



# wwPDB NMR Structure Validation Summary Report ⓘ

Apr 28, 2016 – 07:26 PM EDT

PDB ID : 2MFE  
Title : Csr/Rsm protein-RNA recognition - A molecular affinity ruler: RsmZ(SL2)/  
RsmE(dimer) 2:1 complex  
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Deposited on : 2013-10-11

This is a wwPDB NMR Structure Validation Summary Report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto: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.

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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

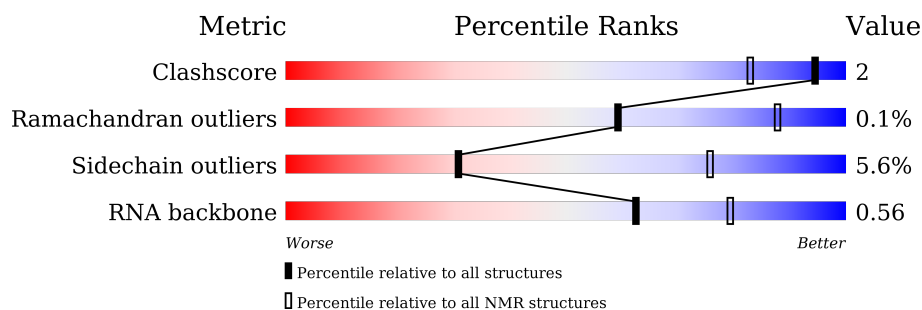
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*SOLUTION NMR*





The overall completeness of chemical shifts assignment is 39%.

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
RNA backbone	3027	600

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  $\geq 3$ , 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	70	
1	C	70	
2	B	22	
2	D	22	

## 2 Ensemble composition and analysis ⓘ

This entry contains 20 models. Model 1 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:1-A:59, C:1-C:57 (116)	0.29	1

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 3 single-model clusters were found.

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

### 3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3264 atoms, of which 1426 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Carbon storage regulator homolog.

Mol	Chain	Residues	Atoms						Trace
1	A	59	Total	C	H	N	O	S	0
			920	280	472	81	86	1	
1	C	59	Total	C	H	N	O	S	0
			920	280	472	81	86	1	

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	60	LYS	-	EXPRESSION TAG	UNP Q5MXB2
A	61	ARG	-	EXPRESSION TAG	UNP Q5MXB2
A	62	GLU	-	EXPRESSION TAG	UNP Q5MXB2
A	63	THR	-	EXPRESSION TAG	UNP Q5MXB2
A	64	PRO	-	EXPRESSION TAG	UNP Q5MXB2
A	65	HIS	-	EXPRESSION TAG	UNP Q5MXB2
A	66	HIS	-	EXPRESSION TAG	UNP Q5MXB2
A	67	HIS	-	EXPRESSION TAG	UNP Q5MXB2
A	68	HIS	-	EXPRESSION TAG	UNP Q5MXB2
A	69	HIS	-	EXPRESSION TAG	UNP Q5MXB2
A	70	HIS	-	EXPRESSION TAG	UNP Q5MXB2
C	60	LYS	-	EXPRESSION TAG	UNP Q5MXB2
C	61	ARG	-	EXPRESSION TAG	UNP Q5MXB2
C	62	GLU	-	EXPRESSION TAG	UNP Q5MXB2
C	63	THR	-	EXPRESSION TAG	UNP Q5MXB2
C	64	PRO	-	EXPRESSION TAG	UNP Q5MXB2
C	65	HIS	-	EXPRESSION TAG	UNP Q5MXB2
C	66	HIS	-	EXPRESSION TAG	UNP Q5MXB2
C	67	HIS	-	EXPRESSION TAG	UNP Q5MXB2
C	68	HIS	-	EXPRESSION TAG	UNP Q5MXB2
C	69	HIS	-	EXPRESSION TAG	UNP Q5MXB2
C	70	HIS	-	EXPRESSION TAG	UNP Q5MXB2

- Molecule 2 is a RNA chain called SL2(RsmZ) RNA.

Mol	Chain	Residues	Atoms						Trace
2	B	22	Total	C	H	N	O	P	0
			712	211	241	89	150	21	

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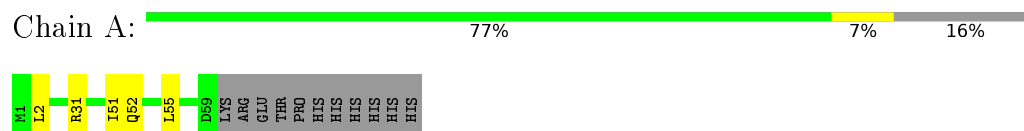
Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	P	
2	D	22	712	211	241	89	150	21	0

## 4 Residue-property plots [i](#)

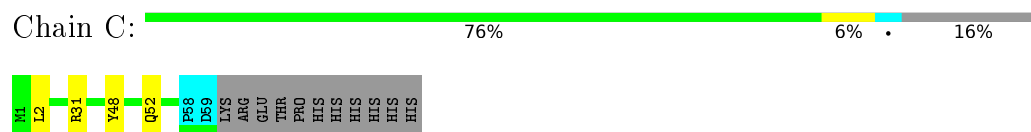
### 4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA 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.

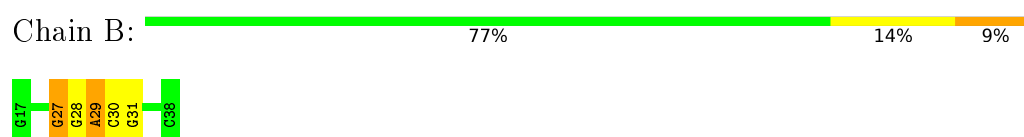
- Molecule 1: Carbon storage regulator homolog



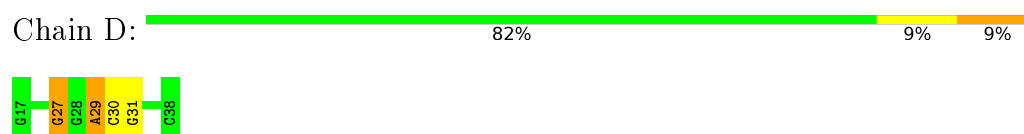
- Molecule 1: Carbon storage regulator homolog



- Molecule 2: SL2(RsmZ) RNA



- Molecule 2: SL2(RsmZ) RNA



### 4.2 Residue scores for the representative (medoid) model from the NMR ensemble

The representative model is number 1. Colouring as in section 4.1 above.

- Molecule 1: Carbon storage regulator homolog

Sequence logo for the 5' region of the 18S rRNA gene. The y-axis represents information content in bits (0.00 to 0.15). The x-axis shows positions from -10 to 10. Positions -10, -9, -8, -7, -6, -5, -4, -3, -2, -1, and 0 are highlighted in yellow. Positions 1 through 10 are highlighted in grey. The sequence at the bottom is: M1, L2, R31, L55, D59, LYS, ARG, GLU, THR, PRO, HIS, HIS, HIS, HIS, HIS, HIS.

- Chain C:  74% 7% • 16%

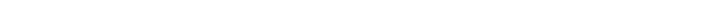
- Chain B:  77% 9% 14%

Diagram of a 1D chain with 8 sites. Sites G17 and C38 are green. Sites G27, G28, A29, C30, and G31 are yellow. Sites G27, G28, and A29 are grouped together in a single yellow box.


- Chain D:  82% 9% 9%

Diagram of a 1D chain with 8 sites. Sites G17, G28, and C38 are green. Sites G27, A29, C30, and G31 are yellow. Sites G28 and G31 are also orange. Horizontal lines connect G17 to G27, G27 to G28, G28 to A29, A29 to C30, C30 to G31, and G31 to C38.

## 5 Refinement protocol and experimental data overview

The models were refined using the following method: *simulated annealing*.

Of the 999 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	
AMBER	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)	2mfe_cs.cif
Number of chemical shift lists	2
Total number of shifts	1048
Number of shifts mapped to atoms	1048
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	39%

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

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	0.40±0.00	0±0/451 (0.0±0.0%)	0.74±0.02	0±0/610 (0.0±0.0%)
1	C	0.38±0.01	0±0/436 (0.0±0.0%)	0.73±0.02	0±0/591 (0.0±0.0%)
2	B	0.97±0.01	0±0/527 (0.0±0.0%)	1.46±0.01	0±0/821 (0.0±0.1%)
2	D	0.96±0.01	0±0/527 (0.0±0.0%)	1.45±0.02	0±0/821 (0.0±0.0%)
All	All	0.76	0/38820 (0.0%)	1.20	9/56860 (0.0%)

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
2	B	0.0±0.0	2.0±0.4
2	D	0.0±0.0	1.8±0.6
All	All	0	75

There are no bond-length outliers.

5 of 6 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
2	D	28	G	O4'-C1'-N9	6.07	113.05	108.20	4	2
2	B	28	G	O4'-C1'-N9	5.74	112.79	108.20	10	3
2	D	30	C	C5'-C4'-C3'	-5.25	107.60	116.00	3	1
2	D	29	A	O4'-C1'-N9	5.20	112.36	108.20	18	1
2	B	30	C	C5'-C4'-C3'	-5.12	107.81	116.00	4	1

There are no chirality outliers.

5 of 6 unique planar outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Group	Models (Total)
2	B	29	A	Sidechain	20
2	B	27	G	Sidechain	18
2	D	29	A	Sidechain	18
2	D	27	G	Sidechain	15
2	D	31	G	Sidechain	2

## 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	448	472	472	2±1
1	C	433	461	461	2±1
2	B	471	241	241	1±1
2	D	471	241	241	1±1
All	All	36460	28300	28300	97

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.

5 of 31 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:D:29:A:H2'	2:D:30:C:H5''	0.59	1.74	10	2
2:B:29:A:H2'	2:B:30:C:H5''	0.58	1.75	8	1
1:C:51:ILE:HG22	1:C:52:GLN:HE21	0.48	1.69	14	8
1:A:55:LEU:C	1:A:55:LEU:HD12	0.47	2.30	2	9
1:A:44:ARG:CZ	1:A:47:ILE:HD12	0.46	2.40	19	1

## 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	57/70 (81%)	50±1 (87±1%)	7±1 (13±1%)	0±0 (0±0%)	59 88
1	C	56/70 (80%)	50±1 (88±2%)	6±1 (11±2%)	0±0 (0±0%)	59 88
All	All	2260/2800 (81%)	1986 (88%)	272 (12%)	2 (0%)	59 88

All 2 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	17	ASP	1
1	C	17	ASP	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	49/60 (82%)	46±1 (95±2%)	3±1 (5±2%)	33 77
1	C	47/60 (78%)	44±1 (94±3%)	3±1 (6±3%)	29 74
All	All	1920/2400 (80%)	1813 (94%)	107 (6%)	31 76

5 of 19 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	C	2	LEU	20
1	A	2	LEU	20
1	C	31	ARG	13
1	A	31	ARG	12
1	C	44	ARG	7

### 6.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers	Suiteness
2	B	21/22 (95%)	3±1 (15±4%)	1±1 (6±4%)	0.56±0.02
2	D	21/22 (95%)	3±1 (14±4%)	1±1 (7±3%)	0.57±0.02
All	All	840/880 (95%)	119 (14%)	56 (7%)	0.56

The overall RNA backbone suiteness is 0.56.

5 of 11 unique RNA backbone outliers are listed below:

Mol	Chain	Res	Type	Models (Total)
2	B	30	C	20
2	D	27	G	20
2	D	30	C	20
2	B	27	G	20
2	B	31	G	16

5 of 7 unique RNA pucker outliers are listed below:

Mol	Chain	Res	Type	Models (Total)
2	D	29	A	19
2	B	29	A	15
2	B	30	C	9
2	D	30	C	7
2	B	28	G	3

## 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 39% for the well-defined parts and 38% for the entire structure.

### 7.1 Chemical shift list 1

File name: 2mfe\_cs.cif

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	743
Number of shifts mapped to atoms	743
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

#### 7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	65	$-0.16 \pm 0.17$	None needed ( $< 0.5$ ppm)
$^{13}\text{C}_\beta$	58	$0.27 \pm 0.30$	None needed ( $< 0.5$ ppm)
$^{13}\text{C}'$	0	—	—
$^{15}\text{N}$	60	$-0.98 \pm 0.53$	None needed (imprecise)

#### 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 25%, i.e. 571 atoms were assigned a chemical shift out of a possible 2245. 9 out of 18 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^1\text{H}$	$^{13}\text{C}$	$^{15}\text{N}$
Backbone	230/574 (40%)	115/229 (50%)	59/232 (25%)	56/113 (50%)
Sidechain	331/801 (41%)	199/460 (43%)	125/301 (42%)	7/40 (18%)

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	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Aromatic	10/30 (33%)	6/16 (38%)	4/12 (33%)	0/2 (0%)
Overall	571/2245 (25%)	320/1193 (27%)	188/837 (22%)	63/215 (29%)

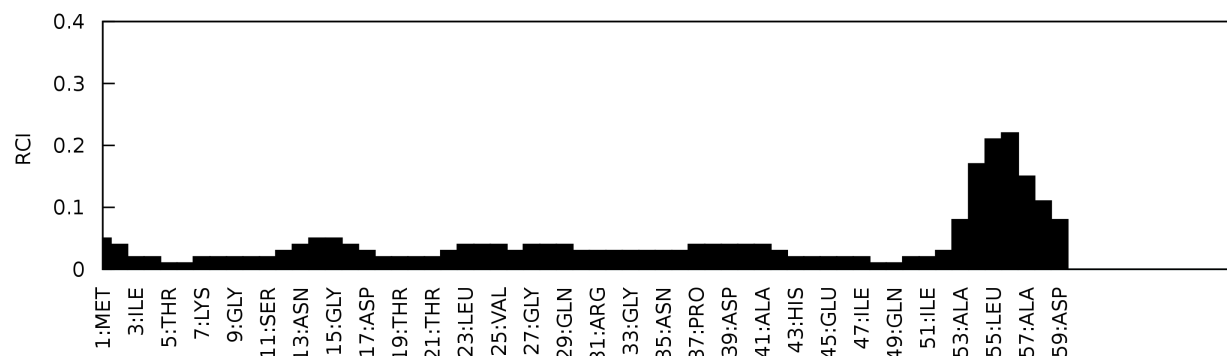
#### 7.1.4 Statistically unusual chemical shifts [i](#)

There are no statistically unusual chemical shifts.

#### 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:



## 7.2 Chemical shift list 2

File name: 2mfe\_cs.cif

Chemical shift list name: *assigned\_chem\_shift\_list\_2*

#### 7.2.1 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	305
Number of shifts mapped to atoms	305
Number of unparsed shifts	0

Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	2

### 7.2.2 Chemical shift referencing [i](#)

No chemical shift referencing corrections were calculated (not enough data).

### 7.2.3 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 13%, i.e. 299 atoms were assigned a chemical shift out of a possible 2245. 0 out of 18 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Backbone	0/574 (0%)	0/229 (0%)	0/232 (0%)	0/113 (0%)
Sidechain	0/801 (0%)	0/460 (0%)	0/301 (0%)	0/40 (0%)
Aromatic	0/30 (0%)	0/16 (0%)	0/12 (0%)	0/2 (0%)
Overall	299/2245 (13%)	158/1193 (13%)	130/837 (16%)	11/215 (5%)

### 7.2.4 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
2	B	26	A	H4'	3.10	5.17 – 3.77	-9.8
2	B	28	G	H5''	2.56	5.11 – 3.31	-9.2

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

No *random coil index* (RCI) plot could be generated from the current chemical shift list (assigned\_chem\_shift\_list\_2). RCI is only applicable to proteins.