



Full wwPDB NMR Structure Validation Report ⓘ

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PDB ID : 1XU0
Title : Solution structure of Xenopus leavis 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

<http://wwpdb.org/validation/2016/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
Mogul : unknown
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
ShiftChecker : rb-20027457
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20027457

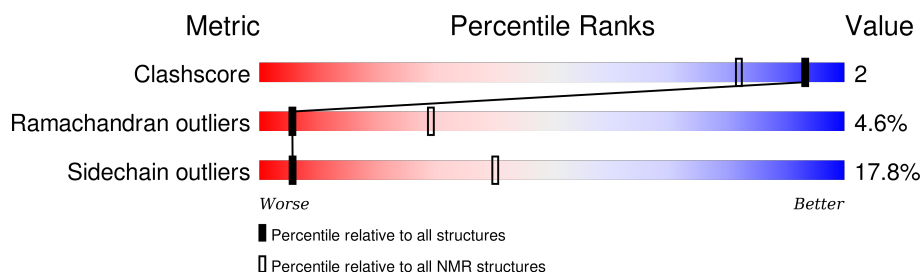
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 81%.

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	114402	11133
Ramachandran outliers	111179	9975
Sidechain outliers	111093	9958

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	 62% 15% • 22%

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)	0.63	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:

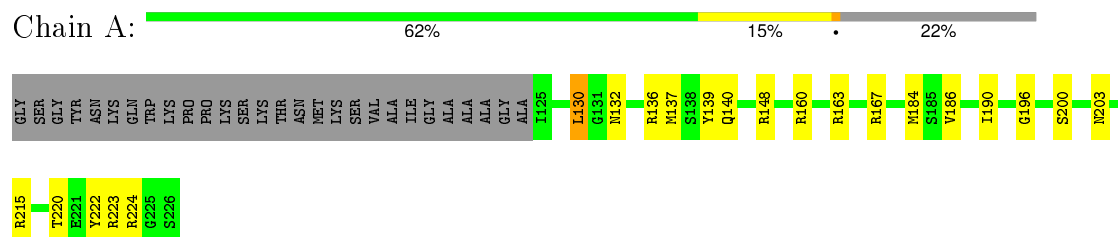
Chain	Residue	Modelled	Actual	Comment	Reference
A	97	GLY	-	CLONING ARTIFACT	UNP Q5S1W7

4 Residue-property plots [i](#)

4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA 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: prion protein

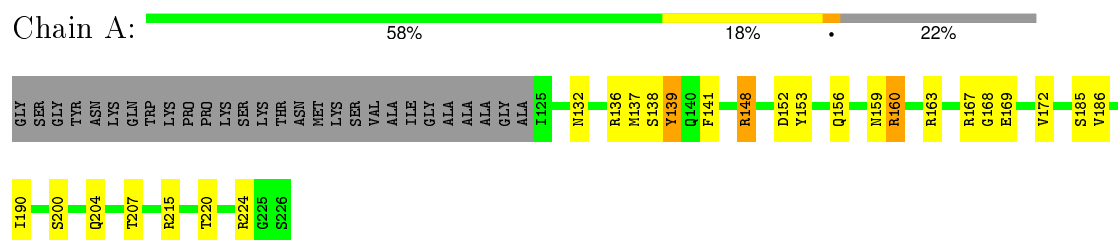


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1 (medoid)

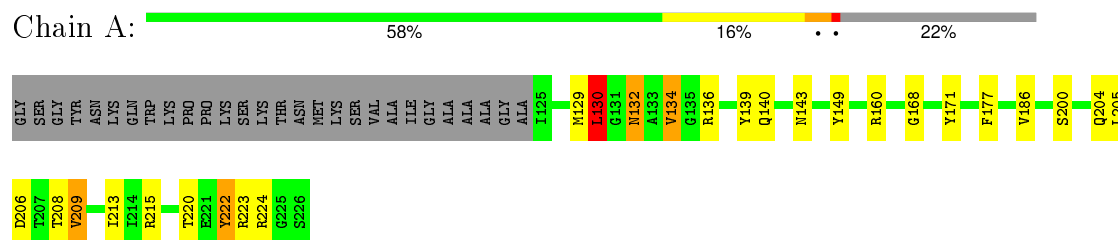
- Molecule 1: prion protein



4.2.2 Score per residue for model 2

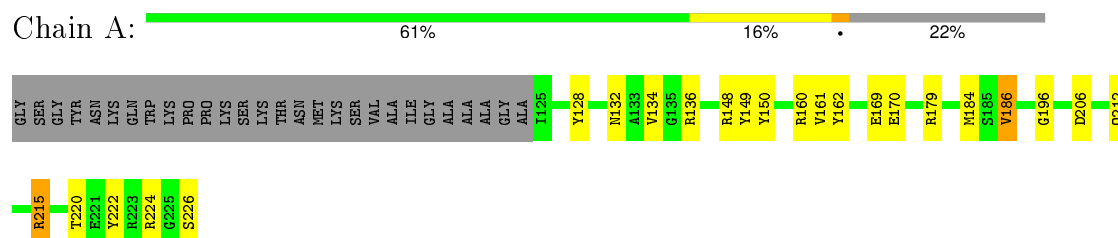
- Molecule 1: prion protein





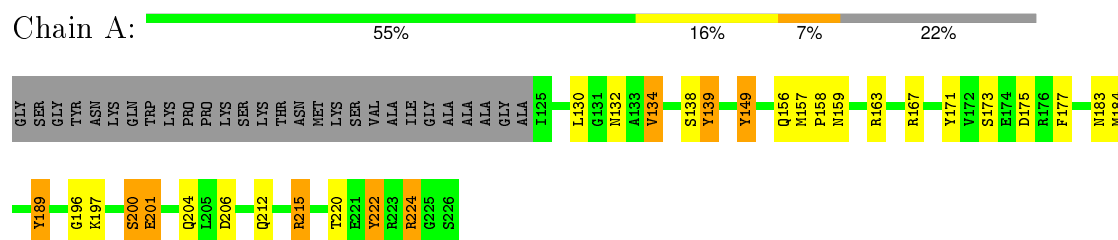
4.2.7 Score per residue for model 7

- Molecule 1: prion protein



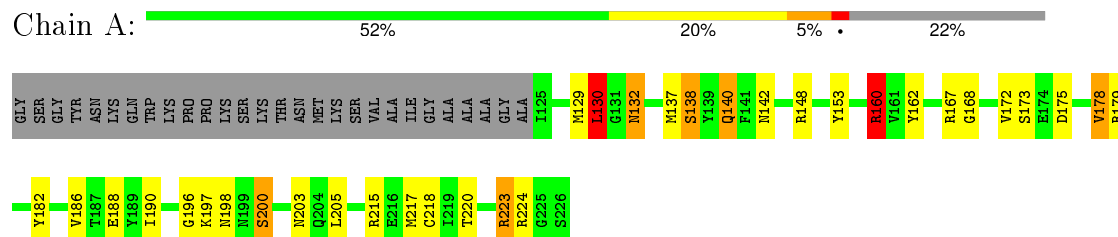
4.2.8 Score per residue for model 8

- Molecule 1: prion protein



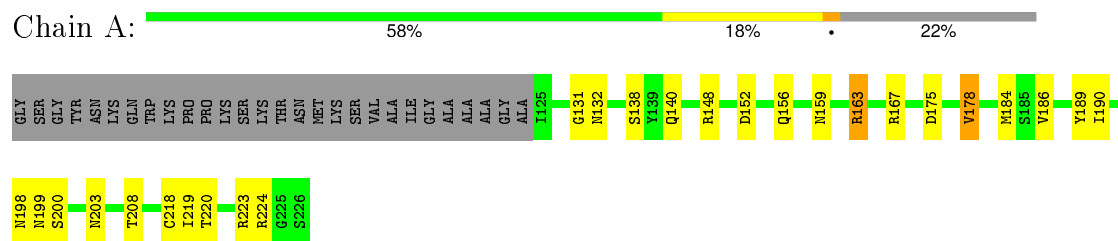
4.2.9 Score per residue for model 9

- Molecule 1: prion protein



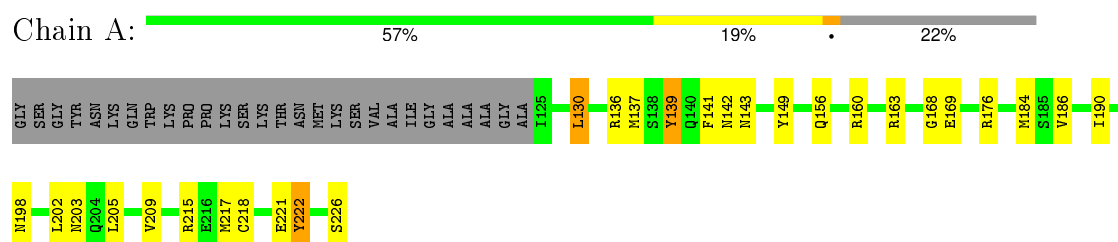
4.2.10 Score per residue for model 10

- Molecule 1: prion protein



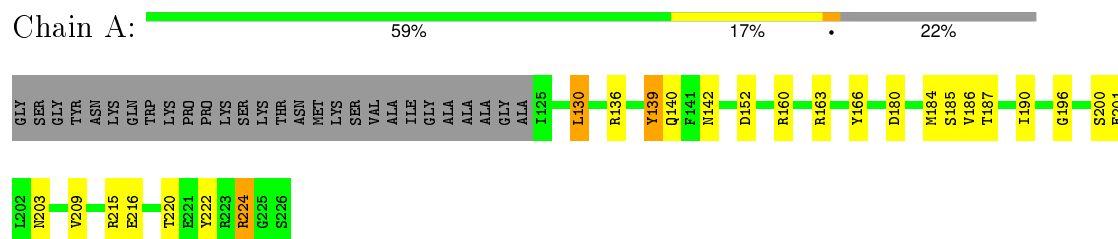
4.2.11 Score per residue for model 11

- Molecule 1: prion protein



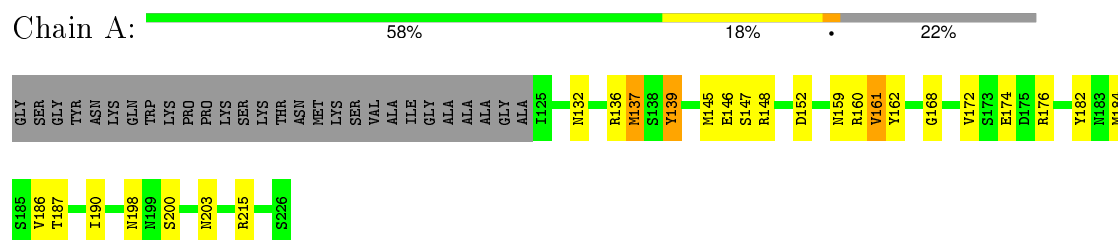
4.2.12 Score per residue for model 12

- Molecule 1: prion protein



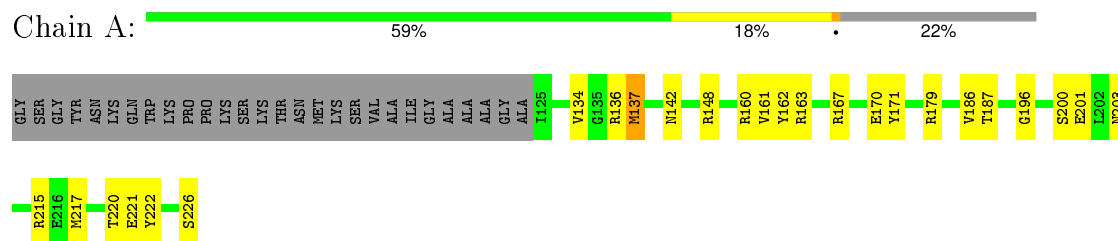
4.2.13 Score per residue for model 13

- Molecule 1: prion protein



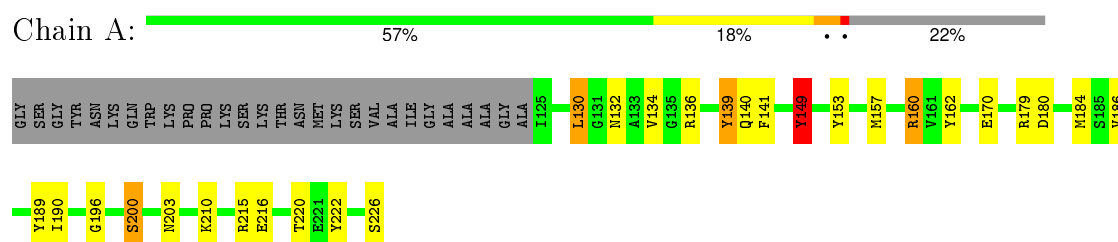
4.2.14 Score per residue for model 14

- Molecule 1: prion protein



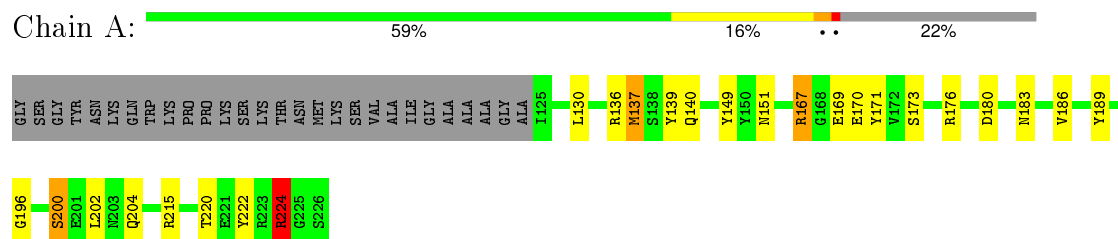
4.2.15 Score per residue for model 15

- Molecule 1: prion protein



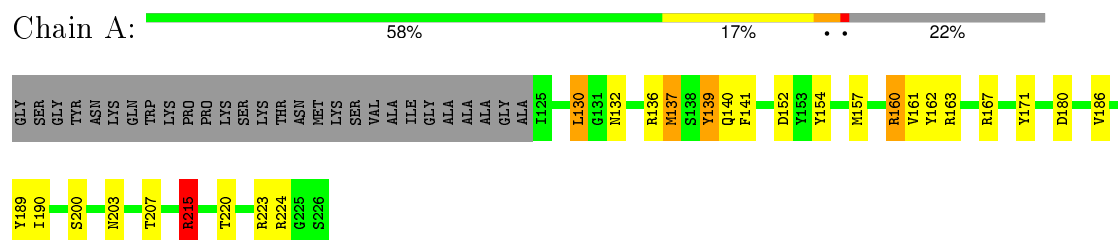
4.2.16 Score per residue for model 16

- Molecule 1: prion protein



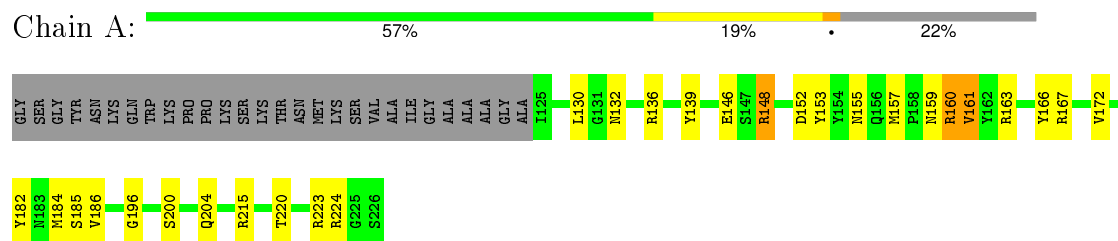
4.2.17 Score per residue for model 17

- Molecule 1: prion protein



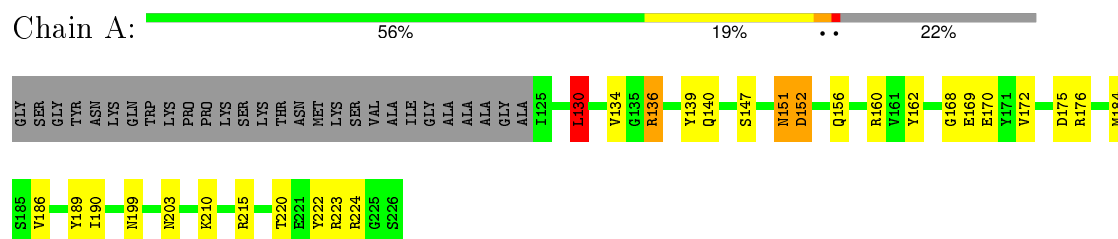
4.2.18 Score per residue for model 18

- Molecule 1: prion protein



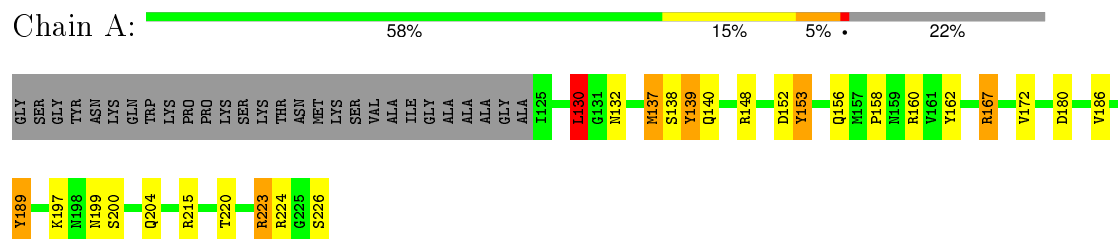
4.2.19 Score per residue for model 19

- 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	

The following table shows chemical shift validation statistics as aggregates over all chemical shift files. Detailed validation can be found in section 7 of this report.

Chemical shift file(s)	BMRB entry 6382
Number of chemical shift lists	1
Total number of shifts	1474
Number of shifts mapped to atoms	1474
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	81%

No validations of the models with respect to experimental NMR restraints is performed at this time.

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±0/867 (0.0±0.0%)	1.15±0.03	2±2/1166 (0.2±0.1%)
All	All	0.69	0/17340 (0.0%)	1.15	44/23320 (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	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	167	ARG	NE-CZ-NH2	-7.75	116.43	120.30	16	1
1	A	209	VAL	CA-CB-CG1	7.64	122.36	110.90	12	1
1	A	139	TYR	CB-CG-CD1	-7.55	116.47	121.00	4	3
1	A	162	TYR	CB-CG-CD2	-7.46	116.52	121.00	14	3
1	A	163	ARG	NE-CZ-NH1	7.19	123.89	120.30	10	1
1	A	209	VAL	CA-CB-CG2	6.85	121.17	110.90	6	1
1	A	139	TYR	CB-CG-CD2	-6.72	116.97	121.00	6	2
1	A	224	ARG	NE-CZ-NH2	-6.71	116.94	120.30	12	2
1	A	161	VAL	CA-CB-CG2	6.21	120.22	110.90	18	3
1	A	167	ARG	NE-CZ-NH1	6.18	123.39	120.30	16	1
1	A	153	TYR	CB-CG-CD1	-6.01	117.39	121.00	1	1
1	A	175	ASP	CB-CG-OD1	6.00	123.70	118.30	19	1
1	A	186	VAL	CA-CB-CG1	5.98	119.87	110.90	5	3
1	A	130	LEU	CB-CA-C	5.82	121.26	110.20	6	1
1	A	172	VAL	CA-CB-CG1	5.73	119.50	110.90	18	3

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	163	ARG	NE-CZ-NH2	-5.58	117.51	120.30	10	1
1	A	134	VAL	CA-CB-CG2	5.58	119.27	110.90	7	1
1	A	149	TYR	CB-CG-CD1	-5.47	117.72	121.00	15	1
1	A	223	ARG	NE-CZ-NH2	-5.47	117.57	120.30	6	2
1	A	223	ARG	CD-NE-CZ	5.45	131.24	123.60	20	1
1	A	136	ARG	NE-CZ-NH2	-5.37	117.61	120.30	19	1
1	A	215	ARG	NE-CZ-NH2	-5.37	117.62	120.30	17	1
1	A	222	TYR	CB-CG-CD1	-5.27	117.84	121.00	6	1
1	A	223	ARG	NE-CZ-NH1	5.23	122.92	120.30	19	3
1	A	160	ARG	NE-CZ-NH1	5.15	122.88	120.30	9	1
1	A	178	VAL	CA-CB-CG1	5.14	118.61	110.90	9	2
1	A	176	ARG	NE-CZ-NH2	-5.14	117.73	120.30	19	1
1	A	171	TYR	CB-CG-CD2	-5.06	117.96	121.00	17	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	163	ARG	Sidechain,Peptide	5
1	A	215	ARG	Sidechain	5
1	A	189	TYR	Sidechain	4
1	A	160	ARG	Sidechain	4
1	A	167	ARG	Sidechain	4
1	A	148	ARG	Sidechain	4
1	A	149	TYR	Sidechain	4
1	A	223	ARG	Sidechain	3
1	A	154	TYR	Sidechain	2
1	A	153	TYR	Sidechain	2
1	A	176	ARG	Sidechain	2
1	A	171	TYR	Sidechain	2
1	A	222	TYR	Sidechain	2
1	A	224	ARG	Sidechain	1
1	A	136	ARG	Sidechain	1
1	A	166	TYR	Sidechain	1
1	A	150	TYR	Sidechain	1
1	A	128	TYR	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	3±2
All	All	17000	16060	16080	55

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:186:VAL:CG2	1:A:190:ILE:HD12	0.55	2.30	11	6
1:A:139:TYR:CE2	1:A:216:GLU:HB3	0.51	2.41	15	1
1:A:175:ASP:HA	1:A:178:VAL:HG12	0.50	1.83	10	2
1:A:149:TYR:CE2	1:A:157:MET:CE	0.50	2.94	8	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: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:137:MET:SD	1:A:139:TYR:CD2	0.44	3.10	20	1
1:A:182:TYR:O	1:A:186:VAL:HG13	0.44	2.13	18	1
1:A:182:TYR:O	1:A:186:VAL:HG12	0.44	2.13	13	2
1:A:134:VAL:HG11	1:A:217:MET:SD	0.43	2.54	14	1
1:A:149:TYR:CD2	1:A:209:VAL:HG11	0.43	2.49	11	1
1:A:158:PRO:HB3	1:A:189:TYR:CZ	0.43	2.48	8	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:149:TYR:CE1	1:A:157:MET:CE	0.42	3.02	15	1
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: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

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
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: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 [i](#)

6.3.1 Protein backbone [i](#)

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%)	5	29
All	All	2000/2600 (77%)	1620 (81%)	288 (14%)	92 (5%)	5	29

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	197	LYS	5
1	A	132	ASN	5
1	A	130	LEU	5
1	A	139	TYR	5
1	A	140	GLN	4
1	A	172	VAL	3
1	A	201	GLU	3
1	A	134	VAL	3
1	A	141	PHE	3
1	A	171	TYR	3
1	A	166	TYR	2
1	A	198	ASN	2
1	A	186	VAL	1

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Mol	Chain	Res	Type	Models (Total)
1	A	128	TYR	1
1	A	131	GLY	1
1	A	169	GLU	1
1	A	136	ARG	1
1	A	138	SER	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±3 (82±3%)	17±3 (18±3%)	6	40
All	All	1860/2240 (83%)	1529 (82%)	331 (18%)	6	40

All 69 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	215	ARG	18
1	A	220	THR	16
1	A	130	LEU	15
1	A	224	ARG	14
1	A	136	ARG	13
1	A	203	ASN	12
1	A	184	MET	11
1	A	140	GLN	10
1	A	200	SER	9
1	A	152	ASP	9
1	A	132	ASN	9
1	A	222	TYR	9
1	A	204	GLN	9
1	A	148	ARG	8
1	A	167	ARG	8
1	A	160	ARG	7
1	A	226	SER	6
1	A	163	ARG	6
1	A	159	ASN	6
1	A	156	GLN	6

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Mol	Chain	Res	Type	Models (Total)
1	A	180	ASP	6
1	A	161	VAL	6
1	A	138	SER	6
1	A	223	ARG	6
1	A	169	GLU	5
1	A	199	ASN	5
1	A	137	MET	5
1	A	179	ARG	4
1	A	153	TYR	4
1	A	134	VAL	4
1	A	173	SER	4
1	A	142	ASN	4
1	A	139	TYR	4
1	A	186	VAL	3
1	A	185	SER	3
1	A	212	GLN	3
1	A	189	TYR	3
1	A	201	GLU	3
1	A	221	GLU	3
1	A	187	THR	3
1	A	210	LYS	3
1	A	157	MET	2
1	A	208	THR	2
1	A	174	GLU	2
1	A	198	ASN	2
1	A	205	LEU	2
1	A	175	ASP	2
1	A	147	SER	2
1	A	213	ILE	2
1	A	143	ASN	2
1	A	151	ASN	2
1	A	206	ASP	2
1	A	207	THR	2
1	A	202	LEU	2
1	A	129	MET	2
1	A	146	GLU	2
1	A	155	ASN	1
1	A	181	CYS	1
1	A	172	VAL	1
1	A	219	ILE	1
1	A	188	GLU	1
1	A	177	PHE	1

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Mol	Chain	Res	Type	Models (Total)
1	A	197	LYS	1
1	A	176	ARG	1
1	A	171	TYR	1
1	A	170	GLU	1
1	A	218	CYS	1
1	A	145	MET	1
1	A	183	ASN	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 carbohydrates 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

The completeness of assignment taking into account all chemical shift lists is 81% for the well-defined parts and 81% for the entire structure.

7.1 Chemical shift list 1

File name: BMRB entry 6382

Chemical shift list name: *assigned_chem_shift_list_1*

7.1.1 Bookkeeping

The following table shows the results of parsing the chemical shift list and reports the number of nuclei with statistically unusual chemical shifts.

Total number of shifts	1474
Number of shifts mapped to atoms	1474
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	12

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	129	-0.49 ± 0.17	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	119	-0.17 ± 0.10	None needed (< 0.5 ppm)
$^{13}\text{C}'$	0	—	—
^{15}N	122	0.33 ± 0.27	None needed (< 0.5 ppm)

7.1.3 Completeness of resonance assignments

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 81%, i.e. 1076 atoms were assigned a chemical shift out of a possible 1322. 9 out of 9 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	398/502 (79%)	199/200 (100%)	102/204 (50%)	97/98 (99%)
Sidechain	592/706 (84%)	372/420 (89%)	196/239 (82%)	24/47 (51%)

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	Total	¹H	¹³C	¹⁵N
Aromatic	86/114 (75%)	58/58 (100%)	28/56 (50%)	0/0 (—%)
Overall	1076/1322 (81%)	629/678 (93%)	326/499 (65%)	121/145 (83%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 81%, i.e. 1076 atoms were assigned a chemical shift out of a possible 1322. 9 out of 9 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Backbone	398/502 (79%)	199/200 (100%)	102/204 (50%)	97/98 (99%)
Sidechain	592/706 (84%)	372/420 (89%)	196/239 (82%)	24/47 (51%)
Aromatic	86/114 (75%)	58/58 (100%)	28/56 (50%)	0/0 (—%)
Overall	1076/1322 (81%)	629/678 (93%)	326/499 (65%)	121/145 (83%)

7.1.4 Statistically unusual chemical shifts ⓘ

The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

Mol	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	176	ARG	NE	109.90	92.63 – 76.73	15.9
1	A	223	ARG	NE	108.90	92.63 – 76.73	15.2
1	A	148	ARG	NE	108.90	92.63 – 76.73	15.2
1	A	179	ARG	NE	108.40	92.63 – 76.73	14.9
1	A	163	ARG	NE	107.90	92.63 – 76.73	14.6
1	A	160	ARG	NE	107.90	92.63 – 76.73	14.6
1	A	167	ARG	NE	107.80	92.63 – 76.73	14.5
1	A	224	ARG	NE	107.70	92.63 – 76.73	14.5
1	A	136	ARG	NE	107.50	92.63 – 76.73	14.4
1	A	215	ARG	NE	106.90	92.63 – 76.73	14.0
1	A	160	ARG	CG	35.40	33.23 – 21.23	6.8
1	A	174	GLU	HA	2.07	6.30 – 2.20	-5.3

7.1.5 Random Coil Index (RCI) plots ⓘ

The image below reports *random coil index* values for the protein chains in the structure. The height of each bar gives a probability of a given residue to be disordered, as predicted from the available chemical shifts and the amino acid sequence. A value above 0.2 is an indication of significant predicted disorder. The colour of the bar shows whether the residue is in the well-defined core (black) or in the ill-defined residue ranges (cyan), as described in section 2 on ensemble composition.

Random coil index (RCI) for chain A:

