



Full wwPDB NMR Structure Validation Report ⓘ

Apr 21, 2024 – 04:27 PM EDT

PDB ID : 2LQ6
BMRB ID : 18296
Title : Solution structure of BRD1 PHD2 finger
Authors : Liu, L.; Wu, J.
Deposited on : 2012-02-25

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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 : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
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) : 2.36.2

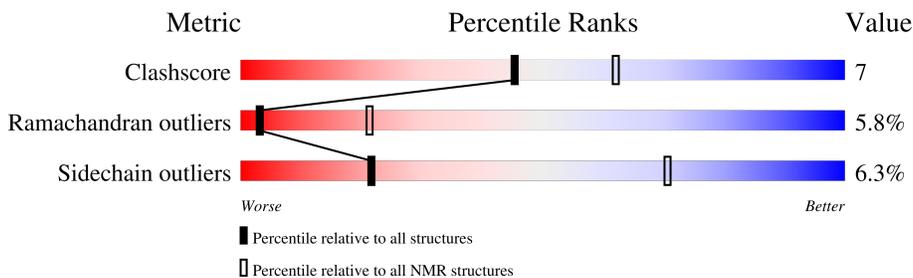
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 87%.

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	158937	12864
Ramachandran outliers	154571	11451
Sidechain outliers	154315	11428

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	87	

2 Ensemble composition and analysis i

This entry contains 20 models. Model 3 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *minimized average structure*.

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:325-A:390 (66)	1.49	3

Ill-defined regions of proteins are excluded from the global statistics.

Ligands and non-protein polymers are included in the analysis.

NmrClust was unable to cluster the ensemble.

Error message: Inconsistent models

3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 1201 atoms, of which 599 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Bromodomain-containing protein 1.

Mol	Chain	Residues	Atoms					Trace	
			Total	C	H	N	O		S
1	A	79	1199	379	599	105	107	9	0

There are 11 discrepancies between the modelled and reference sequences:

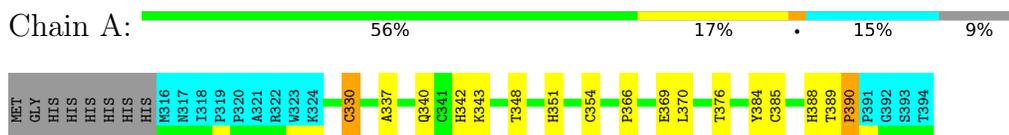
Chain	Residue	Modelled	Actual	Comment	Reference
A	308	MET	-	expression tag	UNP O95696
A	309	GLY	-	expression tag	UNP O95696
A	310	HIS	-	expression tag	UNP O95696
A	311	HIS	-	expression tag	UNP O95696
A	312	HIS	-	expression tag	UNP O95696
A	313	HIS	-	expression tag	UNP O95696
A	314	HIS	-	expression tag	UNP O95696
A	315	HIS	-	expression tag	UNP O95696
A	316	MET	-	expression tag	UNP O95696
A	338	SER	CYS	engineered mutation	UNP O95696
A	393	SER	CYS	engineered mutation	UNP O95696

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	
			Total	Zn
2	A	2	2	2

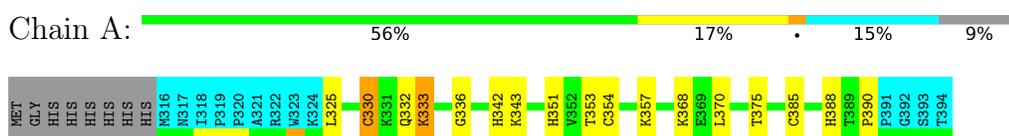
4.2.3 Score per residue for model 3 (medoid)

- Molecule 1: Bromodomain-containing protein 1



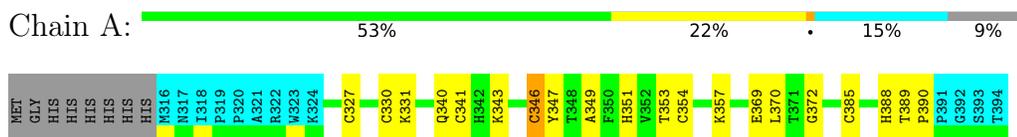
4.2.4 Score per residue for model 4

- Molecule 1: Bromodomain-containing protein 1



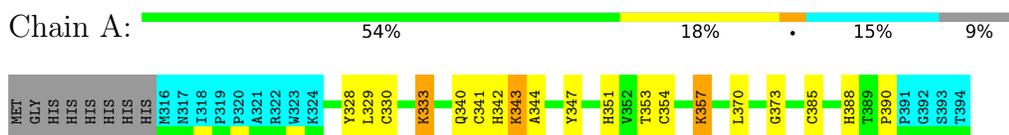
4.2.5 Score per residue for model 5

- Molecule 1: Bromodomain-containing protein 1



4.2.6 Score per residue for model 6

- Molecule 1: Bromodomain-containing protein 1



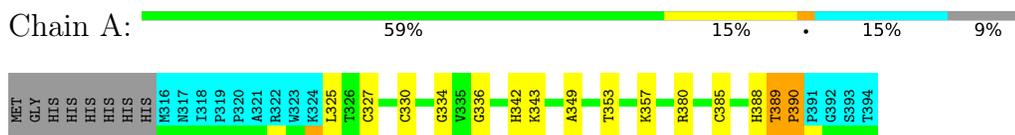
4.2.7 Score per residue for model 7

- Molecule 1: Bromodomain-containing protein 1



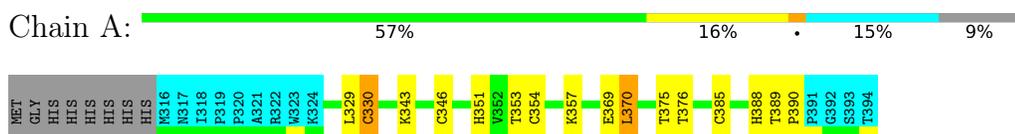
4.2.8 Score per residue for model 8

- Molecule 1: Bromodomain-containing protein 1



4.2.9 Score per residue for model 9

- Molecule 1: Bromodomain-containing protein 1



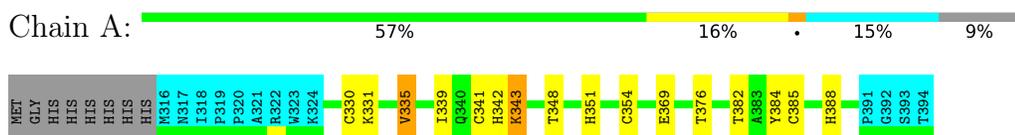
4.2.10 Score per residue for model 10

- Molecule 1: Bromodomain-containing protein 1



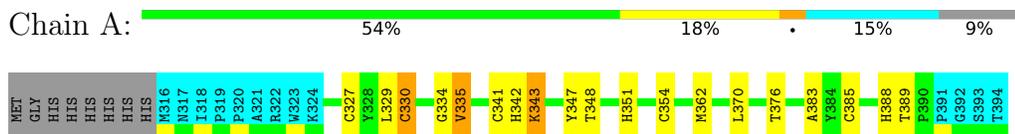
4.2.11 Score per residue for model 11

- Molecule 1: Bromodomain-containing protein 1



4.2.12 Score per residue for model 12

- Molecule 1: Bromodomain-containing protein 1



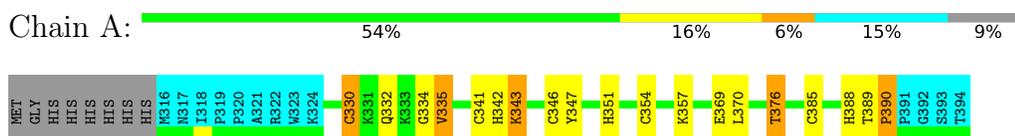
4.2.13 Score per residue for model 13

- Molecule 1: Bromodomain-containing protein 1



4.2.14 Score per residue for model 14

- Molecule 1: Bromodomain-containing protein 1



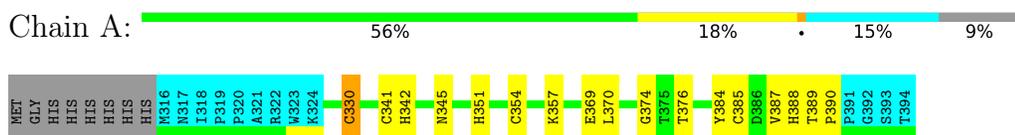
4.2.15 Score per residue for model 15

- Molecule 1: Bromodomain-containing protein 1



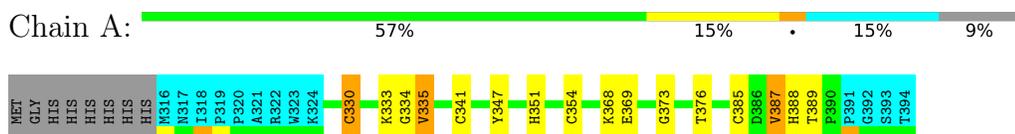
4.2.16 Score per residue for model 16

- Molecule 1: Bromodomain-containing protein 1



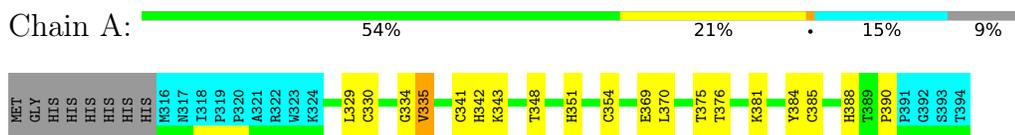
4.2.17 Score per residue for model 17

- Molecule 1: Bromodomain-containing protein 1



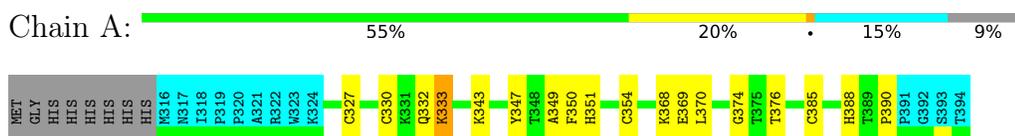
4.2.18 Score per residue for model 18

- Molecule 1: Bromodomain-containing protein 1



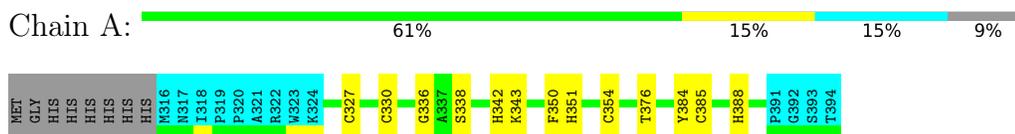
4.2.19 Score per residue for model 19

- Molecule 1: Bromodomain-containing protein 1



4.2.20 Score per residue for model 20

- Molecule 1: Bromodomain-containing protein 1



5 Refinement protocol and experimental data overview

The models were refined using the following method: *DGSA-distance geometry simulated annealing*.

Of the 200 calculated structures, 20 were deposited, based on the following criterion: *structures with the lowest energy*.

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

Software name	Classification	Version
CNS	structure solution	1.2
CNS	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)	working_cs.cif
Number of chemical shift lists	1
Total number of shifts	887
Number of shifts mapped to atoms	887
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	87%

6 Model quality i

6.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section:
ZN

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

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	498	496	495	7±2
All	All	10000	9920	9891	134

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 7.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:385:CYS:SG	1:A:388:HIS:HB2	0.85	2.12	1	19
1:A:351:HIS:HB2	1:A:354:CYS:SG	0.80	2.16	3	18
1:A:342:HIS:HB3	1:A:384:TYR:CE1	0.74	2.18	18	6
1:A:342:HIS:HB3	1:A:384:TYR:CE2	0.71	2.21	20	1
1:A:389:THR:HB	1:A:390:PRO:HD3	0.63	1.69	8	3
1:A:369:GLU:HB2	1:A:376:THR:OG1	0.63	1.93	2	7
1:A:369:GLU:HB3	1:A:376:THR:OG1	0.60	1.96	19	4
1:A:369:GLU:O	1:A:375:THR:HA	0.60	1.96	7	3
1:A:389:THR:HB	1:A:390:PRO:CD	0.58	2.28	8	2
1:A:327:CYS:HB3	1:A:332:GLN:O	0.57	1.99	19	1
1:A:370:LEU:HD12	1:A:374:GLY:O	0.56	1.99	19	2
1:A:389:THR:CB	1:A:390:PRO:HD3	0.55	2.29	8	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:327:CYS:HA	1:A:349:ALA:O	0.55	2.01	8	5
1:A:330:CYS:SG	1:A:351:HIS:CE1	0.55	2.99	3	4
1:A:334:GLY:O	1:A:335:VAL:HB	0.55	2.02	17	1
1:A:346:CYS:SG	1:A:388:HIS:CE1	0.53	3.02	13	4
1:A:334:GLY:O	1:A:335:VAL:HG22	0.52	2.03	14	3
1:A:353:THR:O	1:A:357:LYS:HG2	0.51	2.05	4	2
1:A:340:GLN:NE2	1:A:347:TYR:HB3	0.50	2.22	7	3
1:A:389:THR:OG1	1:A:390:PRO:HD3	0.50	2.06	16	2
1:A:353:THR:O	1:A:357:LYS:HB2	0.50	2.07	6	5
1:A:329:LEU:O	1:A:330:CYS:SG	0.50	2.70	15	3
1:A:342:HIS:O	1:A:343:LYS:HB2	0.49	2.07	14	4
1:A:367:VAL:HG12	1:A:378:SER:O	0.48	2.08	1	1
1:A:337:ALA:O	1:A:351:HIS:HA	0.48	2.09	3	1
1:A:327:CYS:SG	1:A:350:PHE:HA	0.47	2.50	10	4
1:A:330:CYS:SG	1:A:332:GLN:HG2	0.47	2.49	4	1
1:A:342:HIS:O	1:A:343:LYS:HB3	0.47	2.09	4	1
1:A:389:THR:CG2	1:A:390:PRO:HD3	0.46	2.41	8	1
1:A:341:CYS:SG	1:A:384:TYR:HA	0.46	2.50	11	1
1:A:370:LEU:HA	1:A:375:THR:HA	0.46	1.87	9	2
1:A:334:GLY:O	1:A:335:VAL:HG12	0.46	2.11	12	1
1:A:340:GLN:HA	1:A:348:THR:O	0.46	2.11	3	1
1:A:357:LYS:N	1:A:357:LYS:HE2	0.44	2.27	13	1
1:A:362:MET:HG2	1:A:383:ALA:HB2	0.44	1.88	12	1
1:A:389:THR:CB	1:A:390:PRO:CD	0.43	2.94	8	1
1:A:333:LYS:HD3	1:A:333:LYS:H	0.43	1.73	6	1
1:A:365:GLU:HB2	1:A:380:ARG:CG	0.43	2.44	13	1
1:A:380:ARG:HG3	1:A:380:ARG:O	0.42	2.14	13	1
1:A:369:GLU:CD	1:A:370:LEU:H	0.42	2.17	19	1
1:A:387:VAL:HG22	1:A:387:VAL:O	0.42	2.14	17	1
1:A:328:TYR:CE2	1:A:329:LEU:HG	0.42	2.50	6	1
1:A:341:CYS:HA	1:A:383:ALA:O	0.41	2.14	10	1
1:A:341:CYS:O	1:A:347:TYR:HA	0.41	2.14	6	1
1:A:369:GLU:HB2	1:A:376:THR:HG23	0.41	1.92	14	1
1:A:389:THR:OG1	1:A:390:PRO:HD2	0.41	2.15	14	1
1:A:331:LYS:HG2	1:A:331:LYS:O	0.41	2.15	5	1
1:A:327:CYS:SG	1:A:330:CYS:HB2	0.41	2.56	12	1
1:A:342:HIS:NE2	1:A:382:THR:HG23	0.41	2.30	11	1
1:A:343:LYS:HE2	1:A:343:LYS:HA	0.40	1.93	12	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	66/87 (76%)	53±2 (81±3%)	9±3 (13±4%)	4±1 (6±2%)	3	21
All	All	1320/1740 (76%)	1066 (81%)	178 (13%)	76 (6%)	3	21

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	330	CYS	19
1	A	343	LYS	14
1	A	390	PRO	7
1	A	335	VAL	6
1	A	346	CYS	5
1	A	336	GLY	4
1	A	370	LEU	4
1	A	333	LYS	3
1	A	344	ALA	2
1	A	373	GLY	2
1	A	347	TYR	2
1	A	387	VAL	2
1	A	342	HIS	1
1	A	366	PRO	1
1	A	372	GLY	1
1	A	334	GLY	1
1	A	389	THR	1
1	A	325	LEU	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	54/72 (75%)	51±2 (94±3%)	3±2 (6±3%)	21	70
All	All	1080/1440 (75%)	1012 (94%)	68 (6%)	21	70

All 24 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	341	CYS	9
1	A	370	LEU	6
1	A	347	TYR	6
1	A	357	LYS	5
1	A	368	LYS	4
1	A	369	GLU	3
1	A	325	LEU	3
1	A	333	LYS	3
1	A	389	THR	3
1	A	348	THR	3
1	A	376	THR	3
1	A	377	PHE	2
1	A	329	LEU	2
1	A	339	ILE	2
1	A	350	PHE	2
1	A	380	ARG	2
1	A	342	HIS	2
1	A	335	VAL	2
1	A	371	THR	1
1	A	331	LYS	1
1	A	364	MET	1
1	A	332	GLN	1
1	A	345	ASN	1
1	A	381	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 monosaccharides in this entry.

6.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

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 (i)

The completeness of assignment taking into account all chemical shift lists is 87% for the well-defined parts and 86% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *assigned_chem_shift_list_1*

7.1.1 Bookkeeping (i)

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	887
Number of shifts mapped to atoms	887
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 (i)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	77	0.00 \pm 0.28	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	69	-0.05 \pm 0.22	None needed (< 0.5 ppm)
$^{13}\text{C}'$	75	-2.27 \pm 0.43	Should be applied
^{15}N	72	-1.25 \pm 0.28	Should be applied

7.1.3 Completeness of resonance assignments (i)

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 87%, i.e. 741 atoms were assigned a chemical shift out of a possible 850. 0 out of 9 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	324/332 (98%)	134/136 (99%)	127/132 (96%)	63/64 (98%)
Sidechain	393/440 (89%)	278/289 (96%)	112/137 (82%)	3/14 (21%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	24/78 (31%)	24/38 (63%)	0/36 (0%)	0/4 (0%)
Overall	741/850 (87%)	436/463 (94%)	239/305 (78%)	66/82 (80%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 86%, i.e. 887 atoms were assigned a chemical shift out of a possible 1026. 0 out of 9 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	380/392 (97%)	156/160 (98%)	152/158 (96%)	72/74 (97%)
Sidechain	478/544 (88%)	337/357 (94%)	137/168 (82%)	4/19 (21%)
Aromatic	29/90 (32%)	28/44 (64%)	0/41 (0%)	1/5 (20%)
Overall	887/1026 (86%)	521/561 (93%)	289/367 (79%)	77/98 (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.

List Id	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	318	ILE	CG2	37.01	10.93 – 24.12	14.8

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. If well-defined core and ill-defined regions are not identified then it is shown as gray bars.

Random coil index (RCI) for chain A:

