



Full wwPDB NMR Structure Validation Report ⓘ

Apr 26, 2016 – 02:20 PM BST

PDB ID : 1E1U
Title : HUMAN PRION PROTEIN VARIANT R220K
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Deposited on : 2000-05-11

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

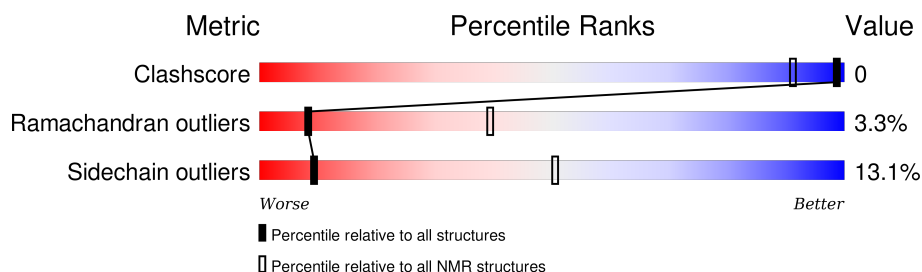
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 80%.

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	104	

2 Ensemble composition and analysis

This entry contains 20 models. Model 3 is the overall representative, medoid model (most similar to other models). The authors have identified model 7 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:128-A:219 (92)	0.54	3

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 5 clusters and 3 single-model clusters were found.

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

3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 1689 atoms, of which 814 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
			1689	544	814	151	171	9	

There is a discrepancy between the modelled and reference sequences:

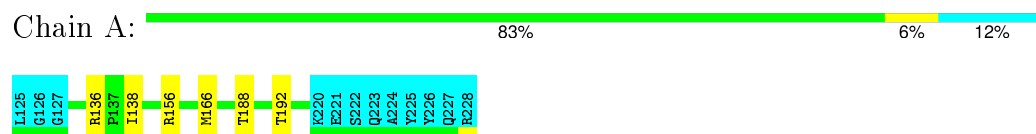
Chain	Residue	Modelled	Actual	Comment	Reference
A	220	LYS	ARG	ENGINEERED MUTATION	UNP P78446

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

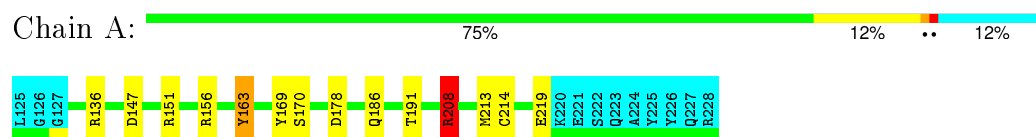


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

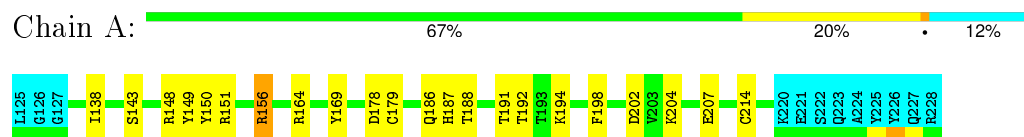
4.2.1 Score per residue for model 1

- Molecule 1: PRION PROTEIN



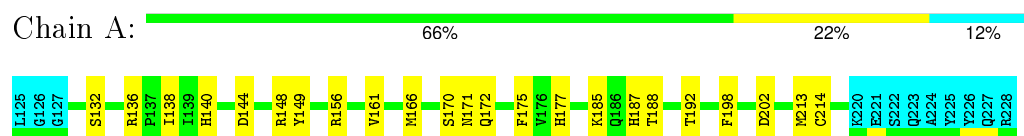
4.2.2 Score per residue for model 2

- Molecule 1: PRION PROTEIN



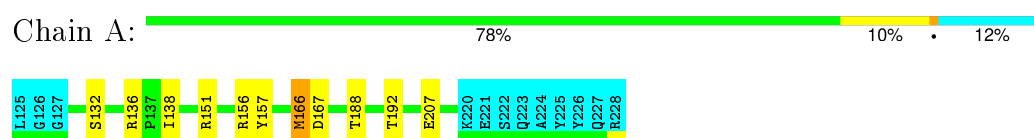
4.2.3 Score per residue for model 3 (medoid)

- Molecule 1: PRION PROTEIN



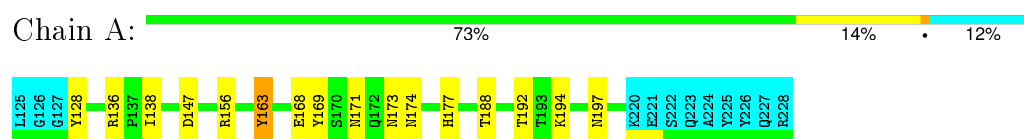
4.2.4 Score per residue for model 4

- Molecule 1: PRION PROTEIN



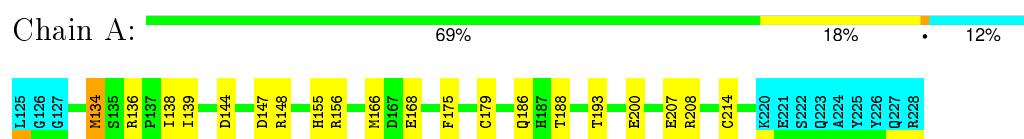
4.2.5 Score per residue for model 5

- Molecule 1: PRION PROTEIN



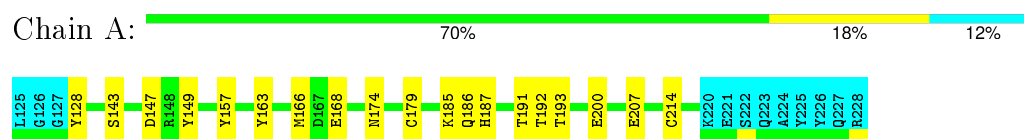
4.2.6 Score per residue for model 6

- Molecule 1: PRION PROTEIN



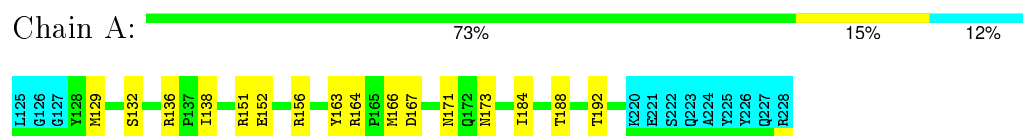
4.2.7 Score per residue for model 7

- Molecule 1: PRION PROTEIN



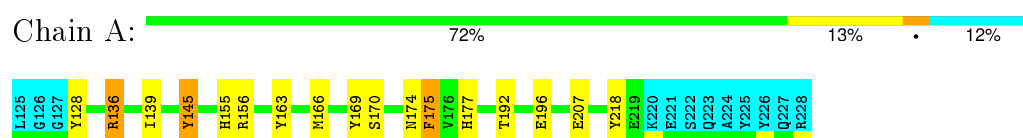
4.2.8 Score per residue for model 8

- Molecule 1: PRION PROTEIN



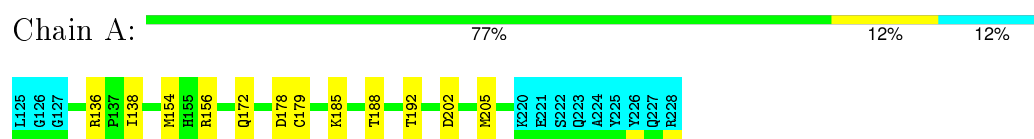
4.2.9 Score per residue for model 9

- Molecule 1: PRION PROTEIN



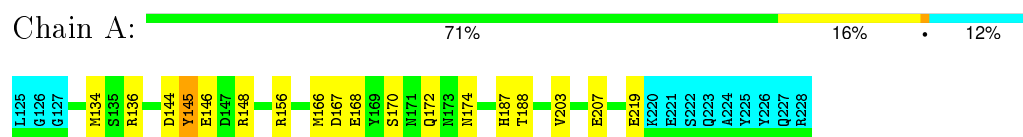
4.2.10 Score per residue for model 10

- Molecule 1: PRION PROTEIN



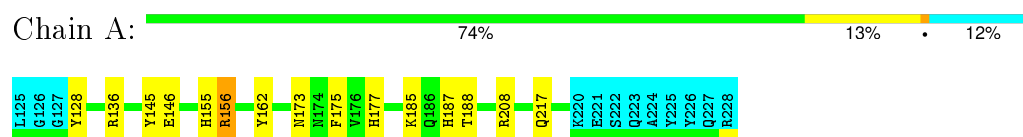
4.2.11 Score per residue for model 11

- Molecule 1: PRION PROTEIN



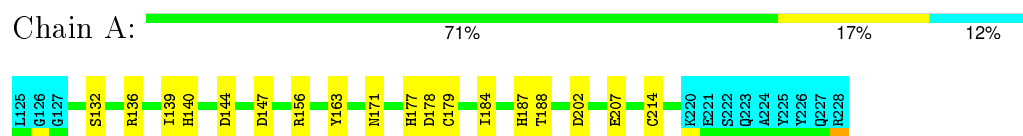
4.2.12 Score per residue for model 12

- Molecule 1: PRION PROTEIN



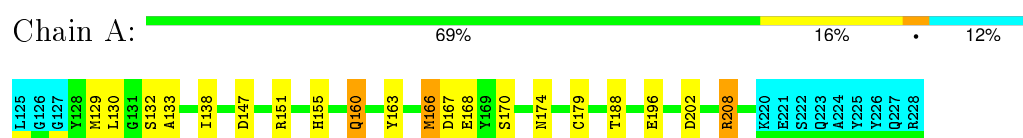
4.2.13 Score per residue for model 13

- Molecule 1: PRION PROTEIN



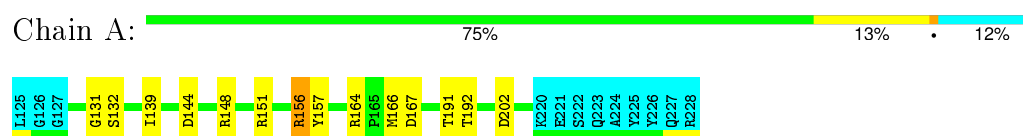
4.2.14 Score per residue for model 14

- Molecule 1: PRION PROTEIN



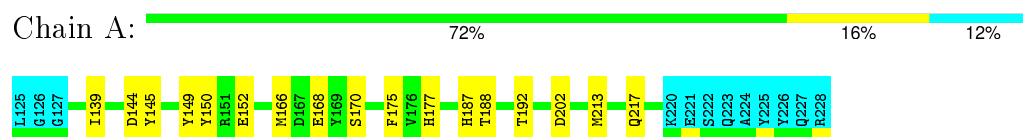
4.2.15 Score per residue for model 15

- Molecule 1: PRION PROTEIN



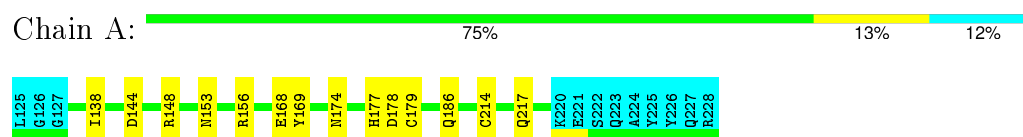
4.2.16 Score per residue for model 16

- Molecule 1: PRION PROTEIN



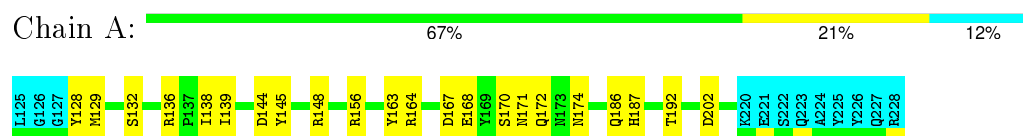
4.2.17 Score per residue for model 17

- Molecule 1: PRION PROTEIN



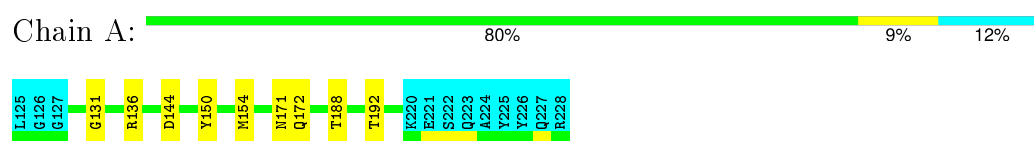
4.2.18 Score per residue for model 18

- Molecule 1: PRION PROTEIN



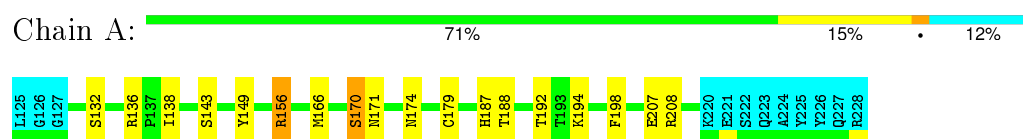
4.2.19 Score per residue for model 19

- 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 20 calculated structures, 20 were deposited, based on the following criterion: ?.

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

Software name	Classification	Version
OPALP	refinement	
DYANA	structure solution	

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 4620
Number of chemical shift lists	1
Total number of shifts	1248
Number of shifts mapped to atoms	1188
Number of unparsed shifts	0
Number of shifts with mapping errors	60
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	80%

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

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	0.67±0.01	0±0/796 (0.0±0.0%)	1.03±0.03	1±1/1077 (0.1±0.1%)
All	All	0.67	0/15920 (0.0%)	1.03	16/21540 (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	1.9±1.4
All	All	0	38

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	151	ARG	NE-CZ-NH2	-6.93	116.84	120.30	2	2
1	A	157	TYR	CB-CG-CD2	-6.19	117.29	121.00	7	3
1	A	163	TYR	CB-CG-CD2	-6.18	117.29	121.00	8	3
1	A	203	VAL	CA-CB-CG1	5.99	119.88	110.90	11	1
1	A	208	ARG	NE-CZ-NH2	-5.79	117.41	120.30	14	2
1	A	148	ARG	NE-CZ-NH2	-5.71	117.44	120.30	15	1
1	A	151	ARG	CD-NE-CZ	5.51	131.32	123.60	2	1
1	A	136	ARG	NE-CZ-NH2	-5.42	117.59	120.30	1	1
1	A	136	ARG	NE-CZ-NH1	5.16	122.88	120.30	1	1
1	A	164	ARG	NE-CZ-NH1	5.14	122.87	120.30	2	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	148	ARG	Sidechain	5
1	A	149	TYR	Sidechain	4
1	A	145	TYR	Sidechain	4
1	A	136	ARG	Sidechain	4
1	A	128	TYR	Sidechain	3
1	A	208	ARG	Sidechain	3
1	A	150	TYR	Sidechain	3
1	A	156	ARG	Sidechain	3
1	A	151	ARG	Sidechain	1
1	A	153	ASN	Peptide	1
1	A	163	TYR	Sidechain	1
1	A	164	ARG	Sidechain	1
1	A	162	TYR	Sidechain	1
1	A	134	MET	Peptide	1
1	A	170	SER	Peptide	1
1	A	167	ASP	Peptide	1
1	A	131	GLY	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	777	721	721	0±1
All	All	15540	14420	14420	6

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:175:PHE:CD2	1:A:218:TYR:CE1	0.50	2.99	9	1
1:A:175:PHE:CD2	1:A:218:TYR:CD1	0.49	3.00	9	1
1:A:145:TYR:CE2	1:A:146:GLU:HG3	0.42	2.50	11	1
1:A:161:VAL:CG1	1:A:213:MET:SD	0.41	3.08	3	1
1:A:145:TYR:CE1	1:A:146:GLU:HG3	0.41	2.50	12	1
1:A:133:ALA:HA	1:A:160:GLN:CG	0.40	2.47	14	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	92/104 (88%)	81±2 (88±2%)	8±2 (9±2%)	3±1 (3±1%)	8	39
All	All	1840/2080 (88%)	1612 (88%)	168 (9%)	60 (3%)	8	39

All 18 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	11
1	A	139	ILE	6
1	A	170	SER	6
1	A	166	MET	5
1	A	167	ASP	5
1	A	168	GLU	4
1	A	169	TYR	3
1	A	198	PHE	3
1	A	172	GLN	3
1	A	136	ARG	2
1	A	132	SER	2
1	A	128	TYR	2
1	A	219	GLU	2
1	A	171	ASN	2
1	A	156	ARG	1
1	A	134	MET	1
1	A	140	HIS	1
1	A	131	GLY	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	88/97 (91%)	76±3 (87±3%)	12±3 (13±3%)	9	50
All	All	1760/1940 (91%)	1529 (87%)	231 (13%)	9	50

All 52 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	156	ARG	16
1	A	188	THR	14
1	A	192	THR	13
1	A	144	ASP	9
1	A	187	HIS	9
1	A	174	ASN	8
1	A	136	ARG	8
1	A	179	CYS	8
1	A	207	GLU	8
1	A	166	MET	8
1	A	202	ASP	8
1	A	177	HIS	7
1	A	214	CYS	7
1	A	163	TYR	6
1	A	186	GLN	6
1	A	147	ASP	6
1	A	132	SER	6
1	A	178	ASP	5
1	A	171	ASN	5
1	A	175	PHE	5
1	A	155	HIS	4
1	A	168	GLU	4
1	A	185	LYS	4
1	A	191	THR	4
1	A	217	GLN	3
1	A	151	ARG	3
1	A	208	ARG	3
1	A	194	LYS	3
1	A	173	ASN	3
1	A	129	MET	3
1	A	143	SER	3
1	A	152	GLU	2
1	A	170	SER	2
1	A	169	TYR	2
1	A	184	ILE	2
1	A	172	GLN	2

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Mol	Chain	Res	Type	Models (Total)
1	A	154	MET	2
1	A	213	MET	2
1	A	196	GLU	2
1	A	200	GLU	2
1	A	164	ARG	2
1	A	193	THR	2
1	A	160	GLN	1
1	A	204	LYS	1
1	A	140	HIS	1
1	A	134	MET	1
1	A	205	MET	1
1	A	145	TYR	1
1	A	130	LEU	1
1	A	149	TYR	1
1	A	197	ASN	1
1	A	148	ARG	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 carbohydrates 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

The completeness of assignment taking into account all chemical shift lists is 80% for the well-defined parts and 80% for the entire structure.

7.1 Chemical shift list 1

File name: BMRB entry 4620

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	1248
Number of shifts mapped to atoms	1188
Number of unparsed shifts	0
Number of shifts with mapping errors	60
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	1

The following assigned chemical shifts were not mapped to the molecules present in the coordinate file.

- Residue not found in structure. All 60 occurrences are reported below.

Chain	Res	Type	Atom	Shift Data		
				Value	Uncertainty	Ambiguity
A	3	VAL	HG21	0.9	-1.0	2
A	3	VAL	CG1	20.9	-1.0	1
A	111	GLY	HA2	3.95	-1.0	1
A	4	VAL	HG13	0.91	-1.0	1
A	112	SER	HB3	3.88	-1.0	1
A	3	VAL	HA	4.18	-1.0	1
A	4	VAL	N	124.8	-1.0	1
A	1	GLY	HA2	3.9	-1.0	1
A	4	VAL	CB	32.4	-1.0	1
A	3	VAL	H	8.39	-1.0	1
A	4	VAL	HA	4.08	-1.0	1
A	1	GLY	CA	43.0	-1.0	1
A	4	VAL	CG2	20.5	-1.0	1
A	4	VAL	HG12	0.91	-1.0	1

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Chain	Res	Type	Atom	Shift Data		
				Value	Uncertainty	Ambiguity
A	4	VAL	H	8.34	-1.0	1
A	112	SER	HB2	3.88	-1.0	1
A	3	VAL	CB	32.5	-1.0	1
A	111	GLY	CA	45.0	-1.0	1
A	4	VAL	HG22	0.91	-1.0	1
A	6	GLY	HA2	3.92	-1.0	1
A	3	VAL	HG23	0.9	-1.0	2
A	2	SER	N	115.7	-1.0	1
A	2	SER	CB	63.7	-1.0	1
A	2	SER	HB3	3.82	-1.0	1
A	112	SER	HA	4.49	-1.0	1
A	6	GLY	N	108.6	-1.0	1
A	111	GLY	HA3	3.95	-1.0	1
A	3	VAL	CA	62.0	-1.0	1
A	4	VAL	HG23	0.91	-1.0	1
A	6	GLY	HA3	3.92	-1.0	1
A	5	GLY	CA	45.2	-1.0	1
A	2	SER	H	8.67	-1.0	1
A	3	VAL	HG22	0.9	-1.0	2
A	112	SER	H	8.16	-1.0	1
A	111	GLY	N	108.6	-1.0	1
A	3	VAL	CG2	20.3	-1.0	1
A	2	SER	HB2	3.82	-1.0	1
A	6	GLY	H	8.3	-1.0	1
A	5	GLY	HA3	3.94	-1.0	1
A	3	VAL	HG11	0.87	-1.0	2
A	3	VAL	HB	2.04	-1.0	1
A	112	SER	CB	63.5	-1.0	1
A	4	VAL	HG11	0.91	-1.0	1
A	4	VAL	HB	2.02	-1.0	1
A	2	SER	HA	4.58	-1.0	1
A	4	VAL	CG1	20.9	-1.0	1
A	5	GLY	HA2	3.94	-1.0	1
A	3	VAL	HG12	0.87	-1.0	2
A	4	VAL	HG21	0.91	-1.0	1
A	5	GLY	H	8.59	-1.0	1
A	2	SER	CA	57.9	-1.0	1
A	111	GLY	H	8.31	-1.0	1
A	3	VAL	HG13	0.87	-1.0	2
A	6	GLY	CA	45.0	-1.0	1
A	3	VAL	N	122.0	-1.0	1

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Chain	Res	Type	Atom	Shift Data		
				Value	Uncertainty	Ambiguity
A	112	SER	CA	58.3	-1.0	1
A	112	SER	N	115.7	-1.0	1
A	1	GLY	HA3	3.9	-1.0	1
A	4	VAL	CA	62.4	-1.0	1
A	5	GLY	N	113.4	-1.0	1

7.1.2 Chemical shift referencing ⓘ

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	110	-0.17 ± 0.09	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	101	0.37 ± 0.14	None needed (< 0.5 ppm)
$^{13}\text{C}'$	0	—	—
^{15}N	104	0.20 ± 0.16	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 80%, i.e. 944 atoms were assigned a chemical shift out of a possible 1186. 8 out of 8 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	351/454 (77%)	176/181 (97%)	90/184 (49%)	85/89 (96%)
Sidechain	508/605 (84%)	318/357 (89%)	172/215 (80%)	18/33 (55%)
Aromatic	85/127 (67%)	55/67 (82%)	30/56 (54%)	0/4 (0%)
Overall	944/1186 (80%)	549/605 (91%)	292/455 (64%)	103/126 (82%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 80%, i.e. 1071 atoms were assigned a chemical shift out of a possible 1340. 9 out of 9 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	399/514 (78%)	200/205 (98%)	102/208 (49%)	97/101 (96%)
Sidechain	575/683 (84%)	361/404 (89%)	193/240 (80%)	21/39 (54%)
Aromatic	97/143 (68%)	63/75 (84%)	34/64 (53%)	0/4 (0%)
Overall	1071/1340 (80%)	624/684 (91%)	329/512 (64%)	118/144 (82%)

7.1.4 Statistically unusual chemical shifts [i](#)

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, <i>ppm</i>	Expected range, <i>ppm</i>	Z-score
1	A	168	GLU	HB2	3.16	3.08 – 0.98	5.4

7.1.5 Random Coil Index (RCI) plots [i](#)

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:

