



Full wwPDB NMR Structure Validation Report ⓘ

Mar 8, 2026 – 09:00 AM UTC

PDB ID : 1XU0 / pdb_00001xu0
Title : Solution structure of Xenopus laevis prion protein
Authors : Perez, D.R.; Wuthrich, K.
Deposited on : 2004-10-25

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

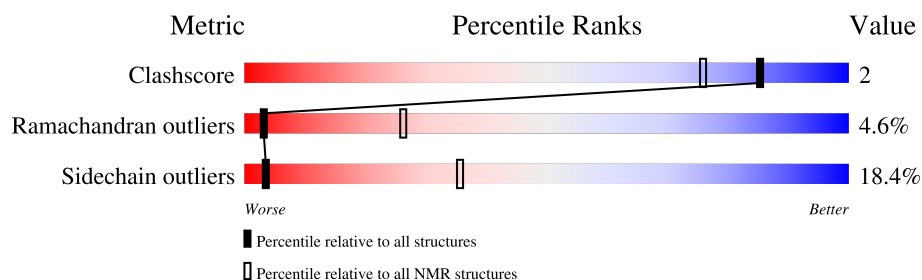
1 Overall quality at a glance

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	130	

2 Ensemble composition and analysis

This entry contains 20 models. Model 1 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:125-A:226 (102)	1.10	1

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 4 single-model clusters were found.

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

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 1653 atoms, of which 803 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called prion protein.

Mol	Chain	Residues	Atoms							Trace
1	A	102	Total	C	H	N	O	S		0
			1653	527	803	149	165	9		

There is a discrepancy between the modelled and reference sequences:

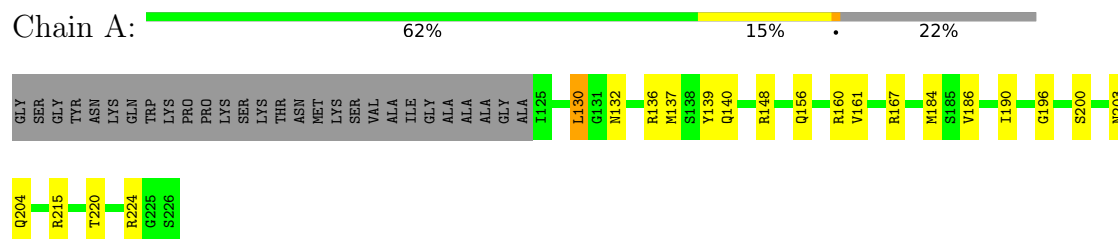
Chain	Residue	Modelled	Actual	Comment	Reference
A	97	GLY	-	cloning artifact	UNP Q5S1W7

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

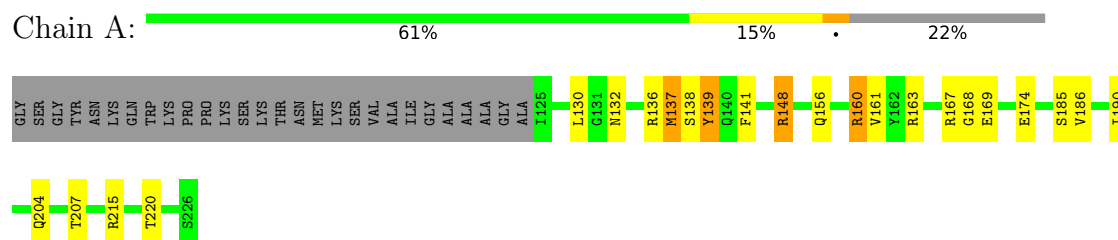


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1 (medoid)

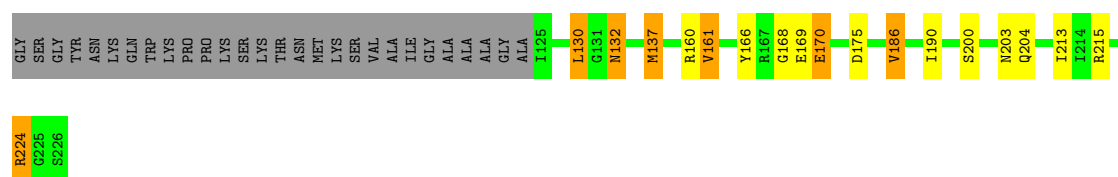
- Molecule 1: prion protein



4.2.2 Score per residue for model 2

- Molecule 1: prion protein

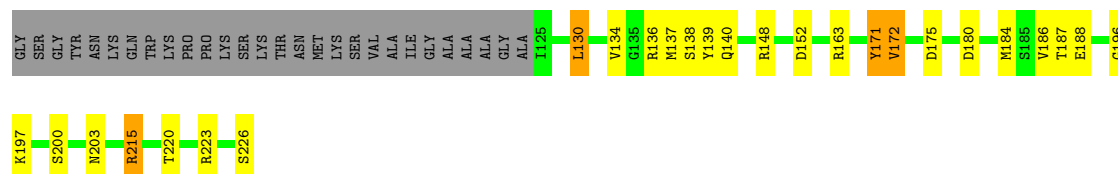




4.2.3 Score per residue for model 3

- Molecule 1: prion protein

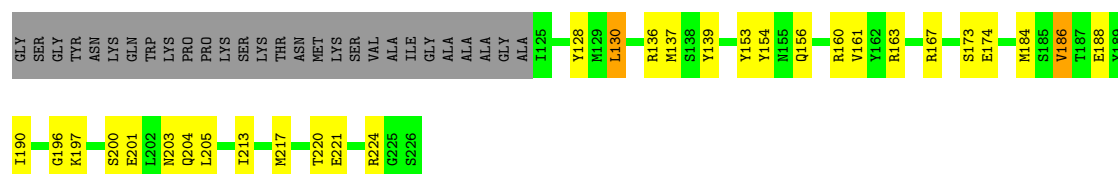
Chain A: 58% 17% 22%



4.2.4 Score per residue for model 4

- Molecule 1: prion protein

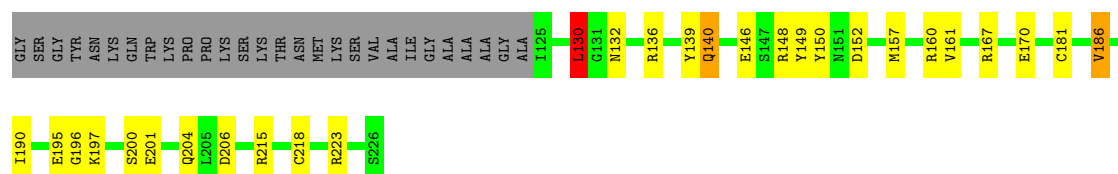
Chain A: 55% 22% 22%



4.2.5 Score per residue for model 5

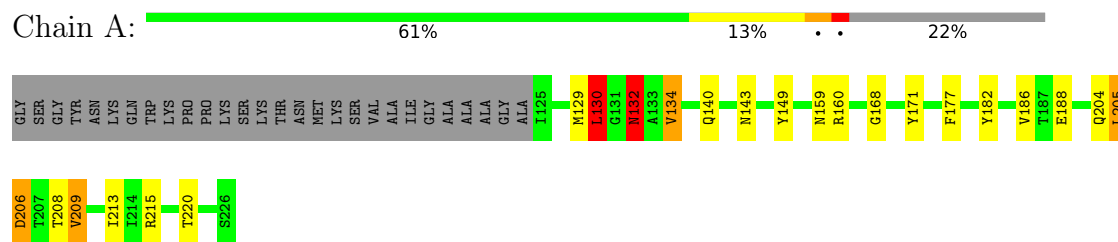
- Molecule 1: prion protein

Chain A: 57% 19% 22%



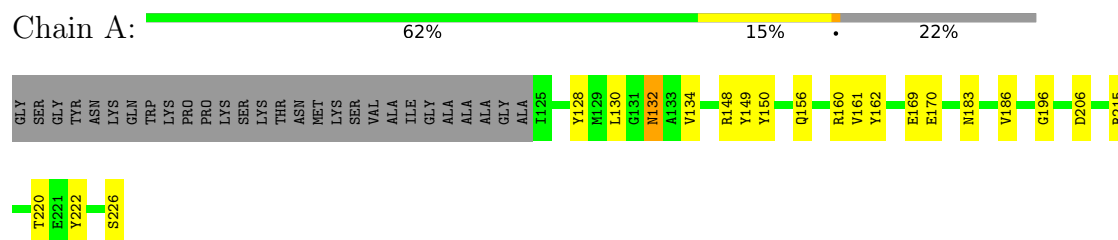
4.2.6 Score per residue for model 6

- Molecule 1: prion protein



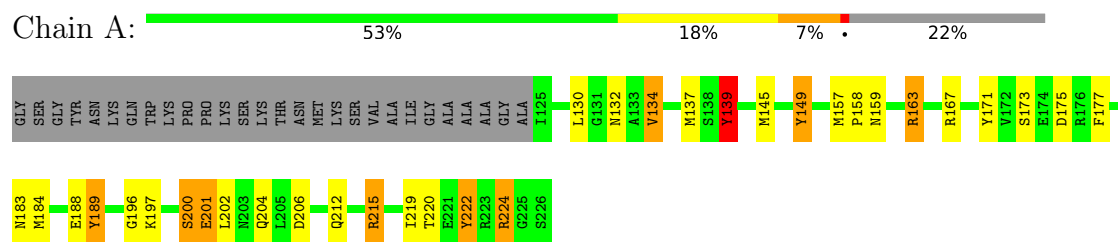
4.2.7 Score per residue for model 7

- Molecule 1: prion protein



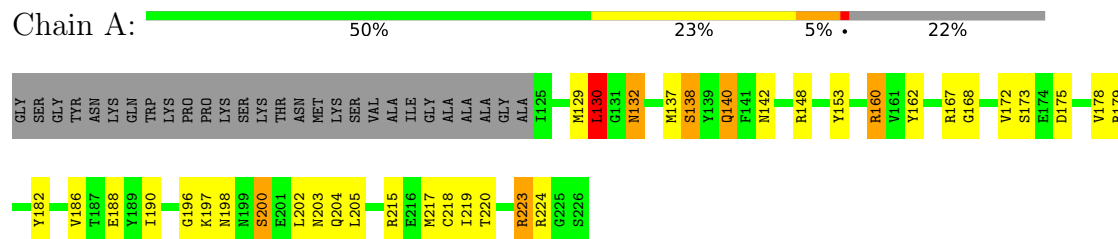
4.2.8 Score per residue for model 8

- Molecule 1: prion protein



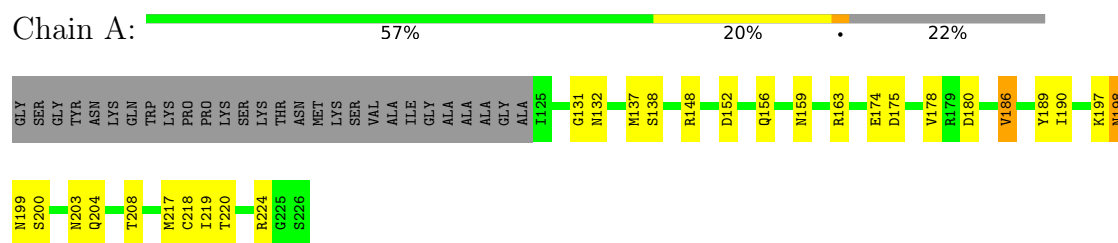
4.2.9 Score per residue for model 9

- Molecule 1: prion protein



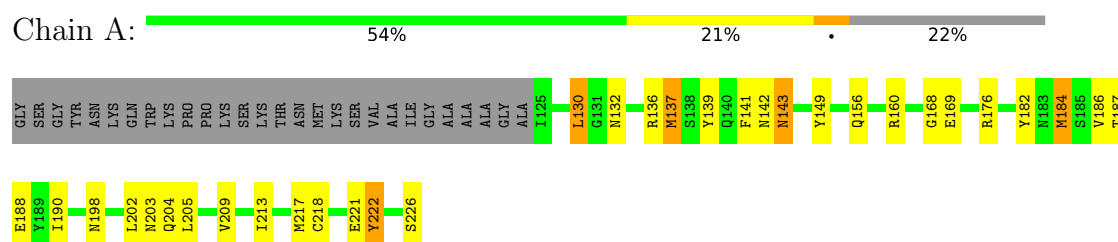
4.2.10 Score per residue for model 10

- Molecule 1: prion protein



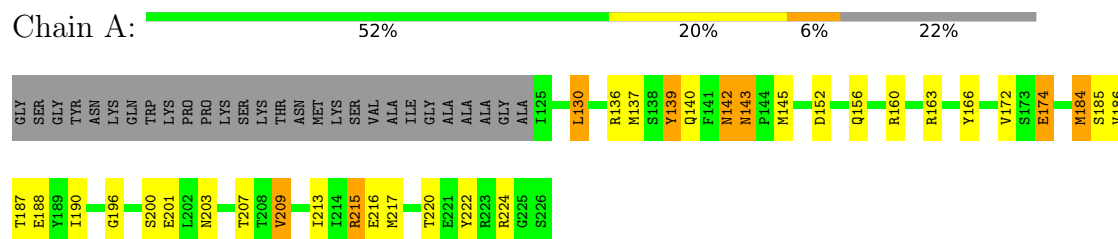
4.2.11 Score per residue for model 11

- Molecule 1: prion protein



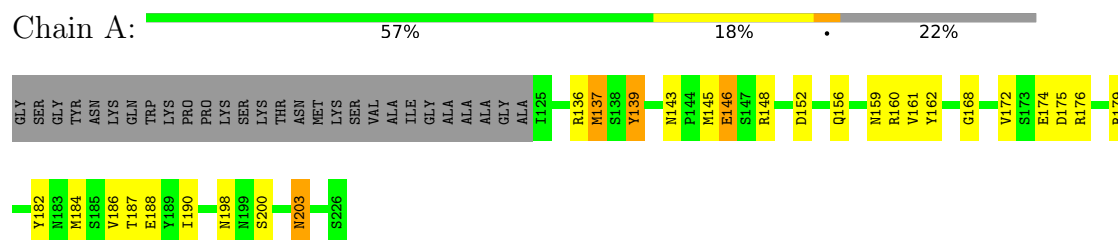
4.2.12 Score per residue for model 12

- Molecule 1: prion protein



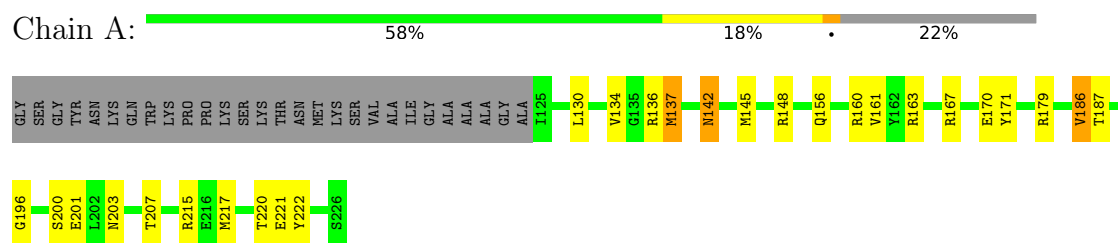
4.2.13 Score per residue for model 13

- Molecule 1: prion protein



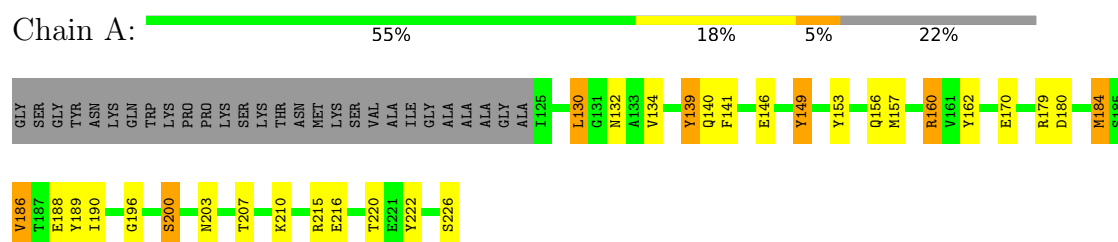
4.2.14 Score per residue for model 14

- Molecule 1: prion protein



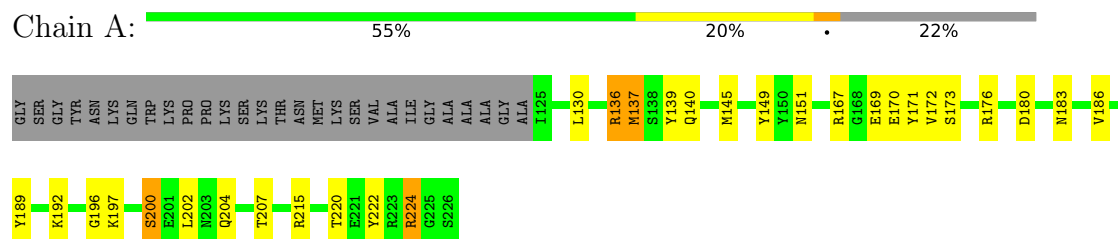
4.2.15 Score per residue for model 15

- Molecule 1: prion protein



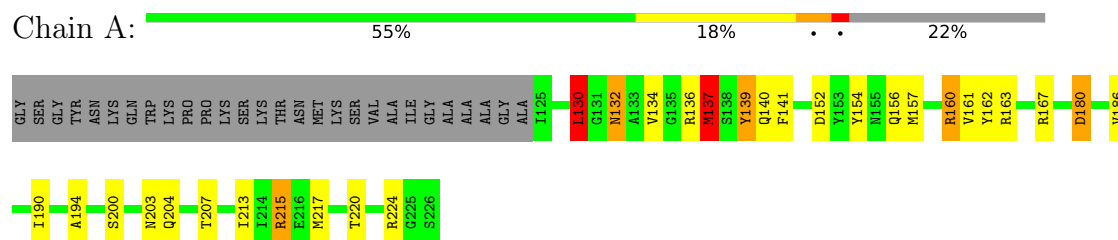
4.2.16 Score per residue for model 16

- Molecule 1: prion protein



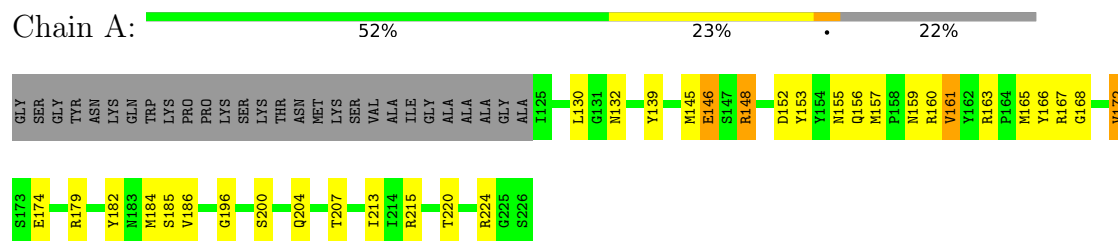
4.2.17 Score per residue for model 17

- Molecule 1: prion protein



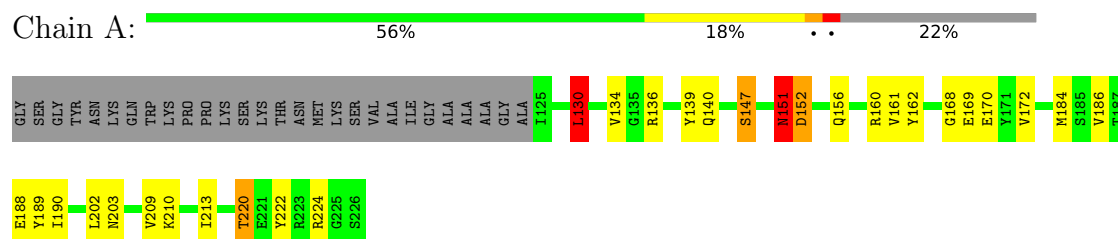
4.2.18 Score per residue for model 18

- Molecule 1: prion protein



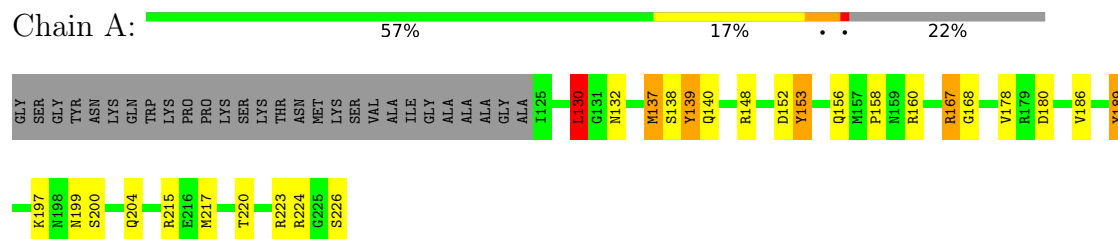
4.2.19 Score per residue for model 19

- Molecule 1: prion protein



4.2.20 Score per residue for model 20

- Molecule 1: 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	6.01
OPALp	refinement	

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	0.66±0.02	0±0/867 (0.0± 0.0%)	1.48±0.04	4±3/1166 (0.4± 0.2%)
All	All	0.66	0/17340 (0.0%)	1.48	90/23320 (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	3.1±1.4
All	All	0	63

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	132	ASN	CA-CB-CG	10.52	123.12	112.60	6	5
1	A	130	LEU	CB-CA-C	7.05	121.26	110.62	6	2
1	A	209	VAL	CA-CB-CG1	7.04	122.36	110.40	12	1
1	A	206	ASP	CA-CB-CG	6.69	119.29	112.60	6	1
1	A	151	ASN	CA-CB-CG	6.58	119.18	112.60	19	1
1	A	142	ASN	CA-CB-CG	6.50	119.09	112.60	14	2
1	A	209	VAL	CA-C-N	6.49	129.30	120.54	19	1
1	A	209	VAL	C-N-CA	6.49	129.30	120.54	19	1
1	A	175	ASP	CA-C-N	6.47	129.24	120.44	2	2
1	A	175	ASP	C-N-CA	6.47	129.24	120.44	2	2
1	A	143	ASN	CA-CB-CG	6.44	119.04	112.60	11	4
1	A	209	VAL	CA-CB-CG2	6.34	121.17	110.40	6	1
1	A	136	ARG	CA-C-N	6.11	133.20	121.54	16	1
1	A	136	ARG	C-N-CA	6.11	133.20	121.54	16	1
1	A	129	MET	CA-C-N	5.86	132.74	121.54	9	1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	129	MET	C-N-CA	5.86	132.74	121.54	9	1
1	A	168	GLY	CA-C-N	5.82	132.66	121.54	18	2
1	A	168	GLY	C-N-CA	5.82	132.66	121.54	18	2
1	A	205	LEU	CA-C-N	5.80	128.37	120.54	6	1
1	A	205	LEU	C-N-CA	5.80	128.37	120.54	6	1
1	A	161	VAL	CA-CB-CG2	5.77	120.22	110.40	18	2
1	A	213	ILE	CA-CB-CG1	5.58	119.88	110.40	19	1
1	A	186	VAL	CA-CB-CG1	5.57	119.87	110.40	5	2
1	A	203	ASN	CA-CB-CG	5.56	118.16	112.60	13	1
1	A	161	VAL	CB-CA-C	5.54	118.78	111.19	5	2
1	A	172	VAL	CB-CA-C	5.48	120.27	111.29	3	1
1	A	146	GLU	CB-CG-CD	5.45	121.86	112.60	15	3
1	A	180	ASP	CA-CB-CG	5.39	117.99	112.60	10	2
1	A	152	ASP	CA-CB-CG	5.39	117.99	112.60	3	1
1	A	172	VAL	CA-CB-CG1	5.35	119.50	110.40	18	1
1	A	182	TYR	CA-C-N	5.32	128.18	120.79	6	2
1	A	182	TYR	C-N-CA	5.32	128.18	120.79	6	2
1	A	224	ARG	N-CA-CB	-5.31	102.72	110.47	2	1
1	A	222	TYR	CA-C-N	5.30	127.39	120.28	11	1
1	A	222	TYR	C-N-CA	5.30	127.39	120.28	11	1
1	A	194	ALA	CA-C-N	5.30	128.12	120.38	17	1
1	A	194	ALA	C-N-CA	5.30	128.12	120.38	17	1
1	A	137	MET	CA-C-N	5.29	131.63	121.54	3	4
1	A	137	MET	C-N-CA	5.29	131.63	121.54	3	4
1	A	178	VAL	CA-C-O	-5.28	115.78	121.27	20	1
1	A	147	SER	CA-C-N	5.28	127.30	120.44	19	1
1	A	147	SER	C-N-CA	5.28	127.30	120.44	19	1
1	A	202	LEU	CA-C-N	5.27	129.52	120.72	19	1
1	A	202	LEU	C-N-CA	5.27	129.52	120.72	19	1
1	A	219	ILE	CA-C-N	5.25	127.26	120.44	8	1
1	A	219	ILE	C-N-CA	5.25	127.26	120.44	8	1
1	A	134	VAL	CB-CA-C	5.23	115.71	111.05	17	1
1	A	134	VAL	CA-CB-CG2	5.22	119.27	110.40	7	1
1	A	197	LYS	CA-C-N	5.16	129.85	122.21	16	1
1	A	197	LYS	C-N-CA	5.16	129.85	122.21	16	1
1	A	165	MET	CA-C-N	5.16	131.39	121.54	18	1
1	A	165	MET	C-N-CA	5.16	131.39	121.54	18	1
1	A	156	GLN	CA-CB-CG	-5.15	103.80	114.10	14	1
1	A	198	ASN	CA-C-N	5.12	131.32	121.54	10	1
1	A	198	ASN	C-N-CA	5.12	131.32	121.54	10	1
1	A	215	ARG	CB-CA-C	5.12	119.38	110.68	12	1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	220	THR	CA-CB-CG2	5.11	119.19	110.50	19	1
1	A	159	ASN	CA-CB-CG	-5.10	107.50	112.60	6	1
1	A	207	THR	CA-C-N	5.07	127.03	120.44	16	1
1	A	207	THR	C-N-CA	5.07	127.03	120.44	16	1
1	A	207	THR	CA-CB-CG2	5.04	119.07	110.50	18	1
1	A	146	GLU	CA-C-N	5.03	126.98	120.44	13	1
1	A	146	GLU	C-N-CA	5.03	126.98	120.44	13	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	139	TYR	Sidechain,Peptide	9
1	A	162	TYR	Sidechain	6
1	A	215	ARG	Sidechain	5
1	A	163	ARG	Sidechain,Peptide	5
1	A	148	ARG	Sidechain	4
1	A	160	ARG	Sidechain	4
1	A	167	ARG	Sidechain	4
1	A	149	TYR	Sidechain	4
1	A	189	TYR	Sidechain	4
1	A	223	ARG	Sidechain	3
1	A	154	TYR	Sidechain	2
1	A	171	TYR	Sidechain	2
1	A	222	TYR	Sidechain	2
1	A	176	ARG	Sidechain	2
1	A	153	TYR	Sidechain	2
1	A	128	TYR	Sidechain	1
1	A	150	TYR	Sidechain	1
1	A	166	TYR	Sidechain	1
1	A	136	ARG	Sidechain	1
1	A	224	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	850	803	804	4±3
All	All	17000	16060	16080	73

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 2.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:186:VAL:HG13	1:A:190:ILE:HD12	0.94	1.38	17	6
1:A:205:LEU:O	1:A:209:VAL:HG13	0.57	2.00	6	1
1:A:130:LEU:HD22	1:A:160:ARG:HD2	0.56	1.77	11	9
1:A:137:MET:HE3	1:A:139:TYR:CD2	0.56	2.35	8	1
1:A:186:VAL:CG2	1:A:190:ILE:HD12	0.55	2.30	11	6
1:A:137:MET:HE3	1:A:217:MET:HG3	0.54	1.79	17	2
1:A:137:MET:HE3	1:A:217:MET:CG	0.53	2.34	12	1
1:A:184:MET:HE2	1:A:184:MET:O	0.51	2.04	11	3
1:A:139:TYR:CE2	1:A:216:GLU:HB3	0.51	2.41	15	1
1:A:184:MET:HE2	1:A:184:MET:C	0.51	2.31	11	1
1:A:175:ASP:HA	1:A:178:VAL:HG12	0.50	1.83	10	2
1:A:184:MET:HE1	1:A:188:GLU:HG3	0.50	1.83	11	1
1:A:149:TYR:CE2	1:A:157:MET:CE	0.50	2.94	8	1
1:A:150:TYR:CD1	1:A:157:MET:HE3	0.49	2.42	5	1
1:A:205:LEU:O	1:A:209:VAL:HG12	0.49	2.07	11	1
1:A:181:CYS:SG	1:A:218:CYS:SG	0.49	3.11	5	1
1:A:141:PHE:CE1	1:A:209:VAL:HG23	0.48	2.42	11	1
1:A:130:LEU:HD22	1:A:160:ARG:CD	0.48	2.38	19	2
1:A:178:VAL:HG23	1:A:218:CYS:HB2	0.46	1.87	9	1
1:A:137:MET:HE3	1:A:217:MET:HG2	0.46	1.88	12	1
1:A:137:MET:HE2	1:A:217:MET:CG	0.45	2.42	20	1
1:A:139:TYR:CE2	1:A:216:GLU:CB	0.45	3.00	12	1
1:A:158:PRO:HB3	1:A:189:TYR:CE2	0.44	2.48	20	2
1:A:182:TYR:O	1:A:186:VAL:HG13	0.44	2.13	18	1
1:A:137:MET:SD	1:A:139:TYR:CD2	0.44	3.10	20	1
1:A:182:TYR:O	1:A:186:VAL:HG12	0.44	2.13	13	2
1:A:140:GLN:H	1:A:140:GLN:CD	0.43	2.21	17	1
1:A:134:VAL:HG11	1:A:217:MET:SD	0.43	2.54	14	1
1:A:158:PRO:HB3	1:A:189:TYR:CZ	0.43	2.48	8	1
1:A:149:TYR:CD2	1:A:209:VAL:HG11	0.43	2.49	11	1
1:A:149:TYR:CZ	1:A:206:ASP:HA	0.43	2.49	5	2
1:A:183:ASN:HA	1:A:186:VAL:HG22	0.42	1.90	16	1
1:A:159:ASN:C	1:A:159:ASN:HD22	0.42	2.22	18	1
1:A:149:TYR:CE1	1:A:157:MET:CE	0.42	3.02	15	1

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:137:MET:CE	1:A:217:MET:HG3	0.42	2.45	9	1
1:A:151:ASN:HD22	1:A:152:ASP:N	0.42	2.13	19	1
1:A:137:MET:HE2	1:A:217:MET:HG2	0.41	1.92	20	1
1:A:137:MET:CE	1:A:217:MET:HG2	0.41	2.46	4	2
1:A:132:ASN:ND2	1:A:224:ARG:HH12	0.41	2.14	8	1
1:A:174:GLU:CD	1:A:174:GLU:H	0.40	2.24	10	1
1:A:149:TYR:CE1	1:A:206:ASP:HA	0.40	2.51	5	1
1:A:177:PHE:CD1	1:A:222:TYR:CE1	0.40	3.09	8	1
1:A:184:MET:HE1	1:A:188:GLU:CG	0.40	2.47	11	1
1:A:174:GLU:H	1:A:174:GLU:CD	0.40	2.24	12	1
1:A:178:VAL:HG23	1:A:218:CYS:CB	0.40	2.46	10	1
1:A:130:LEU:HD13	1:A:160:ARG:CG	0.40	2.46	17	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	100/130 (77%)	81±2 (81±2%)	14±2 (14±2%)	5±2 (5±2%)	3	26
All	All	2000/2600 (77%)	1620 (81%)	288 (14%)	92 (5%)	3	26

All 23 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	200	SER	12
1	A	196	GLY	11
1	A	168	GLY	7
1	A	170	GLU	7
1	A	137	MET	6
1	A	139	TYR	5
1	A	130	LEU	5
1	A	197	LYS	5
1	A	132	ASN	5
1	A	140	GLN	4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Models (Total)
1	A	141	PHE	3
1	A	171	TYR	3
1	A	172	VAL	3
1	A	201	GLU	3
1	A	134	VAL	3
1	A	166	TYR	2
1	A	198	ASN	2
1	A	128	TYR	1
1	A	136	ARG	1
1	A	186	VAL	1
1	A	138	SER	1
1	A	131	GLY	1
1	A	169	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	93/112 (83%)	76±4 (82±4%)	17±4 (18±4%)	3	36
All	All	1860/2240 (83%)	1518 (82%)	342 (18%)	3	36

All 71 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	130	LEU	18
1	A	220	THR	16
1	A	204	GLN	13
1	A	215	ARG	13
1	A	156	GLN	12
1	A	203	ASN	12
1	A	224	ARG	11
1	A	136	ARG	9
1	A	184	MET	9
1	A	188	GLU	9
1	A	132	ASN	8
1	A	148	ARG	8

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Models (Total)
1	A	161	VAL	8
1	A	186	VAL	8
1	A	152	ASP	8
1	A	167	ARG	7
1	A	213	ILE	7
1	A	140	GLN	7
1	A	200	SER	7
1	A	222	TYR	6
1	A	145	MET	6
1	A	137	MET	6
1	A	138	SER	5
1	A	160	ARG	5
1	A	163	ARG	5
1	A	169	GLU	5
1	A	174	GLU	5
1	A	207	THR	5
1	A	180	ASP	5
1	A	187	THR	5
1	A	226	SER	5
1	A	179	ARG	5
1	A	134	VAL	4
1	A	153	TYR	4
1	A	173	SER	4
1	A	139	TYR	4
1	A	202	LEU	4
1	A	142	ASN	4
1	A	172	VAL	4
1	A	185	SER	3
1	A	221	GLU	3
1	A	201	GLU	3
1	A	159	ASN	3
1	A	175	ASP	2
1	A	197	LYS	2
1	A	205	LEU	2
1	A	206	ASP	2
1	A	208	THR	2
1	A	183	ASN	2
1	A	219	ILE	2
1	A	223	ARG	2
1	A	199	ASN	2
1	A	143	ASN	2
1	A	198	ASN	2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Models (Total)
1	A	146	GLU	2
1	A	189	TYR	2
1	A	210	LYS	2
1	A	151	ASN	2
1	A	157	MET	2
1	A	170	GLU	1
1	A	171	TYR	1
1	A	195	GLU	1
1	A	129	MET	1
1	A	177	PHE	1
1	A	212	GLN	1
1	A	176	ARG	1
1	A	218	CYS	1
1	A	209	VAL	1
1	A	192	LYS	1
1	A	155	ASN	1
1	A	147	SER	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 ⓘ

There are no oligosaccharides in this entry.

6.6 Ligand geometry ⓘ

There are no ligands in this entry.

6.7 Other polymers ⓘ

There are no such molecules in this entry.

6.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

7 Chemical shift validation

No chemical shift data were provided