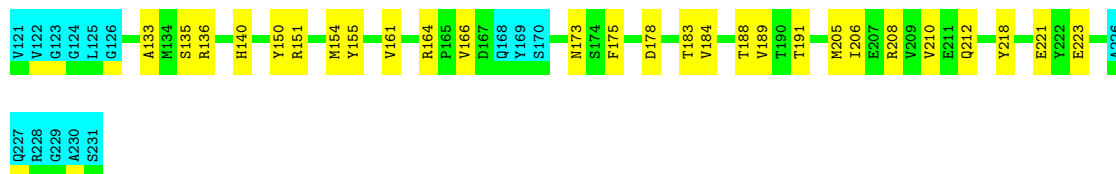
4.2.13 Score per residue for model 13

- Molecule 1: Major prion protein



4.2.14 Score per residue for model 14

- Molecule 1: Major prion protein



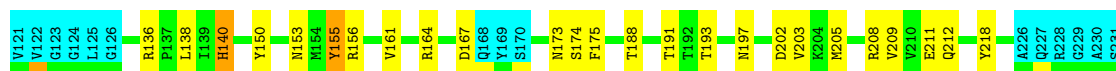
4.2.15 Score per residue for model 15

- Molecule 1: Major prion protein



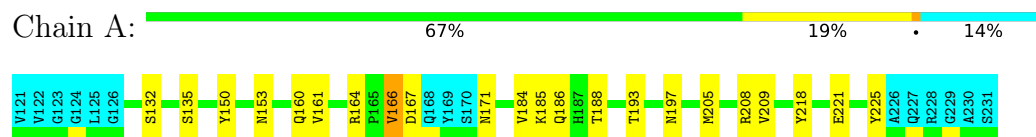
4.2.16 Score per residue for model 16

- Molecule 1: Major prion protein



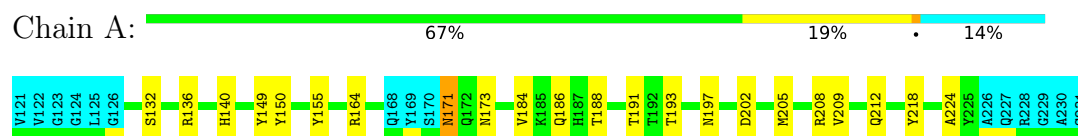
4.2.17 Score per residue for model 17

- Molecule 1: Major prion protein



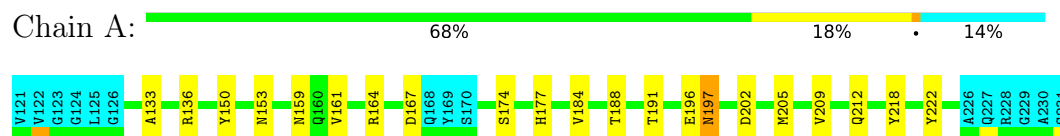
4.2.18 Score per residue for model 18

- Molecule 1: Major prion protein



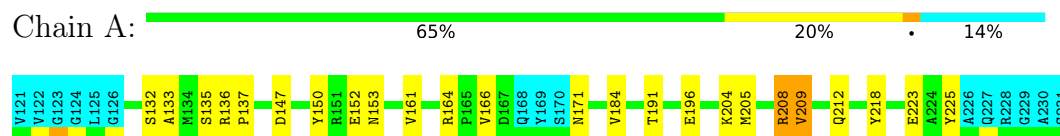
4.2.19 Score per residue for model 19 (medoid)

- Molecule 1: Major prion protein



4.2.20 Score per residue for model 20

- Molecule 1: Major prion protein



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: *target function*.

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

Software name	Classification	Version
DYANA	structure solution	6.2
CANDID	refinement	1.0

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	0.69±0.01	0±0/828 (0.0± 0.0%)	1.45±0.03	3±1/1122 (0.2± 0.1%)
All	All	0.69	0/16560 (0.0%)	1.45	52/22440 (0.2%)

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	1.9±1.4
All	All	0	39

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	213	MET	CA-C-N	6.59	129.00	120.44	5	1
1	A	213	MET	C-N-CA	6.59	129.00	120.44	5	1
1	A	140	HIS	CB-CG-CD2	-6.33	122.98	131.20	16	10
1	A	224	ALA	CA-C-N	6.05	128.64	120.65	18	1
1	A	224	ALA	C-N-CA	6.05	128.64	120.65	18	1
1	A	144	ASP	CA-CB-CG	6.03	118.63	112.60	8	2
1	A	197	ASN	CA-CB-CG	5.97	118.57	112.60	10	2
1	A	209	VAL	CA-CB-CG2	5.74	120.16	110.40	15	1
1	A	167	ASP	CA-CB-CG	-5.70	106.90	112.60	12	2
1	A	221	GLU	CA-C-N	5.70	127.85	120.44	12	3
1	A	221	GLU	C-N-CA	5.70	127.85	120.44	12	3
1	A	166	VAL	CA-C-N	5.62	128.37	120.28	20	4
1	A	166	VAL	C-N-CA	5.62	128.37	120.28	20	4
1	A	161	VAL	CA-CB-CG1	5.52	119.79	110.40	10	2
1	A	221	GLU	N-CA-C	-5.43	107.20	113.88	5	1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	140	HIS	CA-C-N	5.42	127.49	120.44	18	1
1	A	140	HIS	C-N-CA	5.42	127.49	120.44	18	1
1	A	173	ASN	CA-CB-CG	-5.42	107.18	112.60	7	1
1	A	206	ILE	CA-C-N	5.42	127.54	120.28	13	1
1	A	206	ILE	C-N-CA	5.42	127.54	120.28	13	1
1	A	217	GLN	OE1-CD-NE2	-5.40	117.20	122.60	1	1
1	A	160	GLN	CA-C-N	5.39	129.18	121.96	17	1
1	A	160	GLN	C-N-CA	5.39	129.18	121.96	17	1
1	A	210	VAL	CA-C-N	5.37	128.26	120.79	9	1
1	A	210	VAL	C-N-CA	5.37	128.26	120.79	9	1
1	A	178	ASP	CA-CB-CG	5.24	117.84	112.60	14	1
1	A	167	ASP	CA-C-N	5.08	130.15	122.68	7	1
1	A	167	ASP	C-N-CA	5.08	130.15	122.68	7	1
1	A	171	ASN	N-CA-CB	5.03	118.99	110.49	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	151	ARG	Sidechain	6
1	A	155	TYR	Sidechain	5
1	A	148	ARG	Sidechain	4
1	A	136	ARG	Sidechain	3
1	A	222	TYR	Sidechain	3
1	A	208	ARG	Sidechain	2
1	A	218	TYR	Sidechain	2
1	A	156	ARG	Sidechain	2
1	A	128	TYR	Sidechain	2
1	A	164	ARG	Sidechain	2
1	A	149	TYR	Sidechain	2
1	A	225	TYR	Sidechain	1
1	A	162	TYR	Sidechain	1
1	A	163	TYR	Sidechain	1
1	A	135	SER	Peptide	1
1	A	157	TYR	Sidechain	1
1	A	133	ALA	Peptide	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	808	755	755	1±1
All	All	16160	15100	15100	12

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:206:ILE:O	1:A:210:VAL:HG23	0.57	2.00	15	2
1:A:137:PRO:HG2	1:A:209:VAL:HG22	0.55	1.78	20	1
1:A:184:VAL:HG23	1:A:210:VAL:HG21	0.48	1.84	14	1
1:A:161:VAL:HG12	1:A:183:THR:HG21	0.46	1.88	12	2
1:A:133:ALA:HB1	1:A:159:ASN:HD22	0.45	1.71	19	1
1:A:143:SER:HB3	1:A:145:TYR:CE1	0.44	2.47	10	1
1:A:163:TYR:CE1	1:A:217:GLN:NE2	0.43	2.86	4	1
1:A:152:GLU:HG3	1:A:153:ASN:HD22	0.42	1.75	20	1
1:A:143:SER:HB3	1:A:145:TYR:CE2	0.40	2.51	5	1
1:A:128:TYR:CE1	1:A:164:ARG:HG2	0.40	2.51	7	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	96/111 (86%)	85±2 (88±2%)	11±2 (11±2%)	1±1 (1±1%)	18	68
All	All	1920/2220 (86%)	1693 (88%)	211 (11%)	16 (1%)	18	68

All 6 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	171	ASN	5
1	A	133	ALA	4
1	A	197	ASN	3
1	A	132	SER	2
1	A	165	PRO	1
1	A	196	GLU	1

6.3.2 Protein sidechains [i](#)

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	90/99 (91%)	72±3 (80±3%)	18±3 (20±3%)	3	33
All	All	1800/1980 (91%)	1439 (80%)	361 (20%)	3	33

All 53 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	164	ARG	20
1	A	218	TYR	20
1	A	150	TYR	19
1	A	188	THR	18
1	A	209	VAL	18
1	A	184	VAL	16
1	A	205	MET	16
1	A	191	THR	14
1	A	212	GLN	14
1	A	208	ARG	14
1	A	225	TYR	13
1	A	197	ASN	12
1	A	136	ARG	12
1	A	161	VAL	11
1	A	193	THR	9
1	A	135	SER	9
1	A	186	GLN	8
1	A	155	TYR	7
1	A	173	ASN	7
1	A	140	HIS	7

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Models (Total)
1	A	166	VAL	6
1	A	175	PHE	6
1	A	189	VAL	6
1	A	177	HIS	6
1	A	153	ASN	6
1	A	217	GLN	5
1	A	178	ASP	5
1	A	223	GLU	4
1	A	167	ASP	4
1	A	202	ASP	4
1	A	143	SER	4
1	A	154	MET	3
1	A	204	LYS	3
1	A	219	GLN	3
1	A	221	GLU	3
1	A	138	LEU	3
1	A	132	SER	3
1	A	151	ARG	2
1	A	201	THR	2
1	A	156	ARG	2
1	A	171	ASN	2
1	A	185	LYS	2
1	A	147	ASP	2
1	A	174	SER	2
1	A	220	LYS	1
1	A	172	GLN	1
1	A	144	ASP	1
1	A	159	ASN	1
1	A	207	GLU	1
1	A	203	VAL	1
1	A	211	GLU	1
1	A	149	TYR	1
1	A	196	GLU	1

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

No chemical shift data were provided