



Full wwPDB NMR Structure Validation Report ⓘ

Feb 12, 2017 – 07:50 pm GMT

PDB ID : 1S6O
Title : Solution structure and backbone dynamics of the apo-form of the second metal-binding domain of the Menkes protein ATP7A
Authors : Banci, L.; Bertini, I.; Del Conte, R.; D'Onofrio, M.; Rosato, A.; Structural Proteomics in Europe (SPINE)
Deposited on : 2004-01-26

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
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
ShiftChecker : trunk28760
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : recalc28949

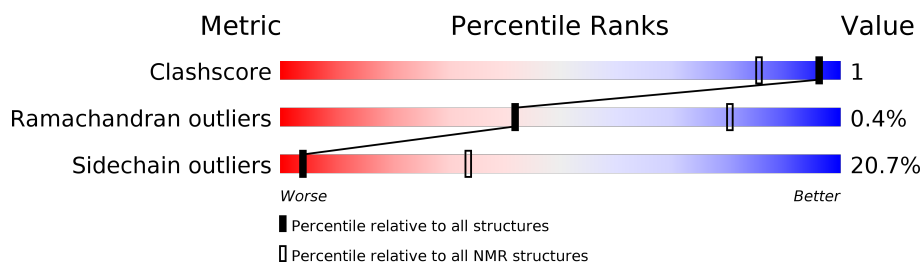
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 90%.

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	125131	11601
Ramachandran outliers	121729	10391
Sidechain outliers	121581	10367

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	76	 67% 14% 18%

2 Ensemble composition and analysis

This entry contains 30 models. Model 20 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:3-A:11, A:18-A:70 (62)	0.26	20

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 1 single-model cluster was found.

Cluster number	Models
1	1, 2, 4, 5, 8, 11, 13, 17, 18, 19, 20, 21, 24, 25, 26, 27, 28
2	10, 12, 14, 15, 23, 29
3	3, 9
4	6, 22
5	7, 30
Single-model clusters	16

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 1209 atoms, of which 621 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Copper-transporting ATPase 1.

Mol	Chain	Residues	Atoms						Trace
1	A	76	Total	C	H	N	O	S	0
			1209	371	621	101	110	6	

There are 4 discrepancies between the modelled and reference sequences:

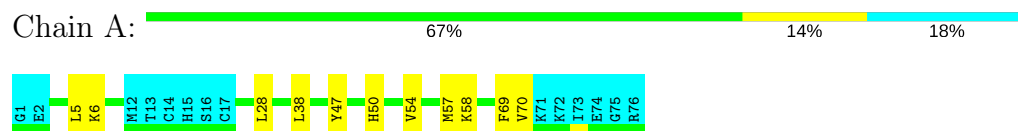
Chain	Residue	Modelled	Actual	Comment	Reference
A	73	ILE	-	CLONING ARTIFACT	UNP Q04656
A	74	GLU	-	CLONING ARTIFACT	UNP Q04656
A	75	GLY	-	CLONING ARTIFACT	UNP Q04656
A	76	ARG	-	CLONING ARTIFACT	UNP Q04656

4 Residue-property plots

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: Copper-transporting ATPase 1

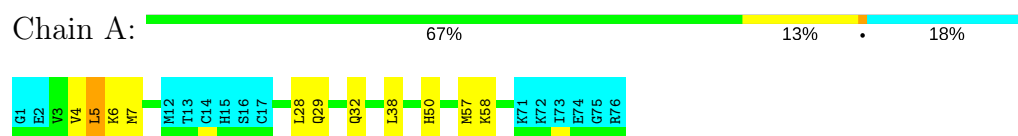


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

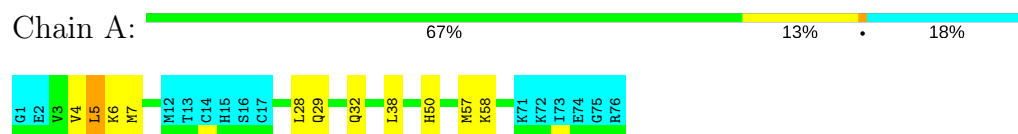
4.2.1 Score per residue for model 1

- Molecule 1: Copper-transporting ATPase 1



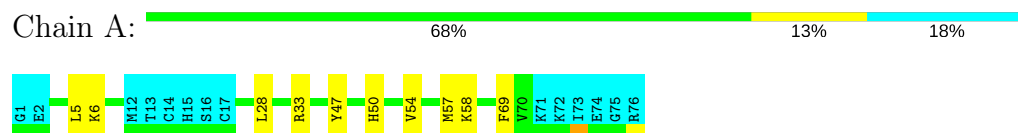
4.2.2 Score per residue for model 2

- Molecule 1: Copper-transporting ATPase 1



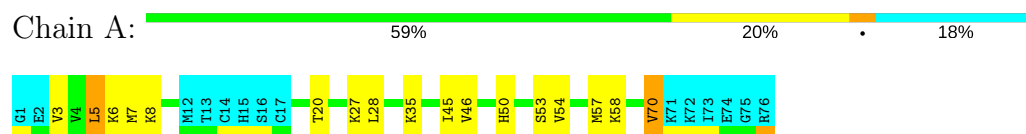
4.2.3 Score per residue for model 3

- Molecule 1: Copper-transporting ATPase 1



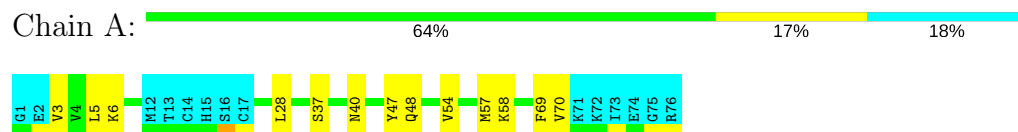
4.2.4 Score per residue for model 4

- Molecule 1: Copper-transporting ATPase 1



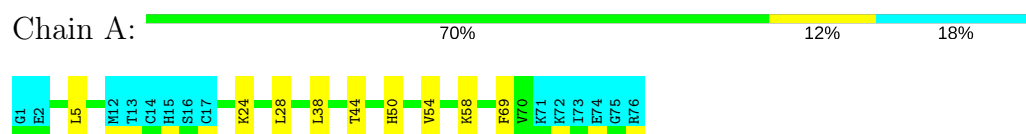
4.2.5 Score per residue for model 5

- Molecule 1: Copper-transporting ATPase 1



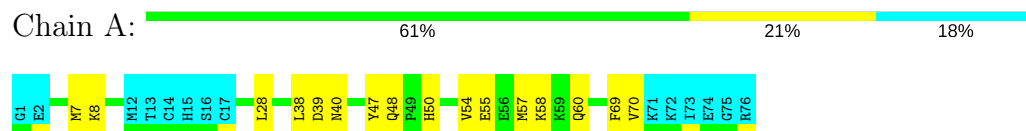
4.2.6 Score per residue for model 6

- Molecule 1: Copper-transporting ATPase 1



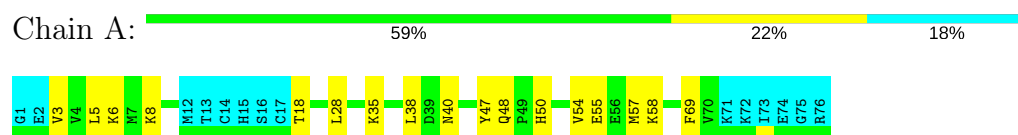
4.2.7 Score per residue for model 7

- Molecule 1: Copper-transporting ATPase 1



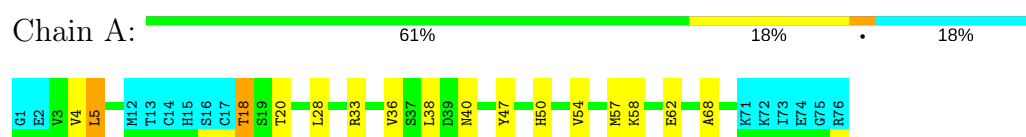
4.2.8 Score per residue for model 8

- Molecule 1: Copper-transporting ATPase 1



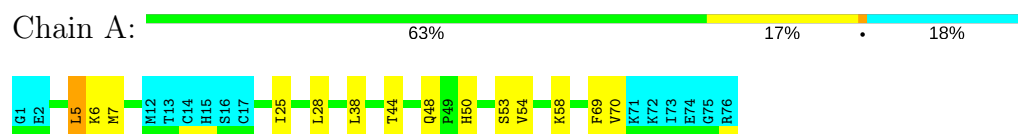
4.2.9 Score per residue for model 9

- Molecule 1: Copper-transporting ATPase 1



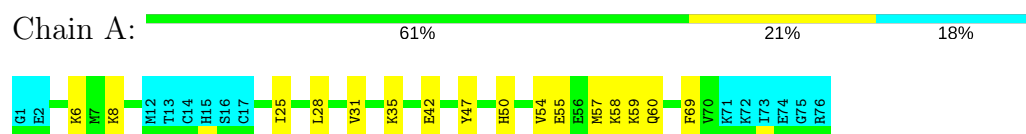
4.2.10 Score per residue for model 10

- Molecule 1: Copper-transporting ATPase 1



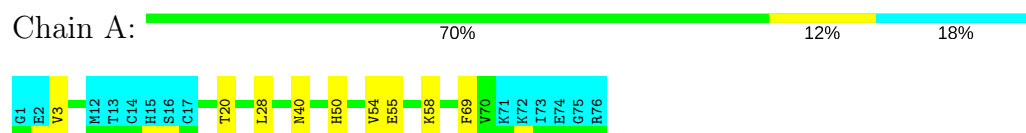
4.2.11 Score per residue for model 11

- Molecule 1: Copper-transporting ATPase 1



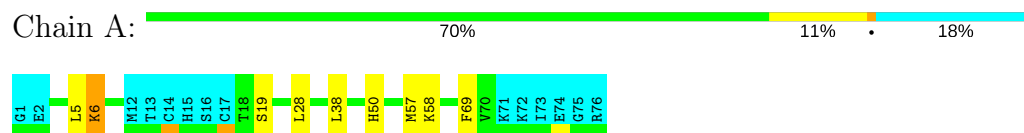
4.2.12 Score per residue for model 12

- Molecule 1: Copper-transporting ATPase 1



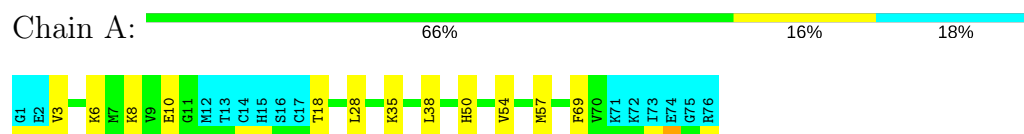
4.2.13 Score per residue for model 13

- Molecule 1: Copper-transporting ATPase 1



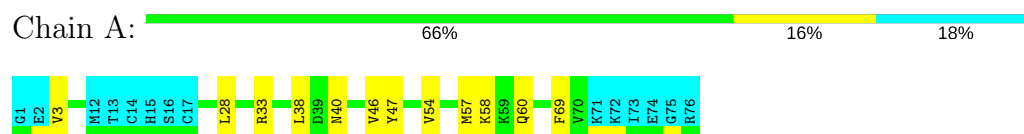
4.2.14 Score per residue for model 14

- Molecule 1: Copper-transporting ATPase 1



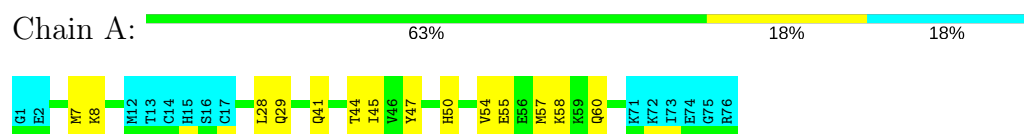
4.2.15 Score per residue for model 15

- Molecule 1: Copper-transporting ATPase 1



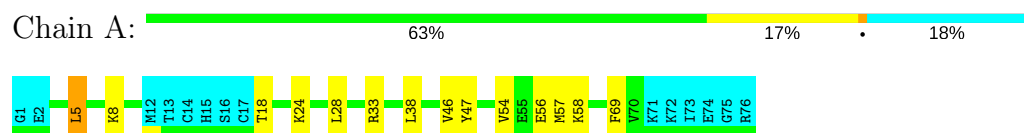
4.2.16 Score per residue for model 16

- Molecule 1: Copper-transporting ATPase 1



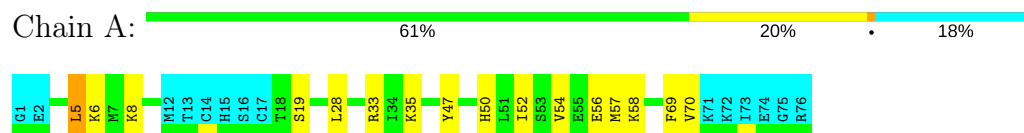
4.2.17 Score per residue for model 17

- Molecule 1: Copper-transporting ATPase 1



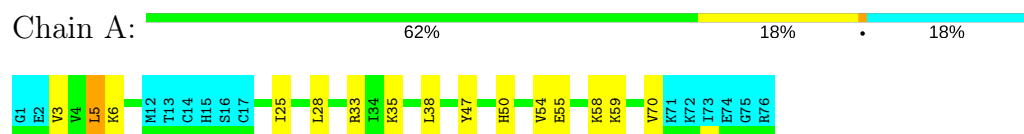
4.2.18 Score per residue for model 18

- Molecule 1: Copper-transporting ATPase 1



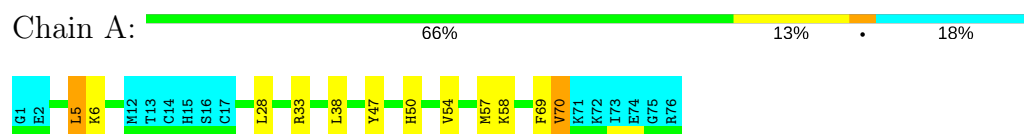
4.2.19 Score per residue for model 19

- Molecule 1: Copper-transporting ATPase 1



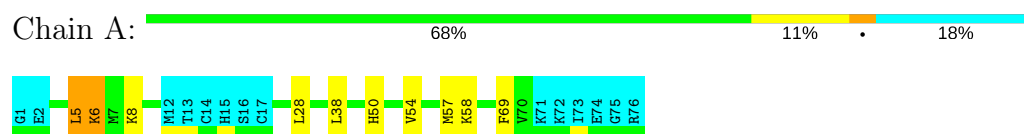
4.2.20 Score per residue for model 20 (medoid)

- Molecule 1: Copper-transporting ATPase 1



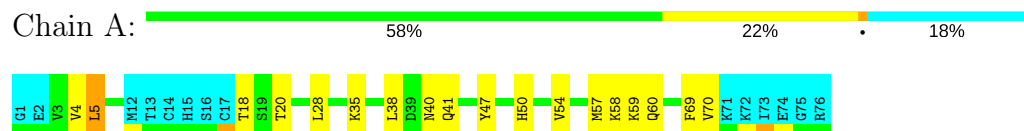
4.2.21 Score per residue for model 21

- Molecule 1: Copper-transporting ATPase 1



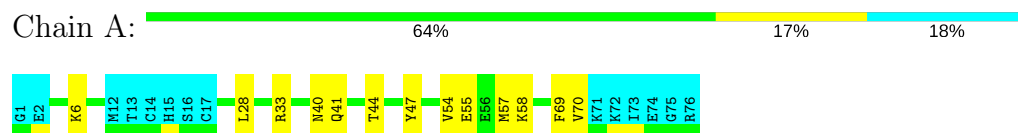
4.2.22 Score per residue for model 22

- Molecule 1: Copper-transporting ATPase 1



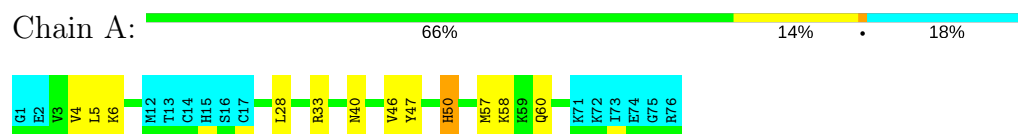
4.2.23 Score per residue for model 23

- Molecule 1: Copper-transporting ATPase 1



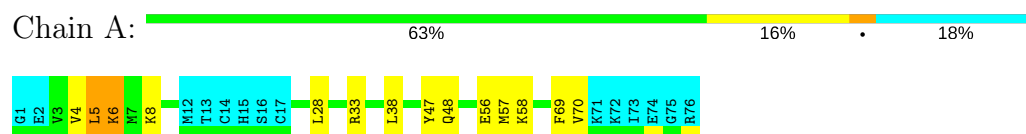
4.2.24 Score per residue for model 24

- Molecule 1: Copper-transporting ATPase 1



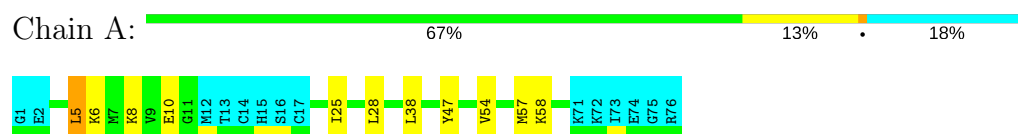
4.2.25 Score per residue for model 25

- Molecule 1: Copper-transporting ATPase 1



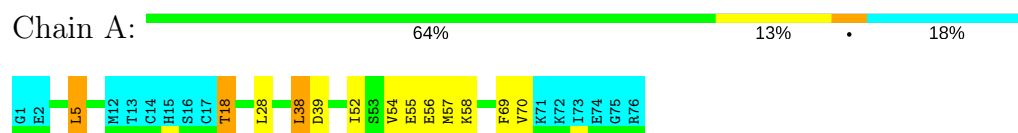
4.2.26 Score per residue for model 26

- Molecule 1: Copper-transporting ATPase 1



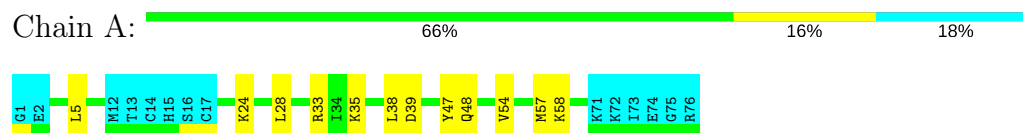
4.2.27 Score per residue for model 27

- Molecule 1: Copper-transporting ATPase 1



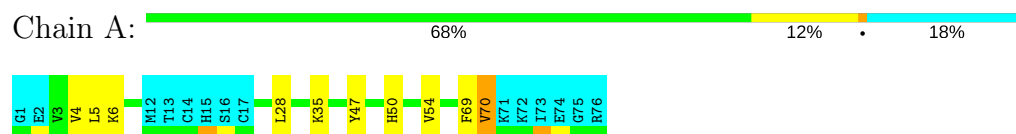
4.2.28 Score per residue for model 28

- Molecule 1: Copper-transporting ATPase 1



4.2.29 Score per residue for model 29

- Molecule 1: Copper-transporting ATPase 1



4.2.30 Score per residue for model 30

- Molecule 1: Copper-transporting ATPase 1



5 Refinement protocol and experimental data overview

The models were refined using the following method: *restrained energy minimization*.

Of the 200 calculated structures, 30 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	1.5
DYANA	refinement	1.5

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 6130
Number of chemical shift lists	1
Total number of shifts	921
Number of shifts mapped to atoms	921
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	90%

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](#)

There are no covalent bond-length or bond-angle outliers.

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	0.7±0.5
All	All	0	21

There are no bond-length outliers.

There are no bond-angle outliers.

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	47	TYR	Sidechain	20
1	A	69	PHE	Sidechain	1

6.2 Too-close contacts [i](#)

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	481	513	513	1±1
All	All	14430	15390	15390	31

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 1.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:31:VAL:HG23	1:A:57:MET:HE2	0.63	1.70	11	1
1:A:5:LEU:HD23	1:A:6:LYS:N	0.60	2.10	13	1
1:A:18:THR:HG22	1:A:36:VAL:HG12	0.58	1.74	9	1
1:A:5:LEU:HD13	1:A:5:LEU:C	0.54	2.22	2	2
1:A:5:LEU:C	1:A:5:LEU:HD13	0.54	2.22	1	4
1:A:31:VAL:HG23	1:A:57:MET:CE	0.51	2.34	11	1
1:A:5:LEU:HD22	1:A:6:LYS:N	0.50	2.21	21	5
1:A:5:LEU:HD22	1:A:5:LEU:C	0.49	2.28	10	3
1:A:5:LEU:HD21	1:A:70:VAL:HG22	0.46	1.86	19	5
1:A:38:LEU:HD13	1:A:39:ASP:N	0.45	2.27	27	1
1:A:7:MET:SD	1:A:45:ILE:HD11	0.44	2.52	16	2
1:A:25:ILE:CG2	1:A:31:VAL:HG21	0.43	2.44	11	1
1:A:5:LEU:HD11	1:A:70:VAL:CG2	0.43	2.43	27	1
1:A:62:GLU:HG2	1:A:68:ALA:HB3	0.42	1.90	9	1
1:A:52:ILE:HD11	1:A:56:GLU:HB3	0.41	1.91	27	2

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	62/76 (82%)	51±2 (82±3%)	11±2 (17±3%)	0±0 (0±1%)	42	80
All	All	1860/2280 (82%)	1534 (82%)	319 (17%)	7 (0%)	42	80

All 3 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	18	THR	4
1	A	50	HIS	2
1	A	29	GLN	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	54/66 (82%)	43±2 (79±4%)	11±2 (21±4%)	4	33
All	All	1620/1980 (82%)	1284 (79%)	336 (21%)	4	33

All 38 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	28	LEU	30
1	A	58	LYS	27
1	A	54	VAL	25
1	A	57	MET	24
1	A	50	HIS	21
1	A	5	LEU	20
1	A	38	LEU	19
1	A	69	PHE	19
1	A	6	LYS	17
1	A	33	ARG	12
1	A	8	LYS	11
1	A	40	ASN	10
1	A	70	VAL	10
1	A	35	LYS	9
1	A	55	GLU	9
1	A	4	VAL	7
1	A	60	GLN	6
1	A	3	VAL	5
1	A	48	GLN	5
1	A	7	MET	5
1	A	44	THR	4
1	A	20	THR	4
1	A	46	VAL	4
1	A	25	ILE	3
1	A	41	GLN	3
1	A	59	LYS	3
1	A	18	THR	3
1	A	39	ASP	3
1	A	24	LYS	3
1	A	29	GLN	2
1	A	53	SER	2
1	A	32	GLN	2
1	A	56	GLU	2

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Mol	Chain	Res	Type	Models (Total)
1	A	19	SER	2
1	A	10	GLU	2
1	A	37	SER	1
1	A	42	GLU	1
1	A	27	LYS	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 90% for the well-defined parts and 87% for the entire structure.

7.1 Chemical shift list 1

File name: BMRB entry 6130

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	921
Number of shifts mapped to atoms	921
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	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
$^{13}\text{C}_\alpha$	76	2.03 ± 0.13	Should be applied
$^{13}\text{C}_\beta$	69	2.40 ± 0.17	Should be applied
$^{13}\text{C}'$	72	2.43 ± 0.17	Should be applied
^{15}N	71	0.95 ± 0.44	Should be applied

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 90%, i.e. 690 atoms were assigned a chemical shift out of a possible 770. 12 out of 12 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	304/306 (99%)	121/122 (99%)	123/124 (99%)	60/60 (100%)
Sidechain	372/431 (86%)	224/251 (89%)	142/164 (87%)	6/16 (38%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	14/33 (42%)	14/18 (78%)	0/14 (0%)	0/1 (0%)
Overall	690/770 (90%)	359/391 (92%)	265/302 (88%)	66/77 (86%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 87%, i.e. 814 atoms were assigned a chemical shift out of a possible 938. 12 out of 12 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	365/376 (97%)	146/150 (97%)	148/152 (97%)	71/74 (96%)
Sidechain	435/522 (83%)	261/306 (85%)	168/195 (86%)	6/21 (29%)
Aromatic	14/40 (35%)	14/22 (64%)	0/16 (0%)	0/2 (0%)
Overall	814/938 (87%)	421/478 (88%)	316/363 (87%)	77/97 (79%)

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, ppm	Expected range, ppm	Z-score
1	A	51	LEU	CG	20.30	32.55 – 21.05	-5.7

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:

