Full wwPDB NMR Structure Validation Report (i)

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PDB ID	:	2MGZ
Title	:	Solution structure of RBFOX family ASD-1 RRM and SUP-12 RRM in ternary complex with RNA
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Deposited on	:	2013-11-12

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 (i) symbol.

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

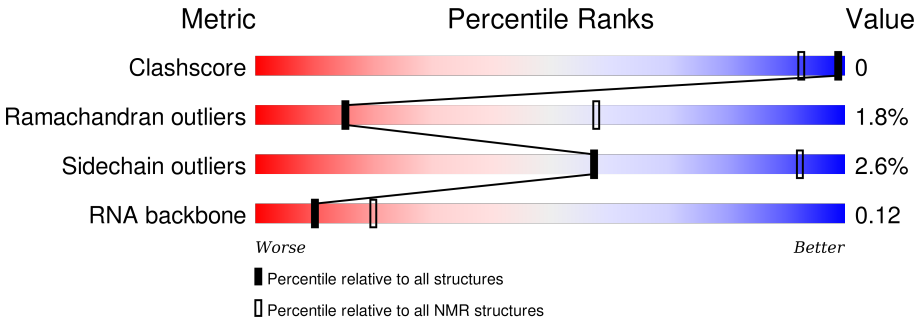
Cyrange	:	Kirchner and Güntert (2011)
NmrClust	:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Mogul	:	unknown
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	rb-20027457
Ideal 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 (i)

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

The overall completeness of chemical shifts assignment is 72%.

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 >=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	94	77% . 19%
2	B	105	71% . 26%
3	C	12	8% 33% 50% 8%

2 Ensemble composition and analysis

This entry contains 20 models. Model 17 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *fewest violations*.

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:101-A:176, B:34-B:69, B:74-B:115 (154)	1.02	17

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 4 clusters and 3 single-model clusters were found.

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

3 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3490 atoms, of which 1676 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Protein ASD-1, isoform a.

Mol	Chain	Residues	Atoms						Trace
1	A	94	Total	C	H	N	O	S	0
			1487	464	743	139	138	3	

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	96	GLY	-	EXPRESSION TAG	UNP G5EEW7

- Molecule 2 is a protein called Protein SUP-12, isoform a.

Mol	Chain	Residues	Atoms						Trace
2	B	105	Total	C	H	N	O	S	0
			1619	508	803	146	159	3	

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	19	GLY	-	EXPRESSION TAG	UNP O45189

- Molecule 3 is a RNA chain called RNA (5'-R(*UP*GP*CP*AP*UP*GP*GP*UP*GP*UP*GP*C)-3').

Mol	Chain	Residues	Atoms						Trace
3	C	12	Total	C	H	N	O	P	0
			384	114	130	44	85	11	

4 Residue-property plots

4.1 Average score per residue in the NMR ensemble

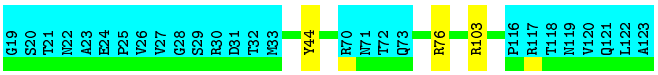
These plots are provided for all protein, RNA and DNA chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-coded according to the number of geometric quality criteria for which they contain 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: Protein ASD-1, isoform a

Chain A:

• Molecule 2: Protein SUP-12, isoform a

Chain B:



• Molecule 3: RNA (5'-R(*UP*GP*CP*AP*UP*GP*GP*UP*GP*UP*GP*C)-3')

Chain C:

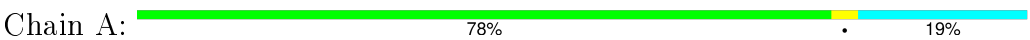
4.2 Scores per residue for each member of the ensemble

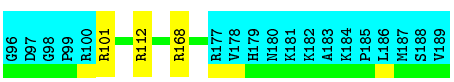
Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

• Molecule 1: Protein ASD-1, isoform a

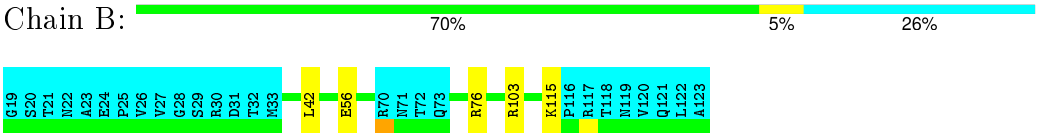
Chain A:





• Molecule 2: Protein SUP-12, isoform a

Chain B:



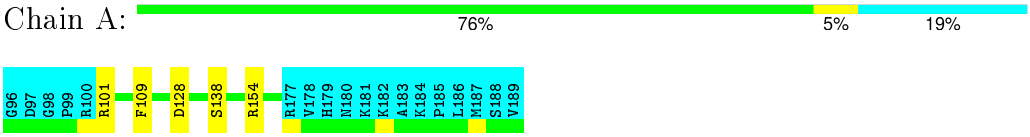
• Molecule 3: RNA (5'-R(*UP*GP*CP*AP*UP*GP*GP*UP*GP*UP*GP*C)-3')

Chain C:

4.2.2 Score per residue for model 2

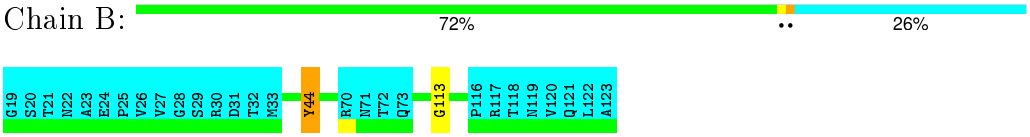
• Molecule 1: Protein ASD-1, isoform a

Chain A:



• Molecule 2: Protein SUP-12, isoform a

Chain B:



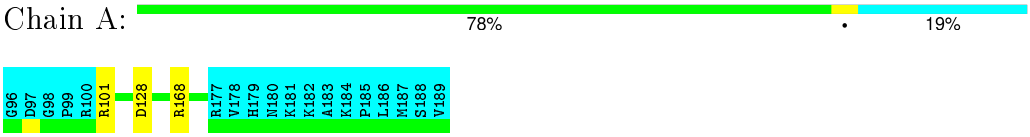
• Molecule 3: RNA (5'-R(*UP*GP*CP*AP*UP*GP*GP*UP*GP*UP*GP*C)-3')

Chain C:

4.2.3 Score per residue for model 3

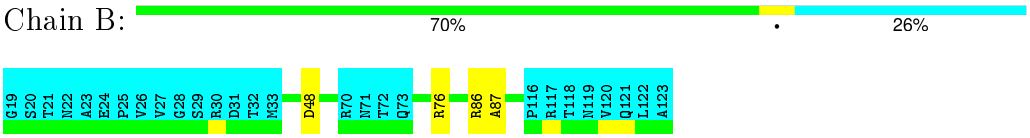
• Molecule 1: Protein ASD-1, isoform a

Chain A:



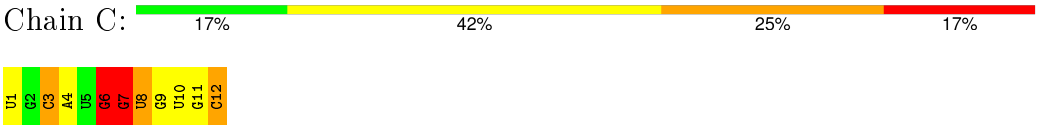
• Molecule 2: Protein SUP-12, isoform a

Chain B:



- Molecule 3: RNA (5'-R(*UP*GP*CP*AP*UP*GP*GP*UP*GP*UP*GP*C)-3')

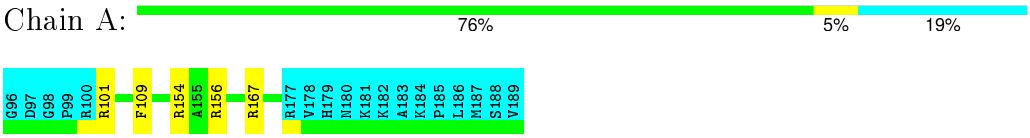
Chain C:



4.2.4 Score per residue for model 4

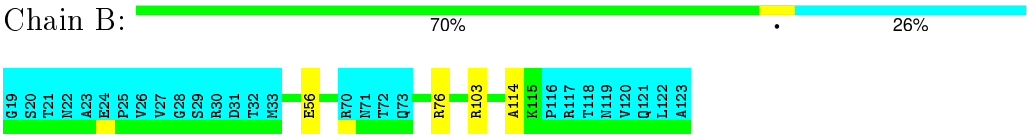
- Molecule 1: Protein ASD-1, isoform a

Chain A:



- Molecule 2: Protein SUP-12, isoform a

Chain B:



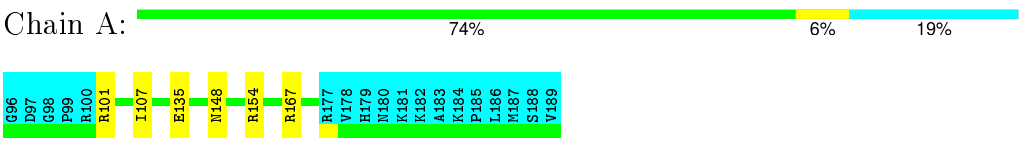
- Molecule 3: RNA (5'-R(*UP*GP*CP*AP*UP*GP*GP*UP*GP*UP*GP*C)-3')

Chain C:

4.2.5 Score per residue for model 5

- Molecule 1: Protein ASD-1, isoform a

Chain A:



- Molecule 2: Protein SUP-12, isoform a

Chain B:

• Molecule 3: RNA (5'-R(*UP*GP*CP*AP*UP*GP*GP*UP*GP*UP*GP*C)-3')

Chain C:

4.2.6 Score per residue for model 6

• Molecule 1: Protein ASD-1, isoform a

Chain A:

• Molecule 2: Protein SUP-12, isoform a

Chain B:

• Molecule 3: RNA (5'-R(*UP*GP*CP*AP*UP*GP*GP*UP*GP*UP*GP*C)-3')

Chain C:

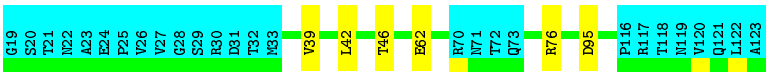
4.2.7 Score per residue for model 7

• Molecule 1: Protein ASD-1, isoform a

Chain A:

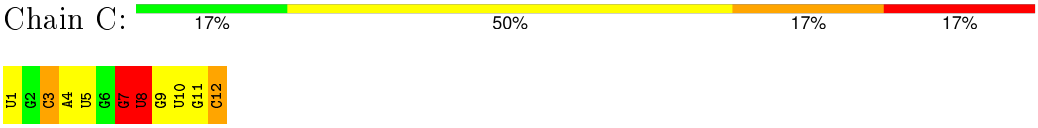
• Molecule 2: Protein SUP-12, isoform a

Chain B:



• Molecule 3: RNA (5'-R(*UP*GP*CP*AP*UP*GP*GP*UP*GP*UP*GP*C)-3')

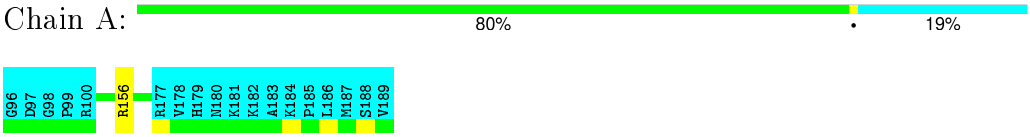
Chain C:



4.2.8 Score per residue for model 8

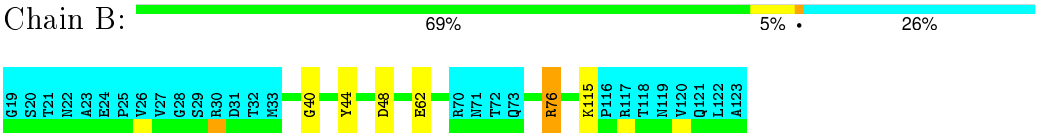
• Molecule 1: Protein ASD-1, isoform a

Chain A:



• Molecule 2: Protein SUP-12, isoform a

Chain B:



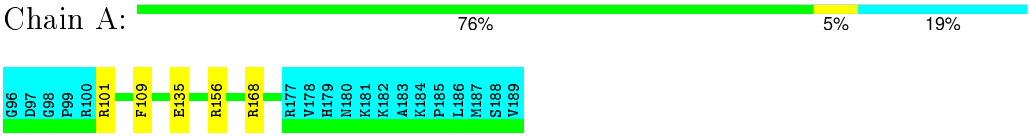
• Molecule 3: RNA (5'-R(*UP*GP*CP*AP*UP*GP*GP*UP*GP*UP*GP*C)-3')

Chain C:

4.2.9 Score per residue for model 9

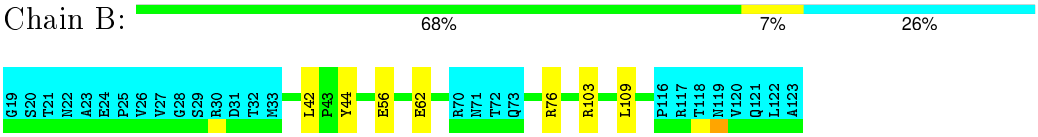
• Molecule 1: Protein ASD-1, isoform a

Chain A:



• Molecule 2: Protein SUP-12, isoform a

Chain B:



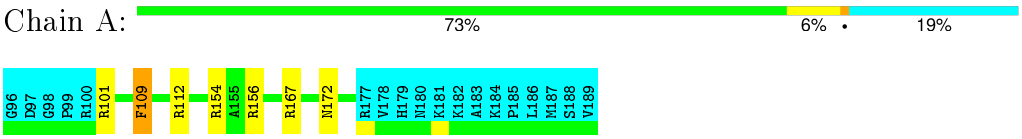
• Molecule 3: RNA (5'-R(*UP*GP*CP*AP*UP*GP*GP*UP*GP*UP*GP*C)-3')

Chain C:

4.2.10 Score per residue for model 10

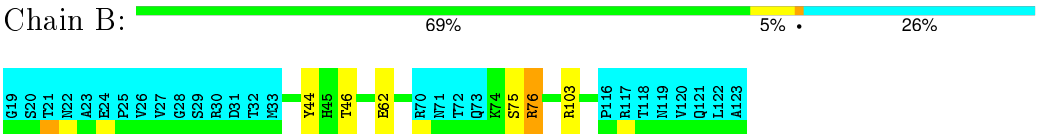
- Molecule 1: Protein ASD-1, isoform a

Chain A:



- Molecule 2: Protein SUP-12, isoform a

Chain B:



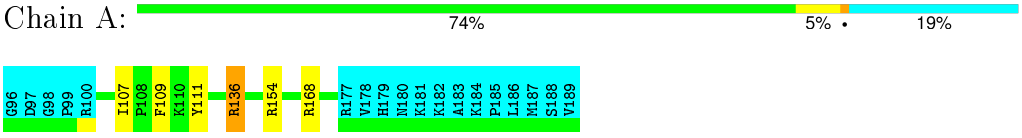
- Molecule 3: RNA (5'-R(*UP*GP*CP*AP*UP*GP*GP*UP*GP*UP*GP*C)-3')

Chain C:

4.2.11 Score per residue for model 11

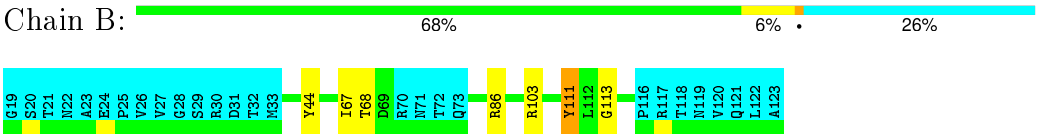
- Molecule 1: Protein ASD-1, isoform a

Chain A:



- Molecule 2: Protein SUP-12, isoform a

Chain B:



- Molecule 3: RNA (5'-R(*UP*GP*CP*AP*UP*GP*GP*UP*GP*UP*GP*C)-3')

Chain C:

4.2.12 Score per residue for model 12

• Molecule 1: Protein ASD-1, isoform a

Chain A:

• Molecule 2: Protein SUP-12, isoform a

Chain B:

• Molecule 3: RNA (5'-R(*UP*GP*CP*AP*UP*GP*GP*UP*GP*UP*GP*C)-3')

Chain C:

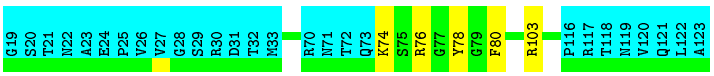
4.2.13 Score per residue for model 13

• Molecule 1: Protein ASD-1, isoform a

Chain A:

• Molecule 2: Protein SUP-12, isoform a

Chain B:



• Molecule 3: RNA (5'-R(*UP*GP*CP*AP*UP*GP*GP*UP*GP*UP*GP*C)-3')

Chain C:

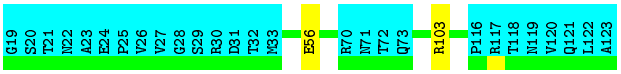
4.2.14 Score per residue for model 14

• Molecule 1: Protein ASD-1, isoform a

Chain A:

• Molecule 2: Protein SUP-12, isoform a

Chain B:



• Molecule 3: RNA (5'-R(*UP*GP*CP*AP*UP*GP*GP*UP*GP*UP*GP*C)-3')

Chain C:

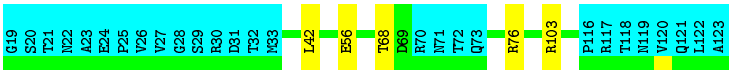
4.2.15 Score per residue for model 15

• Molecule 1: Protein ASD-1, isoform a

Chain A:

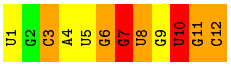
• Molecule 2: Protein SUP-12, isoform a

Chain B:



• Molecule 3: RNA (5'-R(*UP*GP*CP*AP*UP*GP*GP*UP*GP*UP*GP*C)-3')

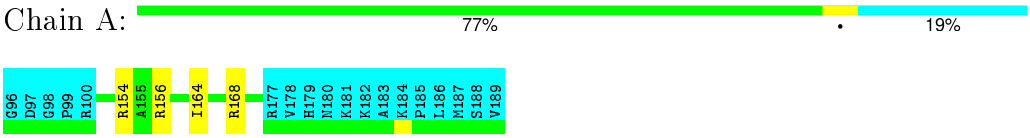
Chain C:



4.2.16 Score per residue for model 16

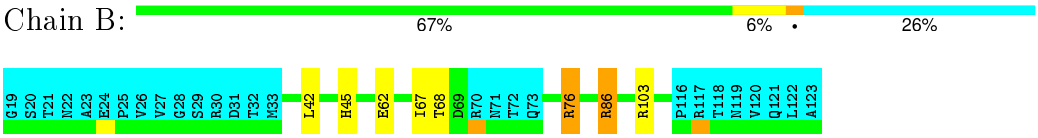
• Molecule 1: Protein ASD-1, isoform a

Chain A:



• Molecule 2: Protein SUP-12, isoform a

Chain B:



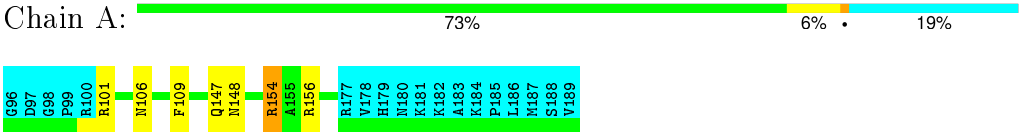
• Molecule 3: RNA (5'-R(*UP*GP*CP*AP*UP*GP*GP*UP*GP*UP*GP*C)-3')

Chain C:

4.2.17 Score per residue for model 17 (medoid)

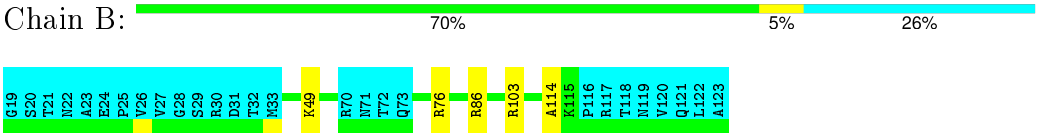
• Molecule 1: Protein ASD-1, isoform a

Chain A:



• Molecule 2: Protein SUP-12, isoform a

Chain B:



• Molecule 3: RNA (5'-R(*UP*GP*CP*AP*UP*GP*GP*UP*GP*UP*GP*C)-3')

Chain C:

4.2.18 Score per residue for model 18

• Molecule 1: Protein ASD-1, isoform a

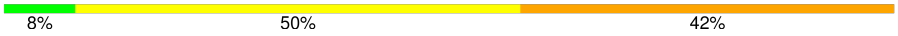
Chain A:

• Molecule 2: Protein SUP-12, isoform a

Chain B:

• Molecule 3: RNA (5'-R(*UP*GP*CP*AP*UP*GP*GP*UP*GP*UP*GP*C)-3')

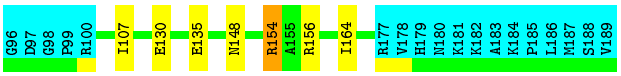
Chain C:



4.2.19 Score per residue for model 19

• Molecule 1: Protein ASD-1, isoform a

Chain A:



• Molecule 2: Protein SUP-12, isoform a

Chain B:

• Molecule 3: RNA (5'-R(*UP*GP*CP*AP*UP*GP*GP*UP*GP*UP*GP*C)-3')

Chain C:

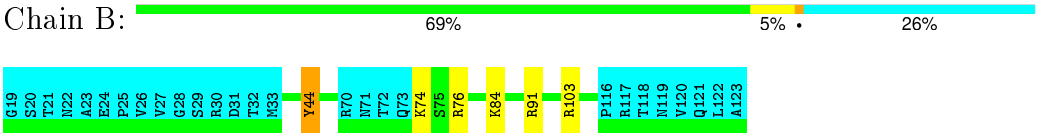
4.2.20 Score per residue for model 20

• Molecule 1: Protein ASD-1, isoform a

Chain A:

• Molecule 2: Protein SUP-12, isoform a

Chain B:



• Molecule 3: RNA (5'-R(*UP*GP*CP*AP*UP*GP*GP*UP*GP*UP*GP*C)-3')

Chain C:

5 Refinement protocol and experimental data overview

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

Of the 400 calculated structures, 20 were deposited, based on the following criterion: *structures with the least restraint violations*.

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

Software name	Classification	Version
AMBER	refinement	9

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)	2mgz_cs.str
Number of chemical shift lists	2
Total number of shifts	1916
Number of shifts mapped to atoms	1916
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	72%

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

6 Model quality

6.1 Standard geometry

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	0.68±0.01	0±0/617 (0.0±0.0%)	1.03±0.03	4±1/834 (0.4±0.1%)
2	B	0.73±0.01	0±0/628 (0.0±0.0%)	0.98±0.03	3±1/848 (0.3±0.1%)
3	C	1.37±0.01	0±0/283 (0.0±0.0%)	2.29±0.04	17±2/440 (3.9±0.6%)
All	All	0.87	0/30560 (0.0%)	1.37	461/42440 (1.1%)

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
1	A	0.0±0.0	0.3±0.5
2	B	0.0±0.0	0.1±0.3
3	C	0.0±0.0	3.5±1.4
All	All	0	78

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
3	C	8	U	O4'-C1'-N1	11.56	117.45	108.20	16	19
3	C	7	G	O4'-C1'-N9	10.22	116.38	108.20	7	20
3	C	4	A	N1-C6-N6	-9.07	113.16	118.60	11	20
3	C	12	C	N3-C2-O2	-8.12	116.22	121.90	7	20
2	B	76	ARG	NE-CZ-NH1	8.12	124.36	120.30	18	15
1	A	154	ARG	NE-CZ-NH1	7.98	124.29	120.30	6	15
2	B	76	ARG	NE-CZ-NH2	-7.94	116.33	120.30	16	7
3	C	11	G	O4'-C1'-N9	7.83	114.47	108.20	20	4
1	A	101	ARG	NE-CZ-NH1	7.74	124.17	120.30	12	15
3	C	4	A	C5-C6-N1	7.71	121.56	117.70	2	20
3	C	10	U	O4'-C1'-N1	7.71	114.36	108.20	4	12

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})	Models	
								Worst	Total
3	C	6	G	O4'-C1'-N9	7.67	114.33	108.20	19	15
2	B	103	ARG	NE-CZ-NH1	7.67	124.13	120.30	13	14
3	C	3	C	O4'-C1'-N1	7.42	114.13	108.20	8	19
3	C	8	U	N3-C2-O2	-7.35	117.05	122.20	15	6
3	C	3	C	N3-C2-O2	-7.21	116.85	121.90	15	20
1	A	156	ARG	NE-CZ-NH1	7.00	123.80	120.30	12	14
1	A	168	ARG	NE-CZ-NH1	6.93	123.77	120.30	12	10
3	C	12	C	N1-C2-O2	6.72	122.94	118.90	7	8
1	A	167	ARG	NE-CZ-NH1	6.71	123.66	120.30	10	6
3	C	9	G	O4'-C1'-N9	6.69	113.55	108.20	8	2
1	A	168	ARG	NE-CZ-NH2	-6.48	117.06	120.30	9	6
2	B	86	ARG	NE-CZ-NH1	6.30	123.45	120.30	5	7
3	C	6	G	N3-C4-C5	-6.17	125.51	128.60	5	14
3	C	4	A	C4-C5-C6	-6.08	113.96	117.00	11	19
3	C	12	C	O4'-C1'-N1	6.04	113.03	108.20	19	3
3	C	10	U	N3-C2-O2	-6.03	117.98	122.20	13	11
3	C	11	G	N1-C6-O6	-5.96	116.32	119.90	2	8
3	C	1	U	O4'-C1'-N1	5.89	112.91	108.20	13	5
1	A	156	ARG	NE-CZ-NH2	-5.85	117.37	120.30	12	3
3	C	8	U	C3'-C2'-C1'	5.85	106.18	101.50	15	1
3	C	7	G	C1'-O4'-C4'	-5.84	105.22	109.90	7	2
3	C	6	G	N1-C6-O6	-5.82	116.41	119.90	20	4
3	C	1	U	N3-C2-O2	-5.77	118.16	122.20	19	13
3	C	7	G	N1-C6-O6	-5.76	116.44	119.90	10	4
3	C	4	A	O4'-C1'-N9	5.72	112.78	108.20	20	1
3	C	9	G	N1-C6-O6	-5.71	116.47	119.90	17	15
3	C	5	U	O4'-C1'-N1	5.69	112.75	108.20	10	10
2	B	44	TYR	CB-CG-CD2	-5.50	117.70	121.00	20	1
3	C	3	C	N1-C2-O2	5.50	122.20	118.90	19	14
2	B	111	TYR	CB-CG-CD2	-5.50	117.70	121.00	11	1
3	C	1	U	N1-C2-N3	5.49	118.19	114.90	5	4
3	C	10	U	C3'-C2'-C1'	5.47	105.87	101.50	15	4
3	C	6	G	C5'-C4'-C3'	-5.46	107.26	116.00	17	1
3	C	10	U	C5'-C4'-C3'	-5.41	107.34	116.00	8	2
3	C	9	G	N3-C4-C5	-5.37	125.92	128.60	20	5
2	B	86	ARG	NE-CZ-NH2	-5.36	117.62	120.30	11	3
2	B	44	TYR	CB-CG-CD1	-5.26	117.84	121.00	2	1
1	A	112	ARG	NE-CZ-NH2	-5.23	117.69	120.30	10	1
3	C	1	U	N1-C1'-C2'	5.22	120.78	114.00	19	2
2	B	91	ARG	NE-CZ-NH1	5.21	122.91	120.30	20	1
1	A	136	ARG	NE-CZ-NH1	5.16	122.88	120.30	11	2

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})	Models	
								Worst	Total
3	C	2	G	N1-C6-O6	-5.12	116.83	119.90	8	4
3	C	1	U	C3'-C2'-C1'	-5.11	97.41	101.50	5	2
3	C	8	U	C5'-C4'-C3'	-5.10	107.84	116.00	13	1
3	C	8	U	C5-C6-N1	-5.08	120.16	122.70	16	1
3	C	6	G	P-O3'-C3'	5.06	125.77	119.70	16	2
3	C	1	U	C5-C6-N1	-5.04	120.18	122.70	5	1
3	C	12	C	N3-C4-N4	-5.01	114.49	118.00	17	1

There are no chirality outliers.

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

Mol	Chain	Res	Type	Group	Models (Total)
3	C	7	G	Sidechain	13
3	C	6	G	Sidechain	11
3	C	11	G	Sidechain	11
3	C	10	U	Sidechain	9
3	C	5	U	Sidechain	6
3	C	8	U	Sidechain	6
3	C	9	G	Sidechain	5
3	C	1	U	Sidechain	5
3	C	12	C	Sidechain	3
1	A	154	ARG	Sidechain	3
1	A	168	ARG	Sidechain	2
2	B	44	TYR	Sidechain	1
1	A	101	ARG	Sidechain	1
3	C	4	A	Sidechain	1
2	B	78	TYR	Sidechain	1

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	605	591	591	0±0
2	B	614	603	603	0±0
3	C	254	130	130	0±0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes
All	All	29460	26480	26480	6

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 0.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:109:PHE:CZ	3:C:1:U:H1'	0.49	2.43	17	4
2:B:44:TYR:CE2	3:C:7:G:H1'	0.45	2.46	6	1
2:B:80:PHE:CZ	3:C:11:G:C8	0.40	3.09	13	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	76/94 (81%)	70±2 (92±2%)	5±2 (7±2%)	1±1 (1±1%)	24	71
2	B	78/105 (74%)	67±3 (86±3%)	9±3 (11±4%)	2±1 (2±1%)	11	48
All	All	3080/3980 (77%)	2746 (89%)	280 (9%)	54 (2%)	15	58

All 20 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
2	B	42	LEU	9
2	B	44	TYR	7
1	A	164	ILE	6
1	A	148	ASN	5
1	A	135	GLU	3
2	B	74	LYS	3
2	B	113	GLY	3
2	B	68	THR	3
2	B	48	ASP	2
2	B	114	ALA	2

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Mol	Chain	Res	Type	Models (Total)
2	B	67	ILE	2
2	B	109	LEU	1
2	B	78	TYR	1
1	A	136	ARG	1
2	B	46	THR	1
2	B	40	GLY	1
2	B	39	VAL	1
2	B	87	ALA	1
2	B	76	ARG	1
2	B	75	SER	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	65/80 (81%)	64±1 (98±1%)	1±1 (2±1%)	64 94
2	B	64/87 (74%)	62±1 (97±2%)	2±1 (3±2%)	52 90
All	All	2580/3340 (77%)	2514 (97%)	66 (3%)	57 92

All 30 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)
2	B	56	GLU	8
2	B	62	GLU	7
1	A	107	ILE	6
2	B	76	ARG	4
1	A	106	ASN	3
2	B	46	THR	3
1	A	128	ASP	3
1	A	109	PHE	3
1	A	130	GLU	2
2	B	95	ASP	2
1	A	138	SER	2
1	A	110	LYS	2
2	B	86	ARG	2
2	B	45	HIS	2

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Mol	Chain	Res	Type	Models (Total)
2	B	115	LYS	2
2	B	36	LYS	1
1	A	167	ARG	1
2	B	111	TYR	1
2	B	67	ILE	1
2	B	78	TYR	1
1	A	111	TYR	1
1	A	136	ARG	1
2	B	50	THR	1
1	A	172	ASN	1
2	B	74	LYS	1
2	B	49	LYS	1
1	A	112	ARG	1
2	B	84	LYS	1
1	A	147	GLN	1
2	B	44	TYR	1

6.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers	Suiteness
3	C	11/12 (92%)	6±1 (52±14%)	2±1 (14±9%)	0.12±0.04
All	All	220/240 (92%)	114 (52%)	30 (14%)	0.12

The overall RNA backbone suiteness is 0.12.

All unique RNA backbone outliers are listed below:

Mol	Chain	Res	Type	Models (Total)
3	C	3	C	20
3	C	8	U	20
3	C	7	G	19
3	C	12	C	11
3	C	6	G	10
3	C	11	G	9
3	C	9	G	7
3	C	5	U	5
3	C	10	U	5
3	C	2	G	5
3	C	4	A	3

All unique RNA pucker outliers are listed below:

Mol	Chain	Res	Type	Models (Total)
3	C	3	C	9
3	C	6	G	7
3	C	7	G	5
3	C	8	U	4
3	C	9	G	3
3	C	5	U	1
3	C	10	U	1

6.4 Non-standard residues in protein, DNA, RNA chains

There are no non-standard protein/DNA/RNA residues in this entry.

6.5 Carbohydrates

There are no carbohydrates in this entry.

6.6 Ligand geometry

There are no ligands in this entry.

6.7 Other polymers

There are no such molecules in this entry.

6.8 Polymer linkage issues

There are no chain breaks in this entry.

7 Chemical shift validation

The completeness of assignment taking into account all chemical shift lists is 72% for the well-defined parts and 64% for the entire structure.

7.1 Chemical shift list 1

File name: 2mgz_cs.str

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	949
Number of shifts mapped to atoms	949
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

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	81	-0.26 ± 0.12	None needed (< 0.5 ppm)
$^{13}C_{\beta}$	78	0.18 ± 0.10	None needed (< 0.5 ppm)
$^{13}C'$	0	—	—
^{15}N	78	0.32 ± 0.51	None needed (< 0.5 ppm)

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 36%, i.e. 763 atoms were assigned a chemical shift out of a possible 2131. 1 out of 20 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	290/756 (38%)	145/301 (48%)	73/308 (24%)	72/147 (49%)
Sidechain	410/990 (41%)	252/579 (44%)	146/357 (41%)	12/54 (22%)

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	Total	^{1}H	^{13}C	^{15}N
Aromatic	63/160 (39%)	35/87 (40%)	28/70 (40%)	0/3 (0%)
Overall	763/2131 (36%)	432/1096 (39%)	247/814 (30%)	84/221 (38%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 32%, i.e. 847 atoms were assigned a chemical shift out of a possible 2681. 1 out of 27 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	318/973 (33%)	159/387 (41%)	81/398 (20%)	78/188 (41%)
Sidechain	462/1316 (35%)	285/772 (37%)	163/466 (35%)	14/78 (18%)
Aromatic	67/167 (40%)	37/91 (41%)	30/72 (42%)	0/4 (0%)
Overall	847/2681 (32%)	481/1379 (35%)	274/1015 (27%)	92/287 (32%)

7.1.4 Statistically unusual chemical shifts (i)

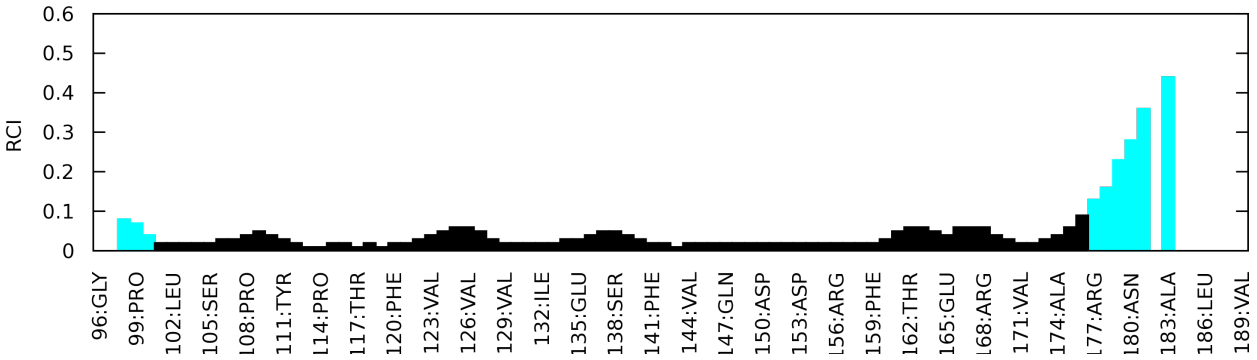
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

Mol	Chain	Res	Type	Atom	Shift, *ppm*	Expected range, *ppm*	Z-score
1	A	168	ARG	NE	110.36	92.63 – 76.73	16.2
1	A	115	ASP	HB3	1.15	4.07 – 1.27	-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.

Random coil index (RCI) for chain A:



7.2 Chemical shift list 2

File name: 2mgz_cs.str

Chemical shift list name: *assigned_chem_shift_list_2*

7.2.1 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	967
Number of shifts mapped to atoms	967
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	4

7.2.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	85	-0.14 ± 0.28	None needed (< 0.5 ppm)
$^{13}C_{\beta}$	77	-0.03 ± 0.22	None needed (< 0.5 ppm)
$^{13}C'$	0	—	—
^{15}N	82	0.52 ± 0.56	None needed (imprecise)

7.2.3 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 37%, i.e. 778 atoms were assigned a chemical shift out of a possible 2131. 2 out of 20 assigned methyl groups (LEU and VAL) were assigned

stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	302/756 (40%)	152/301 (50%)	76/308 (25%)	74/147 (50%)
Sidechain	400/990 (40%)	248/579 (43%)	145/357 (41%)	7/54 (13%)
Aromatic	76/160 (48%)	41/87 (47%)	35/70 (50%)	0/3 (0%)
Overall	778/2131 (37%)	441/1096 (40%)	256/814 (31%)	81/221 (37%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 32%, i.e. 865 atoms were assigned a chemical shift out of a possible 2681. 2 out of 27 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	336/973 (35%)	169/387 (44%)	85/398 (21%)	82/188 (44%)
Sidechain	453/1316 (34%)	282/772 (37%)	161/466 (35%)	10/78 (13%)
Aromatic	76/167 (46%)	41/91 (45%)	35/72 (49%)	0/4 (0%)
Overall	865/2681 (32%)	492/1379 (36%)	281/1015 (28%)	92/287 (32%)

7.2.4 Statistically unusual chemical shifts (i)

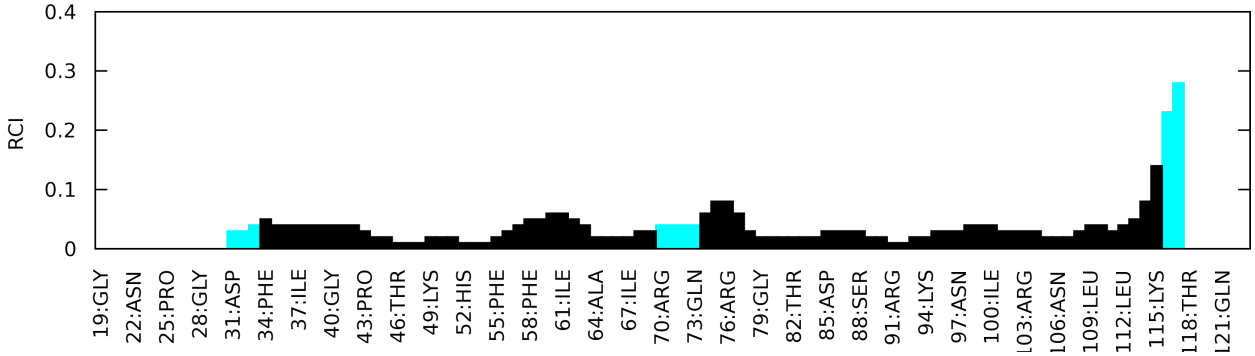
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

Mol	Chain	Res	Type	Atom	Shift, *ppm*	Expected range, *ppm*	Z-score
2	B	103	ARG	NE	125.14	92.63 – 76.73	25.4
2	B	86	ARG	NE	123.78	92.63 – 76.73	24.6
2	B	57	GLN	HG2	0.18	3.67 – 0.97	-7.9
2	B	92	ALA	HA	1.95	6.46 – 2.06	-5.2

7.2.5 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 B:


RCI
0.4
0.3
0.2
0.1
0
19:GLY
22:ASN
25:PRO
28:GLY
31:ASP
34:PHE
37:ILE
40:GLY
43:PRO
46:THR
49:LYS
52:HIS
55:PHE
58:PHE
61:ILE
64:ALA
67:ILE
70:ARG
73:GLN
76:ARG
79:GLY
82:THR
85:ASP
88:SER
91:ARG
94:LYS
97:ASN
100:ILE
103:ARG
106:ASN
109:LEU
112:LEU
115:LYS
118:THR
121:GLN