Full wwPDB NMR Structure Validation Report (i)

Jun 15, 2024 – 11:47 PM EDT

PDB ID	:	2L11
BMRB ID	:	17071
Title	:	Solution NMR structure of the Cbx3 in complex with H3K9me3 peptide
Authors	:	Kaustov, L.; Lemak, A.; Fares, C.; Gutmanas, A.; Quang, H.; Loppnau, P.; Min, J.; Edwards, A.; Arrowsmith, C.; Structural Genomics Consortium (SGC)
Deposited on	:	2010-07-22

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
https://www.wwpdb.org/validation/2017/NMRValidationReportHelp
with specific help available everywhere you see the (i) 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 (1)) were used in the production of this report:

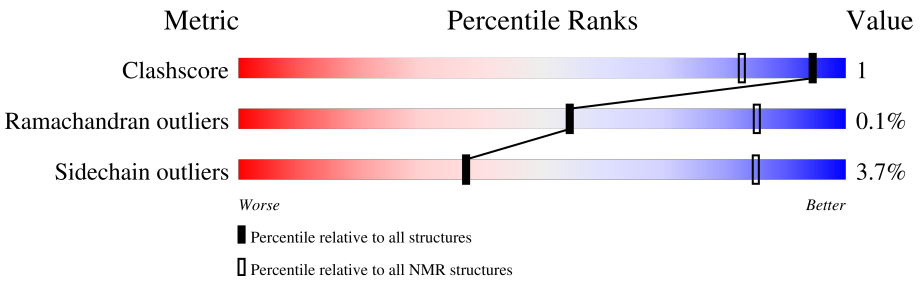
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
SOLUTION NMR

The overall completeness of chemical shifts assignment is 85%.

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 <=5%

Mol	Chain	Length	Quality of chain
1	A	54	91% • 7%
2	B	15	27% 73%

2 Ensemble composition and analysis (i)

This entry contains 20 models. Model 8 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:3-A:52, B:5-B:8 (54)	0.61	8

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 and 2 single-model clusters were found.

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

3 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 1120 atoms, of which 559 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Chromobox protein homolog 3.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	54	880	288	431	72	88	1	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	expression tag	UNP Q13185

- Molecule 2 is a protein called Histone H3.

Mol	Chain	Residues	Atoms					Trace
			Total	C	H	N	O	
2	B	15	240	66	128	25	21	0

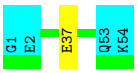
4 Residue-property plots (i)

4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA, DNA and oligosaccharide 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.

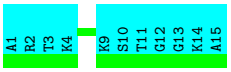
• Molecule 1: Chromobox protein homolog 3

Chain A: 91% • 7%



• Molecule 2: Histone H3

Chain B: 27% 73%



4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

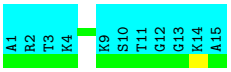
4.2.1 Score per residue for model 1

• Molecule 1: Chromobox protein homolog 3

Chain A: 87% 6% 7%

• Molecule 2: Histone H3

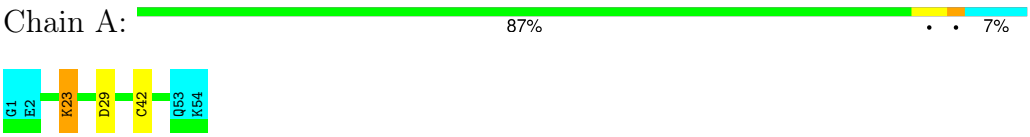
Chain B: 27% 73%



4.2.2 Score per residue for model 2

• Molecule 1: Chromobox protein homolog 3

Chain A:



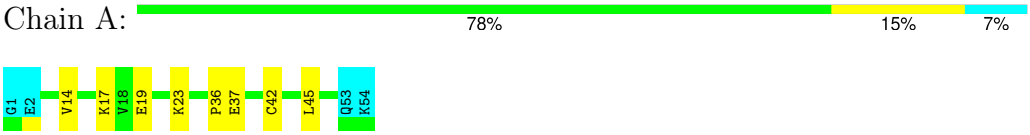
• Molecule 2: Histone H3

Chain B:

4.2.3 Score per residue for model 3

• Molecule 1: Chromobox protein homolog 3

Chain A:



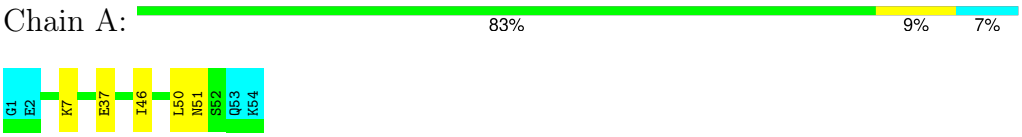
• Molecule 2: Histone H3

Chain B:

4.2.4 Score per residue for model 4

• Molecule 1: Chromobox protein homolog 3

Chain A:



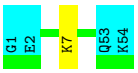
• Molecule 2: Histone H3

Chain B:

4.2.5 Score per residue for model 5

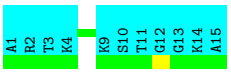
• Molecule 1: Chromobox protein homolog 3

Chain A: 91% 7%



• Molecule 2: Histone H3

Chain B: 27% 73%



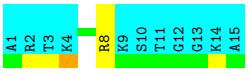
4.2.6 Score per residue for model 6

• Molecule 1: Chromobox protein homolog 3

Chain A: 89% 7%

• Molecule 2: Histone H3

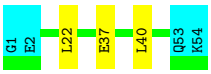
Chain B: 20% 7% 73%



4.2.7 Score per residue for model 7

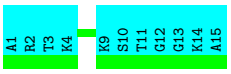
• Molecule 1: Chromobox protein homolog 3

Chain A: 87% 6% 7%



• Molecule 2: Histone H3

Chain B: 27% 73%



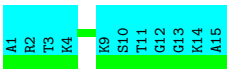
4.2.8 Score per residue for model 8 (medoid)

- Molecule 1: Chromobox protein homolog 3

Chain A:

- Molecule 2: Histone H3

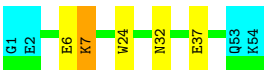
Chain B:



4.2.9 Score per residue for model 9

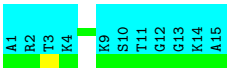
- Molecule 1: Chromobox protein homolog 3

Chain A:



- Molecule 2: Histone H3

Chain B:



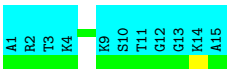
4.2.10 Score per residue for model 10

- Molecule 1: Chromobox protein homolog 3

Chain A:

- Molecule 2: Histone H3

Chain B:



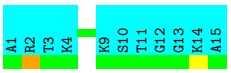
4.2.11 Score per residue for model 11

- Molecule 1: Chromobox protein homolog 3

Chain A: 85% 7% 7%

- Molecule 2: Histone H3

Chain B: 27% 73%



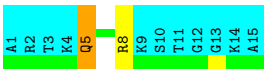
4.2.12 Score per residue for model 12

- Molecule 1: Chromobox protein homolog 3

Chain A: 89% 7%

- Molecule 2: Histone H3

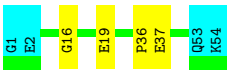
Chain B: 13% 7% 7% 73%



4.2.13 Score per residue for model 13

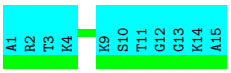
- Molecule 1: Chromobox protein homolog 3

Chain A: 85% 7% 7%



- Molecule 2: Histone H3

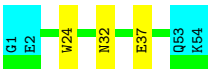
Chain B: 27% 73%



4.2.14 Score per residue for model 14

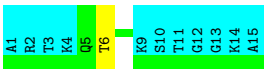
- Molecule 1: Chromobox protein homolog 3

Chain A: 87% 6% 7%



- Molecule 2: Histone H3

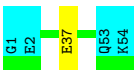
Chain B: 20% 7% 73%



4.2.15 Score per residue for model 15

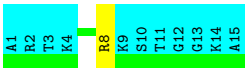
- Molecule 1: Chromobox protein homolog 3

Chain A: 91% • 7%



- Molecule 2: Histone H3

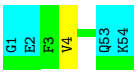
Chain B: 20% 7% 73%



4.2.16 Score per residue for model 16

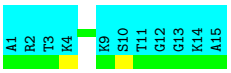
- Molecule 1: Chromobox protein homolog 3

Chain A: 91% • 7%



- Molecule 2: Histone H3

Chain B: 27% 73%



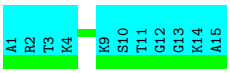
4.2.17 Score per residue for model 17

- Molecule 1: Chromobox protein homolog 3

Chain A:

- Molecule 2: Histone H3

Chain B:



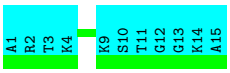
4.2.18 Score per residue for model 18

- Molecule 1: Chromobox protein homolog 3

Chain A:

- Molecule 2: Histone H3

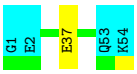
Chain B:



4.2.19 Score per residue for model 19

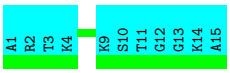
- Molecule 1: Chromobox protein homolog 3

Chain A:



- Molecule 2: Histone H3

Chain B:



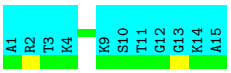
4.2.20 Score per residue for model 20

- Molecule 1: Chromobox protein homolog 3

Chain A:

- Molecule 2: Histone H3

Chain B:



5 Refinement protocol and experimental data overview (i)

The models were refined using the following method: *molecular dynamics*.

Of the 100 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
CYANA	structure solution	
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	721
Number of shifts mapped to atoms	692
Number of unparsed shifts	0
Number of shifts with mapping errors	29
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	85%

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: M3L

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	417	399	399	1±1
2	B	32	33	33	0±0
All	All	8980	8640	8640	19

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:42:CYS:SG	2:B:5:GLN:HG2	0.60	2.37	2	1
1:A:6:GLU:HG3	1:A:7:LYS:HD2	0.59	1.74	10	2
1:A:23:LYS:HD3	1:A:29:ASP:HA	0.55	1.77	2	1
1:A:19:GLU:HA	1:A:36:PRO:HA	0.50	1.82	13	5
1:A:22:LEU:HD11	1:A:40:LEU:HD22	0.50	1.83	7	2
1:A:24:TRP:HD1	1:A:32:ASN:HA	0.44	1.72	14	1
1:A:6:GLU:HB2	1:A:25:LYS:HG3	0.43	1.90	17	1
1:A:46:ILE:O	1:A:50:LEU:HG	0.42	2.14	4	2
1:A:14:VAL:O	1:A:17:LYS:HG2	0.41	2.15	3	1
1:A:42:CYS:SG	1:A:45:LEU:HG	0.41	2.56	3	1
1:A:5:VAL:O	2:B:5:GLN:HB2	0.41	2.16	12	1

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:24:TRP:CD1	1:A:32:ASN:HA	0.41	2.51	9	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	50/54 (93%)	49±1 (98±2%)	1±1 (1±2%)	0±0 (0±0%)	54	85
2	B	4/15 (27%)	4±0 (95±10%)	0±0 (5±10%)	0±0 (0±0%)	100	100
All	All	1080/1380 (78%)	1061 (98%)	18 (2%)	1 (0%)	54	85

All 1 unique Ramachandran outliers are listed below.

Mol	Chain	Res	Type	Models (Total)
1	A	16	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	46/49 (94%)	44±1 (97±2%)	2±1 (3±2%)	40	87
2	B	3/9 (33%)	3±1 (92±18%)	0±1 (8±18%)	15	62
All	All	980/1160 (84%)	944 (96%)	36 (4%)	37	85

All 11 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	37	GLU	15

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Mol	Chain	Res	Type	Models (Total)
1	A	7	LYS	4
1	A	23	LYS	3
2	B	8	ARG	3
1	A	51	ASN	3
1	A	17	LYS	2
1	A	44	GLU	2
1	A	25	LYS	1
2	B	5	GLN	1
2	B	6	THR	1
1	A	32	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)

1 non-standard protein/DNA/RNA residue is modelled in this entry.

In the following table, the Counts columns list the number of bonds for which Mogul statistics could be retrieved, the number of bonds that are observed in the model and the number of bonds that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length is the number of standard deviations the observed value is removed from the expected value. A bond length with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond lengths.

Mol	Type	Chain	Res	Link	Bond lengths		
					Counts	RMSZ	#Z>2
2	M3L	B	9	2	10,11,12	1.04±0.08	0±0 (0±0%)

In the following table, the Counts columns list the number of angles for which Mogul statistics could be retrieved, the number of angles that are observed in the model and the number of angles that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond angle is the number of standard deviations the observed value is removed from the expected value. A bond angle with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond angles.

Mol	Type	Chain	Res	Link	Bond angles		
					Counts	RMSZ	#Z>2
2	M3L	B	9	2	9,14,16	0.27±0.06	0±0 (0±0%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	M3L	B	9	2	-	0±0,9,10,12	-

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6.5 Carbohydrates (i)

There are no monosaccharides 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 85% for the well-defined parts and 74% 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	721
Number of shifts mapped to atoms	692
Number of unparsed shifts	0
Number of shifts with mapping errors	29
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	2

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

- No matching atom found in the structure. All 29 occurrences are reported below.

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	UNMAPPED	3	THR	HA	3.97	0.0300	1
1	UNMAPPED	3	THR	HG21	1.17	0.0300	1
1	UNMAPPED	3	THR	HG22	1.17	0.0300	1
1	UNMAPPED	3	THR	HG23	1.17	0.0300	1
1	UNMAPPED	5	GLN	HA	4.26	0.0300	1
1	UNMAPPED	5	GLN	HB2	1.97	0.0300	2
1	UNMAPPED	5	GLN	HB3	1.94	0.0300	2
1	UNMAPPED	5	GLN	HE21	6.71	0.0300	2
1	UNMAPPED	5	GLN	HG2	2.23	0.0300	2
1	UNMAPPED	5	GLN	HG3	2.0	0.0300	2
1	UNMAPPED	6	THR	HA	4.04	0.0300	1
1	UNMAPPED	6	THR	HB	4.15	0.0300	1
1	UNMAPPED	6	THR	HG21	1.06	0.0300	1
1	UNMAPPED	6	THR	HG22	1.06	0.0300	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	UNMAPPED	6	THR	HG23	1.06	0.0300	1
1	UNMAPPED	7	ALA	HA	3.92	0.0300	1
1	UNMAPPED	7	ALA	HB1	1.34	0.0300	1
1	UNMAPPED	7	ALA	HB2	1.34	0.0300	1
1	UNMAPPED	7	ALA	HB3	1.34	0.0300	1
1	UNMAPPED	8	ARG	HA	4.28	0.0300	1
1	UNMAPPED	8	ARG	HB2	1.72	0.0300	2
1	UNMAPPED	8	ARG	HB3	1.65	0.0300	2
1	UNMAPPED	8	ARG	HD2	3.07	0.0300	2
1	UNMAPPED	8	ARG	HD3	3.07	0.0300	2
1	UNMAPPED	8	ARG	HG2	1.52	0.0300	2
1	UNMAPPED	8	ARG	HG3	1.52	0.0300	2
1	UNMAPPED	10	SER	HA	4.44	0.0300	1
1	UNMAPPED	10	SER	HB2	3.91	0.0300	2
1	UNMAPPED	10	SER	HB3	3.87	0.0300	2

7.1.2 Chemical shift referencing (i)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	54	-0.15 ± 0.30	None needed (< 0.5 ppm)
$^{13}C_{\beta}$	51	-0.06 ± 0.17	None needed (< 0.5 ppm)
$^{13}C'$	49	0.24 ± 0.37	None needed (< 0.5 ppm)
^{15}N	49	0.01 ± 0.55	None needed (< 0.5 ppm)

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 85%, i.e. 647 atoms were assigned a chemical shift out of a possible 763. 0 out of 11 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	240/268 (90%)	98/108 (91%)	96/108 (89%)	46/52 (88%)
Sidechain	347/422 (82%)	236/270 (87%)	107/134 (80%)	4/18 (22%)
Aromatic	60/73 (82%)	35/36 (97%)	23/35 (66%)	2/2 (100%)
Overall	647/763 (85%)	369/414 (89%)	226/277 (82%)	52/72 (72%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 74%, i.e. 692 atoms were assigned a chemical shift out of a possible

933. 0 out of 11 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	258/341 (76%)	106/139 (76%)	103/136 (76%)	49/66 (74%)
Sidechain	374/519 (72%)	254/331 (77%)	115/163 (71%)	5/25 (20%)
Aromatic	60/73 (82%)	35/36 (97%)	23/35 (66%)	2/2 (100%)
Overall	692/933 (74%)	395/506 (78%)	241/334 (72%)	56/93 (60%)

7.1.4 Statistically unusual chemical shifts (i)

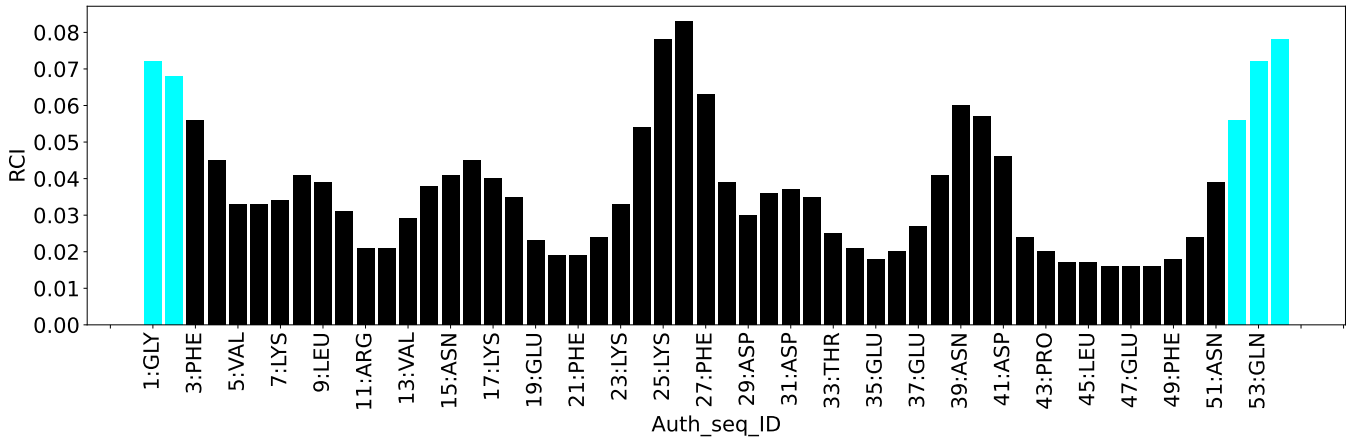
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, *ppm*	Expected range, *ppm*	Z-score
1	A	21	PHE	HB3	-0.14	1.03 – 4.85	-8.1
1	A	12	ARG	HD2	1.89	1.97 – 4.26	-5.4

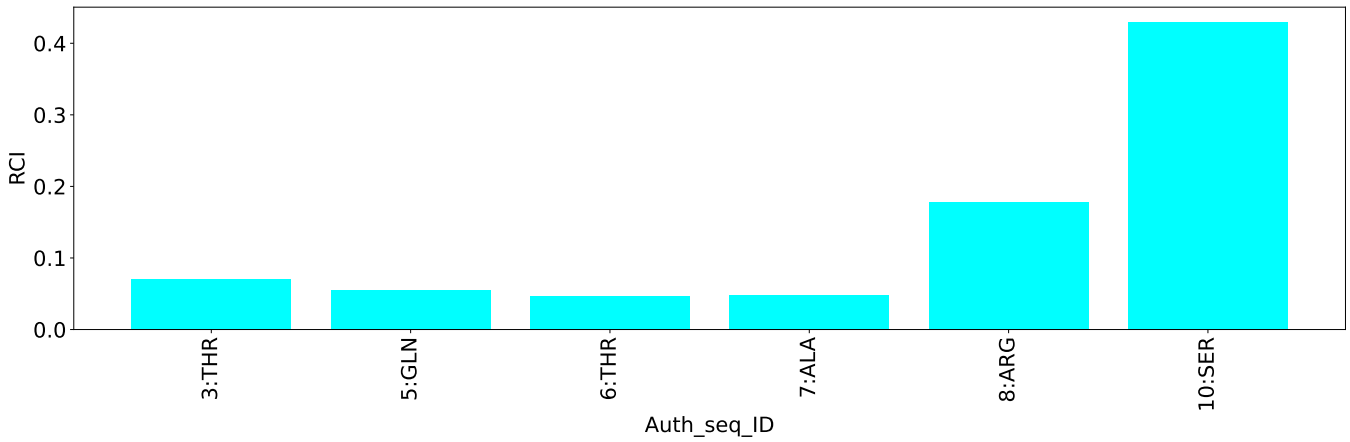
7.1.5 Random Coil Index (RCI) plots (i)

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.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:



Random coil index (RCI) for chain UNMAPPED:


0.4
0.3
0.2
0.1
0.0
RCI
3:THR
5:GLN
6:THR
7:ALA
8:ARG
10:SER
Auth_seq_ID