wwPDB NMR Structure Validation Summary Report (i)

Apr 27, 2016 – 03:05 AM BST

PDB ID	:	2MC0
Title	:	Structural Basis of a Thiopeptide Antibiotic Multidrug Resistance System from Streptomyces lividans:Nosiheptide in Complex with TipAS
Authors	:	Habazettl, J.; Allan, M.G.; Jensen, P.; Sass, H.; Grzesiek, S.
Deposited on	:	2013-08-12

This is a wwPDB NMR Structure Validation Summary 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 (i) symbol.

The following versions of software and data (see references (i)) were used in the production of this report:

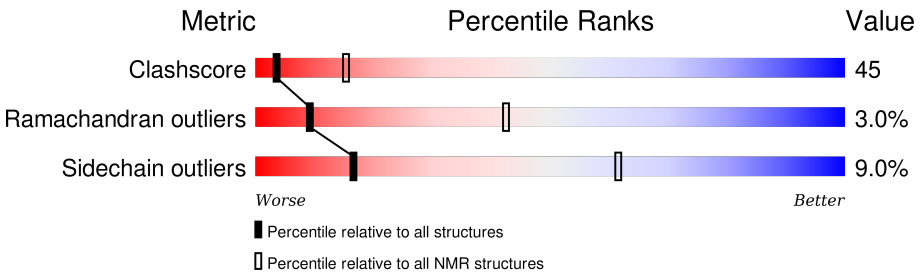
Cyrange	:	Kirchner and Güntert (2011)
NmrClust	:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Mogul	:	1.7.1 (RC1), CSD as537be (2016)
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	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 (i)

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

The overall completeness of chemical shifts assignment is 88%.

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 <=5%

Mol	Chain	Length	Quality of chain
1	A	144	33% 59% • • •
2	B	13	8% 15% 8% 69%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA and RNA chains that are outliers for geometric criteria:

Mol	Chain	Compound	Res	Total models with violations	
				Chirality	Geometry
2	B	BB9	509	-	10

2 Ensemble composition and analysis (i)

This entry contains 10 models. Model 4 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:112-A:209, A:214-A:253, B:501-B:501, B:503-B:503, B:508-B:508, B:512-B:512 (142)	0.31	4

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 3 clusters and 1 single-model cluster was found.

Cluster number	Models
1	3, 6, 8, 9
2	1, 2, 5
3	4, 10
Single-model clusters	7

3 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 2330 atoms, of which 1094 are hydrogens and 0 are deuteriums.

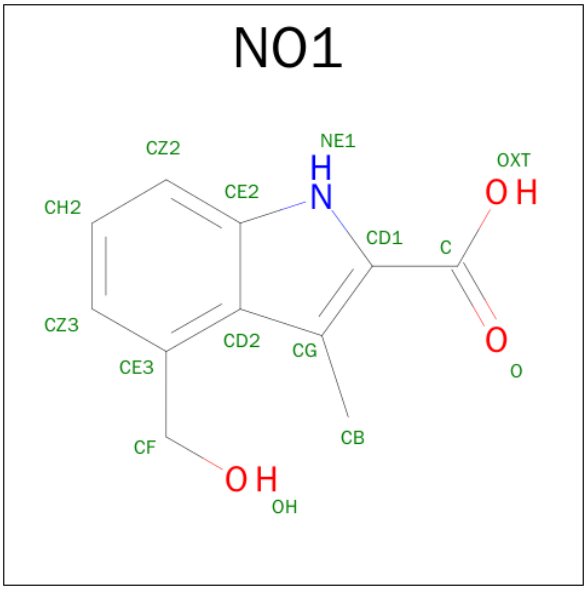
- Molecule 1 is a protein called HTH-type transcriptional activator TipA.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	143	2207	706	1053	204	237	7	0

- Molecule 2 is a protein called nosiheptide.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
2	B	13	101	40	32	12	11	6	1

- Molecule 3 is 4-(HYDROXYMETHYL)-3-METHYL-1H-INDOLE-2-CARBOXYLIC ACID (three-letter code: NO1) (formula: $C_{11}H_{11}NO_3$).



Mol	Chain	Residues	Atoms				
			Total	C	H	N	O
3	B	1	22	11	9	1	1

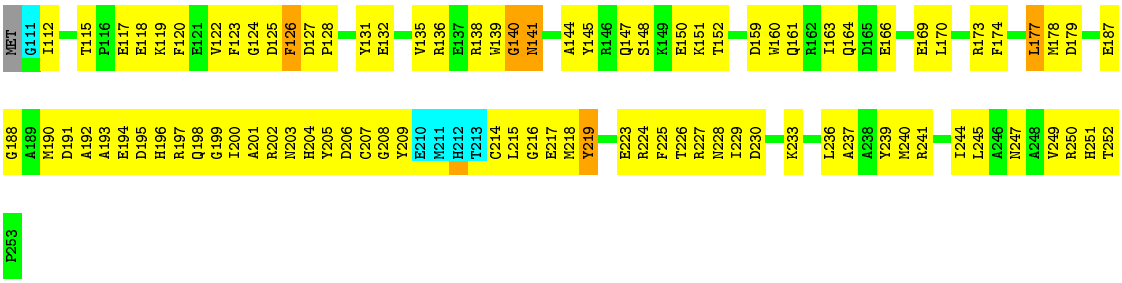
4 Residue-property plots (i)

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.

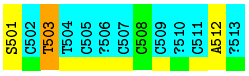
- Molecule 1: HTH-type transcriptional activator TipA

Chain A:



- Molecule 2: nosiheptide

Chain B:

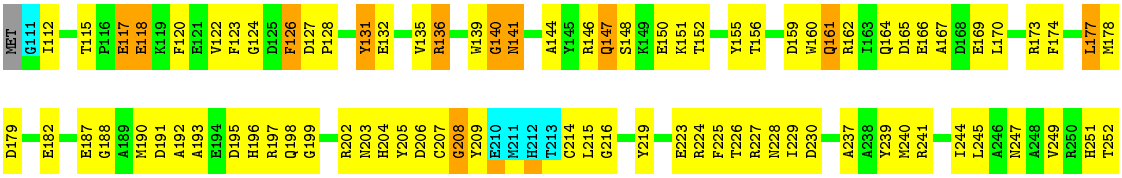


4.2 Residue scores for the representative (medoid) model from the NMR ensemble

The representative model is number 4. Colouring as in section 4.1 above.

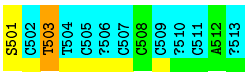
- Molecule 1: HTH-type transcriptional activator TipA

Chain A:



- Molecule 2: nosiheptide

Chain B:



5 Refinement protocol and experimental data overview (i)

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

Of the 100 calculated structures, 10 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
Xplor-NIH	structure solution	2.30
Xplor-NIH	refinement	2.30

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)	2mc0_cs.str
Number of chemical shift lists	1
Total number of shifts	1736
Number of shifts mapped to atoms	1736
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	88%

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)

Bond lengths and bond angles in the following residue types are not validated in this section: 3GL, BB9, NH2, MH6, DBU, NO1

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	0.27±0.00	0±0/1139 (0.0±0.0%)	0.47±0.01	0±0/1537 (0.0±0.0%)
2	B	2.65±0.03	1±0/16 (6.2±0.0%)	1.40±0.05	1±1/16 (3.1±3.1%)
All	All	0.41	10/11550 (0.1%)	0.49	5/15530 (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	1.0±0.0	0.0±0.0
All	All	10	0

All unique bond outliers are listed below.

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
2	B	501	SER	CA-CB	-10.29	1.37	1.52	1	10

All unique angle outliers are listed below.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
2	B	501	SER	CB-CA-C	5.24	120.06	110.10	10	5

All unique chiral outliers are listed below.

Mol	Chain	Res	Type	Atoms	Models (Total)
2	B	501	SER	CA	10

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	1116	1021	1020	99±8
2	B	20	15	16	1±1
3	B	13	9	7	2±2
All	All	11490	10450	10430	988

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 45.

5 of 518 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:174:PHE:CE1	1:A:192:ALA:HB1	0.97	1.94	7	10
1:A:159:ASP:O	1:A:163:ILE:HD13	0.90	1.66	2	3
1:A:245:LEU:O	1:A:249:VAL:HG23	0.87	1.70	7	4
1:A:230:ASP:OD1	1:A:237:ALA:HB2	0.82	1.73	3	3
1:A:118:GLU:OE1	1:A:118:GLU:N	0.82	2.13	1	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	137/144 (95%)	129±3 (94±2%)	6±2 (4±1%)	3±1 (2±1%)	13 53
2	B	3/13 (23%)	1±1 (27±25%)	1±1 (30±23%)	1±0 (43±15%)	0 0
All	All	1400/1570 (89%)	1293 (92%)	65 (5%)	42 (3%)	9 42

5 of 7 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	140	GLY	10
2	B	503	THR	10
1	A	141	ASN	10
1	A	125	ASP	4
1	A	208	GLY	3

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	113/118 (96%)	103±3 (91±3%)	10±3 (9±3%)	16	61
2	B	2/3 (67%)	2±0 (95±15%)	0±0 (5±15%)	35	79
All	All	1150/1210 (95%)	1046 (91%)	104 (9%)	16	61

5 of 45 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	126	PHE	9
1	A	177	LEU	9
1	A	219	TYR	7
1	A	147	GLN	6
1	A	250	ARG	4

6.3.3 RNA (i)

There are no RNA molecules in this entry.

6.4 Non-standard residues in protein, DNA, RNA chains (i)

8 non-standard protein/DNA/RNA residues are 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	BB9	B	502	2	3,5,6	1.59±0.04	0±0 (0±0%)
2	DBU	B	504	2	4,4,6	1.38±0.04	0±0 (0±0%)
2	BB9	B	505	2	3,5,6	1.53±0.06	0±0 (0±0%)
2	3GL	B	506	3,2	5,8,10	0.71±0.12	0±0 (0±0%)
2	BB9	B	507	2	3,5,6	1.49±0.05	0±0 (0±0%)
2	BB9	B	509	2	2,4,6	1.99±0.04	0±0 (0±0%)
2	MH6	B	510	2	3,4,6	2.17±0.03	0±0 (0±0%)
2	BB9	B	511	2	3,5,6	1.53±0.04	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	BB9	B	502	2	1,5,7	3.47±0.25	0±0 (0±0%)
2	DBU	B	504	2	1,4,7	3.94±0.56	0±0 (10±30%)
2	BB9	B	505	2	1,5,7	2.68±0.21	0±0 (0±0%)
2	3GL	B	506	3,2	6,10,13	0.76±0.08	0±0 (0±0%)
2	BB9	B	507	2	1,5,7	2.82±0.15	0±0 (0±0%)
2	BB9	B	509	2	3,4,7	3.51±0.04	1±1 (16±16%)
2	MH6	B	510	2	1,4,7	0.39±0.10	0±0 (0±0%)
2	BB9	B	511	2	1,5,7	2.90±0.09	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	BB9	B	502	2	-	0±0,0,4,6	0±0,0,0,0
2	DBU	B	504	2	-	0±0,1,2,6	0±0,0,0,0
2	BB9	B	505	2	-	0±0,0,4,6	0±0,0,0,0
2	3GL	B	506	3,2	-	0±0,4,8,12	0±0,0,0,0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	BB9	B	507	2	-	0±0,0,4,6	0±0,0,0,0
2	BB9	B	509	2	-	0±0,0,2,6	0±0,0,0,0
2	MH6	B	510	2	-	0±0,1,2,6	0±0,0,0,0
2	BB9	B	511	2	-	0±0,0,4,6	0±0,0,0,0

There are no bond-length outliers.

All 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(^{o})	Ideal(^{o})	Models	
								Worst	Total
2	B	509	BB9	C-CA-CB	5.14	127.66	120.96	10	5
2	B	504	DBU	C-CA-N	5.07	122.37	116.52	7	1

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6.5 Carbohydrates (i)

There are no carbohydrates in this entry.

6.6 Ligand geometry (i)

1 ligand 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
3	NO1	B	601	2	13,14,16	1.49±0.05	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
3	NO1	B	601	2	12,20,23	2.11±0.22	1±0 (8±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
3	NO1	B	601	2	-	0±0,0,2,6	0±0,2,2,2

There are no bond-length outliers.

All unique angle outliers are listed below.

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})	Models	
								Worst	Total
3	B	601	NO1	O-C-CD1	7.80	117.94	124.47	1	10

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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 88% for the well-defined parts and 88% for the entire structure.

7.1 Chemical shift list 1

File name: 2mc0_cs.str

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	1736
Number of shifts mapped to atoms	1736
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	6

7.1.2 Chemical shift referencing (i)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	143	-0.67 ± 0.16	Should be applied
$^{13}C_{\beta}$	132	0.32 ± 0.11	None needed (< 0.5 ppm)
$^{13}C'$	132	-0.56 ± 0.09	Should be applied
^{15}N	138	0.42 ± 0.42	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 88%, i.e. 1529 atoms were assigned a chemical shift out of a possible 1734. 5 out of 11 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	675/700 (96%)	275/279 (99%)	267/284 (94%)	133/137 (97%)
Sidechain	720/887 (81%)	465/520 (89%)	243/316 (77%)	12/51 (24%)

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	Total	^{1}H	^{13}C	^{15}N
Aromatic	134/147 (91%)	69/77 (90%)	63/64 (98%)	2/6 (33%)
Overall	1529/1734 (88%)	809/876 (92%)	573/664 (86%)	147/194 (76%)

7.1.4 Statistically unusual chemical shifts (i)

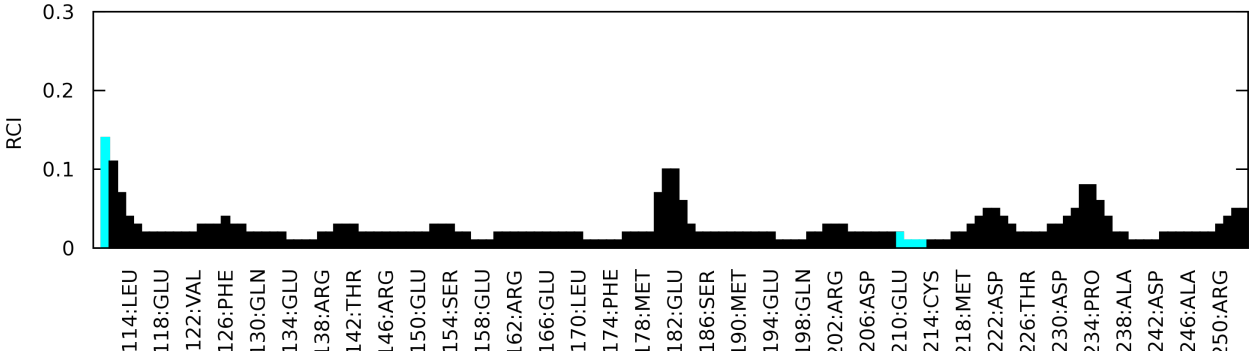
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

Mol	Chain	Res	Type	Atom	Shift, *ppm*	Expected range, *ppm*	Z-score
2	B	512	ALA	HB1	6.39	2.61 – 0.11	20.1
2	B	512	ALA	HB2	5.87	2.61 – 0.11	18.0
2	B	501	SER	HB2	7.03	5.18 – 2.58	12.1
2	B	501	SER	HB3	7.03	5.25 – 2.45	11.3
1	A	138	ARG	HG3	-0.26	3.00 – 0.10	-6.2
1	A	138	ARG	HG2	-0.04	2.92 – 0.22	-5.9

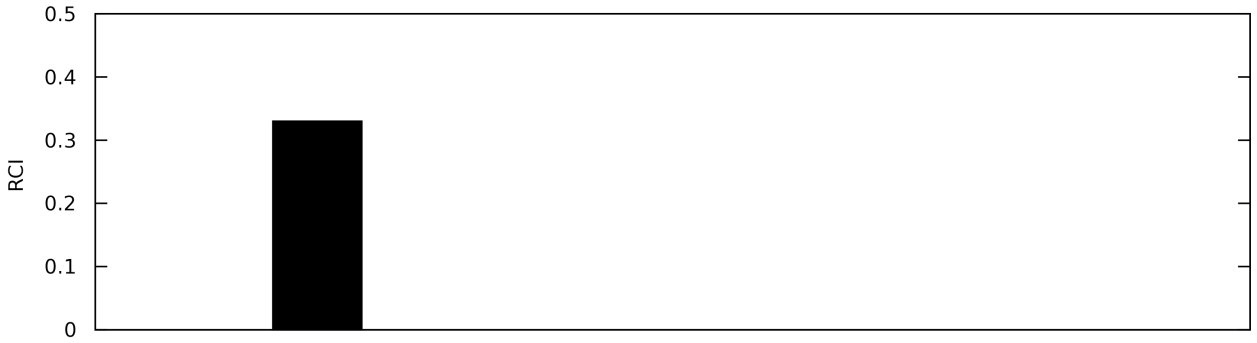
7.1.5 Random Coil Index (RCI) plots (i)

The images below report *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:



Random coil index (RCI) for chain B:


0.5
0.4
0.3
0.2
0.1
0
RCI