



Full wwPDB NMR Structure Validation Report ⓘ

Apr 26, 2016 – 10:43 PM BST

PDB ID : 2KE9
Title : NMR solution structure of the CASKIN SH3 domain
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Deposited on : 2009-01-27

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

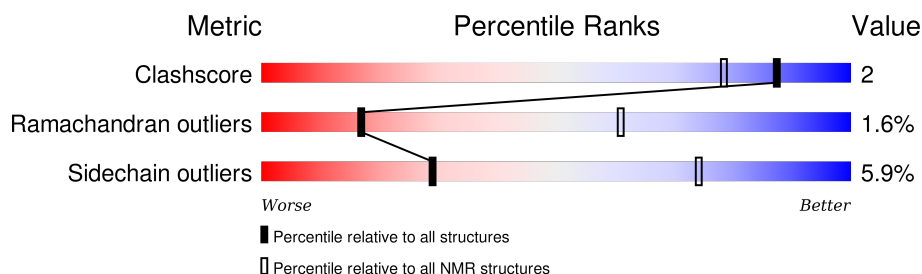
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 76%.

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	83	

2 Ensemble composition and analysis

This entry contains 15 models. Model 5 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *lowest energy*.

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:283-A:325, A:333-A:348 (59)	0.90	5

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 2 clusters. No single-model clusters were found.

Cluster number	Models
1	1, 3, 5, 7, 8, 9, 10, 11, 12, 13, 14, 15
2	2, 4, 6

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 896 atoms, of which 359 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Caskin-2.

Mol	Chain	Residues	Atoms					Trace
1	A	67	Total	C	H	N	O	0
			896	339	359	103	95	

There are 18 discrepancies between the modelled and reference sequences:

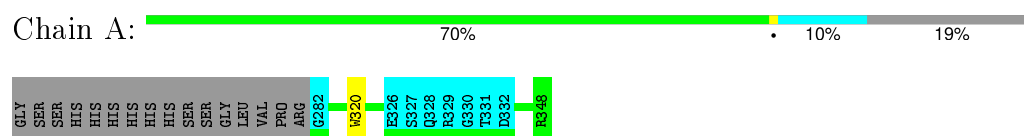
Chain	Residue	Modelled	Actual	Comment	Reference
A	266	GLY	-	EXPRESSION TAG	UNP Q8WXE0
A	267	SER	-	EXPRESSION TAG	UNP Q8WXE0
A	268	SER	-	EXPRESSION TAG	UNP Q8WXE0
A	269	HIS	-	EXPRESSION TAG	UNP Q8WXE0
A	270	HIS	-	EXPRESSION TAG	UNP Q8WXE0
A	271	HIS	-	EXPRESSION TAG	UNP Q8WXE0
A	272	HIS	-	EXPRESSION TAG	UNP Q8WXE0
A	273	HIS	-	EXPRESSION TAG	UNP Q8WXE0
A	274	HIS	-	EXPRESSION TAG	UNP Q8WXE0
A	275	SER	-	EXPRESSION TAG	UNP Q8WXE0
A	276	SER	-	EXPRESSION TAG	UNP Q8WXE0
A	277	GLY	-	EXPRESSION TAG	UNP Q8WXE0
A	278	LEU	-	EXPRESSION TAG	UNP Q8WXE0
A	279	VAL	-	EXPRESSION TAG	UNP Q8WXE0
A	280	PRO	-	EXPRESSION TAG	UNP Q8WXE0
A	281	ARG	-	EXPRESSION TAG	UNP Q8WXE0
A	282	GLY	-	EXPRESSION TAG	UNP Q8WXE0
A	283	SER	-	EXPRESSION TAG	UNP Q8WXE0

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: Caskin-2

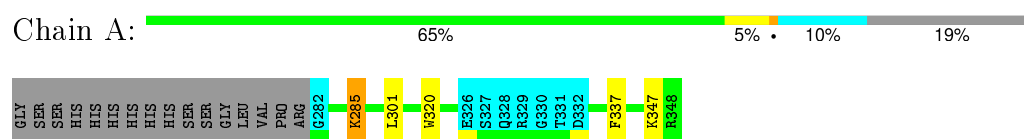


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

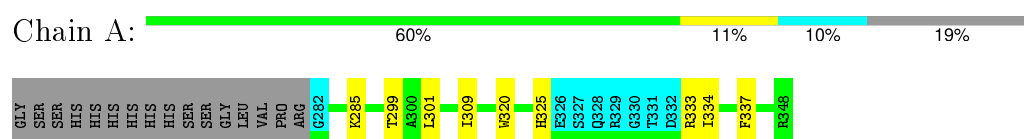
4.2.1 Score per residue for model 1

- Molecule 1: Caskin-2



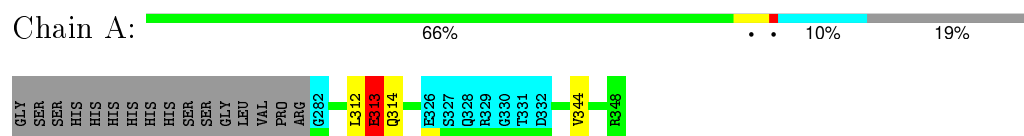
4.2.2 Score per residue for model 2

- Molecule 1: Caskin-2



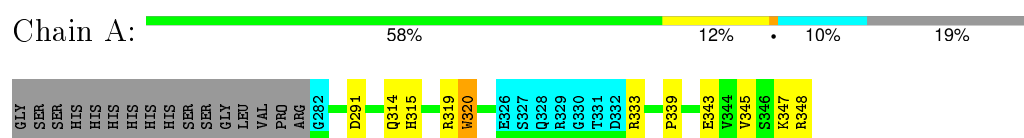
4.2.3 Score per residue for model 3

- Molecule 1: Caskin-2



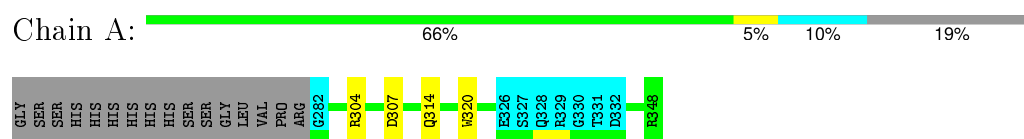
4.2.4 Score per residue for model 4

- Molecule 1: Caskin-2



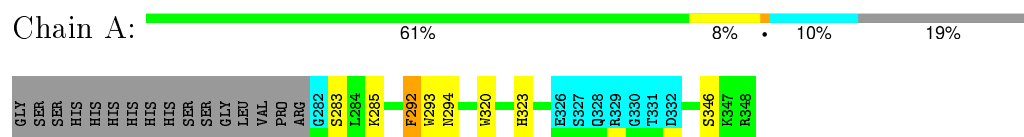
4.2.5 Score per residue for model 5 (medoid)

- Molecule 1: Caskin-2



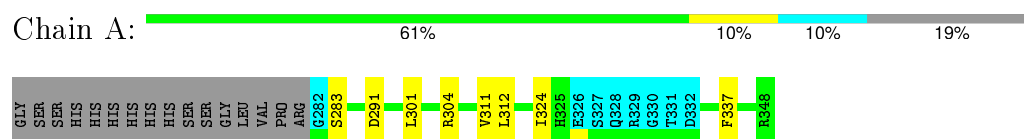
4.2.6 Score per residue for model 6

- Molecule 1: Caskin-2



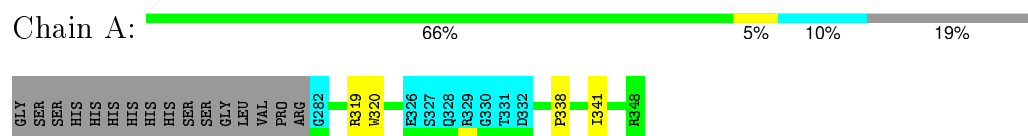
4.2.7 Score per residue for model 7

- Molecule 1: Caskin-2



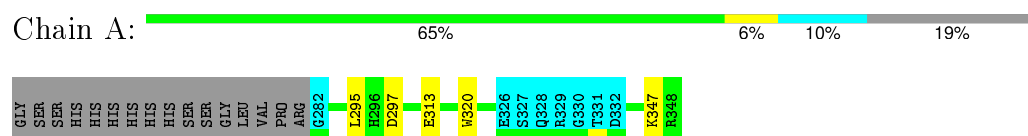
4.2.8 Score per residue for model 8

- Molecule 1: Caskin-2



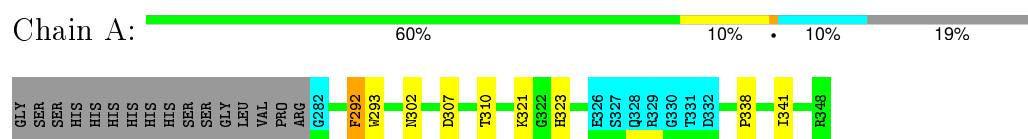
4.2.9 Score per residue for model 9

- Molecule 1: Caskin-2



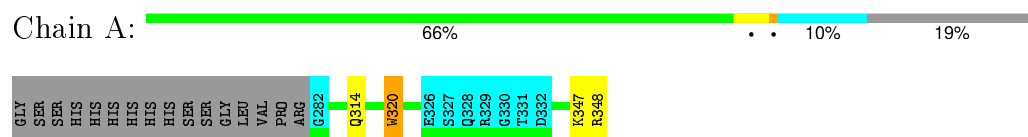
4.2.10 Score per residue for model 10

- Molecule 1: Caskin-2



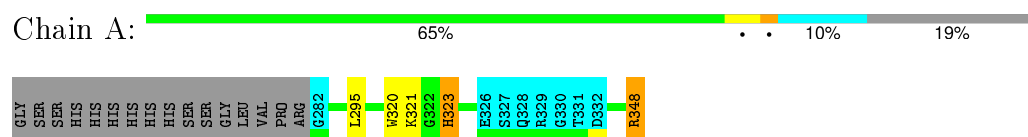
4.2.11 Score per residue for model 11

- Molecule 1: Caskin-2



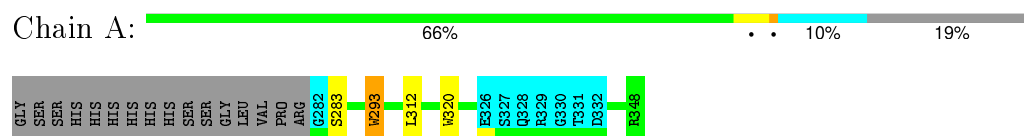
4.2.12 Score per residue for model 12

- Molecule 1: Caskin-2



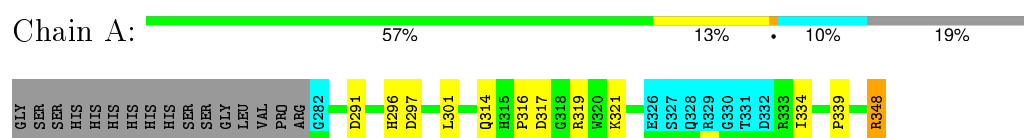
4.2.13 Score per residue for model 13

- Molecule 1: Caskin-2



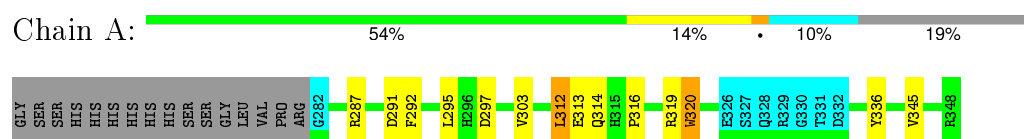
4.2.14 Score per residue for model 14

- Molecule 1: Caskin-2



4.2.15 Score per residue for model 15

- Molecule 1: Caskin-2



5 Refinement protocol and experimental data overview

The models were refined using the following method: *torsion angle dynamics, water refinement*.

Of the 25 calculated structures, 15 were deposited, based on the following criterion: ?.

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

Software name	Classification	Version
CYANA	structure solution	2.1
X-PLOR NIH	refinement	2.21

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 16139
Number of chemical shift lists	1
Total number of shifts	684
Number of shifts mapped to atoms	684
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	76%

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

6 Model quality

6.1 Standard geometry

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

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	479	329	484	2±2
All	All	7185	4935	7260	36

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:287:ARG:HG3	1:A:345:VAL:O	0.53	2.04	15	1
1:A:348:ARG:HD3	1:A:348:ARG:O	0.49	2.06	14	1
1:A:338:PRO:O	1:A:341:ILE:HG12	0.47	2.09	8	2
1:A:295:LEU:HD23	1:A:295:LEU:H	0.47	1.70	9	1
1:A:285:LYS:HA	1:A:309:ILE:O	0.46	2.10	2	1
1:A:316:PRO:O	1:A:339:PRO:HG3	0.46	2.10	14	1
1:A:291:ASP:OD2	1:A:304:ARG:HD2	0.46	2.10	7	1
1:A:301:LEU:HD22	1:A:337:PHE:CD1	0.45	2.46	7	3
1:A:304:ARG:HB2	1:A:307:ASP:OD2	0.45	2.11	5	1
1:A:314:GLN:HA	1:A:320:TRP:CZ3	0.45	2.47	11	2
1:A:347:LYS:HD3	1:A:347:LYS:O	0.44	2.13	9	1
1:A:320:TRP:O	1:A:336:TYR:HA	0.44	2.13	15	1
1:A:321:LYS:HG2	1:A:334:ILE:CG2	0.44	2.43	14	1
1:A:310:THR:O	1:A:323:HIS:HB3	0.43	2.13	10	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:312:LEU:HD23	1:A:312:LEU:H	0.43	1.73	7	2
1:A:292:PHE:CE1	1:A:294:ASN:HB2	0.43	2.49	6	1
1:A:301:LEU:HD22	1:A:337:PHE:CG	0.43	2.48	2	1
1:A:321:LYS:HG2	1:A:334:ILE:HG22	0.43	1.90	14	1
1:A:347:LYS:HD3	1:A:348:ARG:N	0.42	2.29	4	1
1:A:319:ARG:O	1:A:319:ARG:HG3	0.42	2.15	4	1
1:A:292:PHE:O	1:A:302:ASN:HA	0.42	2.15	10	1
1:A:292:PHE:HB3	1:A:303:VAL:HG12	0.41	1.91	15	1
1:A:285:LYS:H	1:A:285:LYS:HD2	0.41	1.74	1	1
1:A:316:PRO:HG3	1:A:320:TRP:CG	0.41	2.50	15	1
1:A:296:HIS:O	1:A:297:ASP:HB2	0.41	2.14	14	1
1:A:312:LEU:HG	1:A:313:GLU:H	0.41	1.76	15	1
1:A:283:SER:HA	1:A:312:LEU:O	0.41	2.16	13	1
1:A:348:ARG:HD3	1:A:348:ARG:C	0.40	2.35	12	1
1:A:283:SER:HA	1:A:311:VAL:O	0.40	2.16	7	1
1:A:312:LEU:O	1:A:313:GLU:HB2	0.40	2.16	3	1
1:A:320:TRP:CZ2	1:A:339:PRO:HB3	0.40	2.52	4	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	58/83 (70%)	52±2 (90±3%)	5±1 (8±2%)	1±1 (2±2%)	17	61
All	All	870/1245 (70%)	787 (90%)	69 (8%)	14 (2%)	17	61

All 11 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	297	ASP	2
1	A	314	GLN	2
1	A	293	TRP	2
1	A	325	HIS	1
1	A	333	ARG	1

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Mol	Chain	Res	Type	Models (Total)
1	A	313	GLU	1
1	A	345	VAL	1
1	A	315	HIS	1
1	A	283	SER	1
1	A	344	VAL	1
1	A	346	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	51/71 (72%)	48±2 (94±3%)	3±2 (6±3%)	29	74
All	All	765/1065 (72%)	720 (94%)	45 (6%)	29	74

All 21 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	320	TRP	11
1	A	348	ARG	3
1	A	291	ASP	3
1	A	319	ARG	3
1	A	347	LYS	2
1	A	313	GLU	2
1	A	314	GLN	2
1	A	321	LYS	2
1	A	292	PHE	2
1	A	285	LYS	2
1	A	293	TRP	2
1	A	295	LEU	2
1	A	343	GLU	1
1	A	317	ASP	1
1	A	333	ARG	1
1	A	307	ASP	1
1	A	312	LEU	1
1	A	323	HIS	1
1	A	299	THR	1

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Mol	Chain	Res	Type	Models (Total)
1	A	301	LEU	1
1	A	334	ILE	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 [i](#)

The completeness of assignment taking into account all chemical shift lists is 76% for the well-defined parts and 70% for the entire structure.

7.1 Chemical shift list 1

File name: BMRB entry 16139

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	684
Number of shifts mapped to atoms	684
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
$^{13}\text{C}_\alpha$	61	-0.06 ± 0.21	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	52	-0.17 ± 0.21	None needed (< 0.5 ppm)
$^{13}\text{C}'$	54	0.36 ± 0.22	None needed (< 0.5 ppm)
^{15}N	53	-2.77 ± 0.58	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 76%, i.e. 579 atoms were assigned a chemical shift out of a possible 763. 11 out of 12 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	261/287 (91%)	102/114 (89%)	109/118 (92%)	50/55 (91%)
Sidechain	280/402 (70%)	165/236 (70%)	115/144 (80%)	0/22 (0%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	38/74 (51%)	25/42 (60%)	11/30 (37%)	2/2 (100%)
Overall	579/763 (76%)	292/392 (74%)	235/292 (80%)	52/79 (66%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 70%, i.e. 596 atoms were assigned a chemical shift out of a possible 849. 11 out of 12 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	275/327 (84%)	107/130 (82%)	115/134 (86%)	53/63 (84%)
Sidechain	283/448 (63%)	166/263 (63%)	117/159 (74%)	0/26 (0%)
Aromatic	38/74 (51%)	25/42 (60%)	11/30 (37%)	2/2 (100%)
Overall	596/849 (70%)	298/435 (69%)	243/323 (75%)	55/91 (60%)

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	313	GLU	HG2	0.58	3.33 – 1.23	-8.1

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:

