



Full wwPDB NMR Structure Validation Report ⓘ

Apr 16, 2023 – 08:04 AM EDT

PDB ID : 8B8S
BMRB ID : 34761
Title : Solution structure of tandem RRM1 and RRM2 domains of yeast NPL3
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Deposited on : 2022-10-04

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We welcome your comments at validation@mail.wwpdb.org

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<https://www.wwpdb.org/validation/2017/NMRValidationReportHelp>

with specific help available everywhere you see the ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
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) : 2.32.2

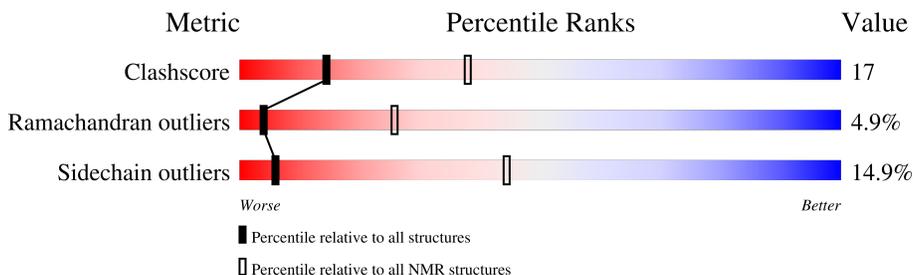
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR, SOLUTION SCATTERING

The overall completeness of chemical shifts assignment is 74%.

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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	161	

2 Ensemble composition and analysis

This entry contains 10 models. Model 6 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:124-A:193 (70)	0.03	10
2	A:197-A:276 (80)	0.07	6

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 1 clusters and 4 single-model clusters were found.

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

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 2542 atoms, of which 1257 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Serine/arginine (SR)-type shuttling mRNA binding protein NPL3.

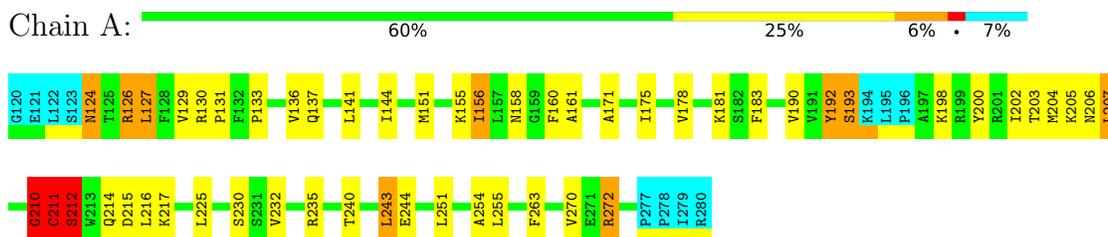
Mol	Chain	Residues	Atoms					Trace	
			Total	C	H	N	O		S
1	A	161	2542	814	1257	215	253	3	0

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: Serine/arginine (SR)-type shuttling mRNA binding protein NPL3

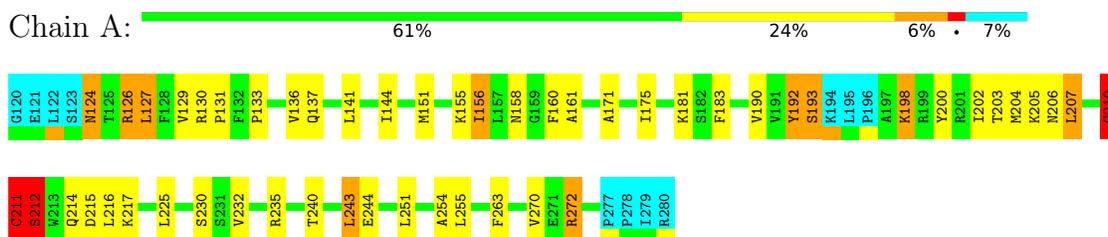


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

- Molecule 1: Serine/arginine (SR)-type shuttling mRNA binding protein NPL3



4.2.2 Score per residue for model 2

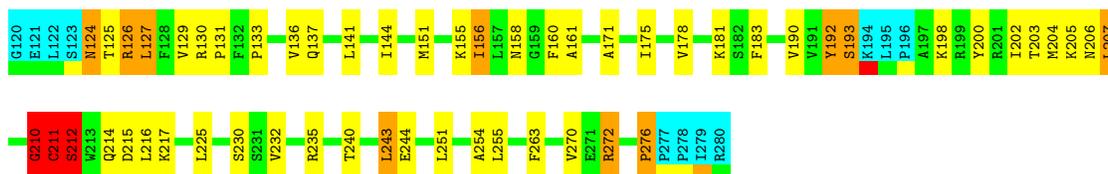
- Molecule 1: Serine/arginine (SR)-type shuttling mRNA binding protein NPL3





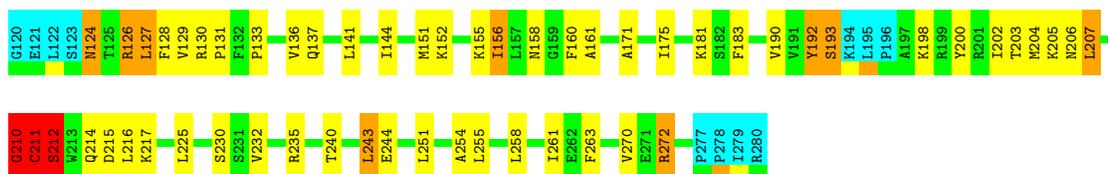
4.2.3 Score per residue for model 3

- Molecule 1: Serine/arginine (SR)-type shuttling mRNA binding protein NPL3



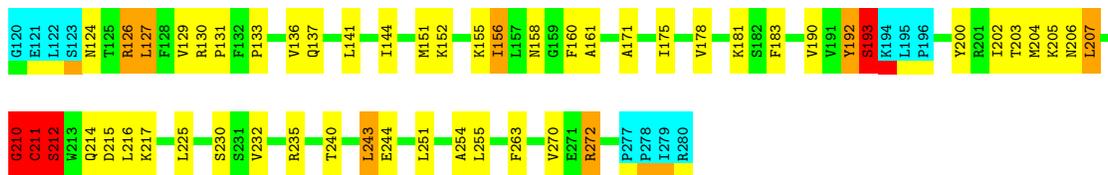
4.2.4 Score per residue for model 4

- Molecule 1: Serine/arginine (SR)-type shuttling mRNA binding protein NPL3



4.2.5 Score per residue for model 5

- Molecule 1: Serine/arginine (SR)-type shuttling mRNA binding protein NPL3



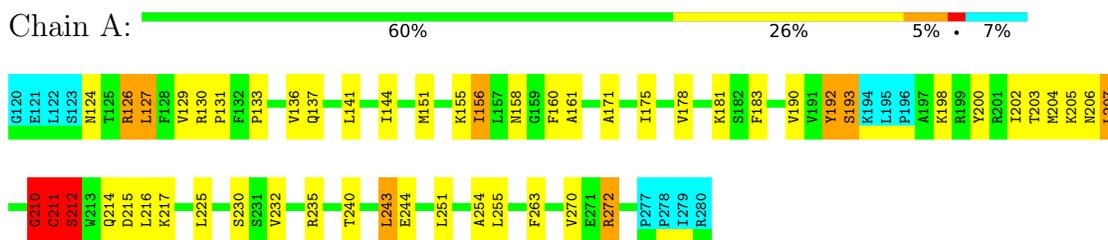
4.2.6 Score per residue for model 6 (medoid)

- Molecule 1: Serine/arginine (SR)-type shuttling mRNA binding protein NPL3



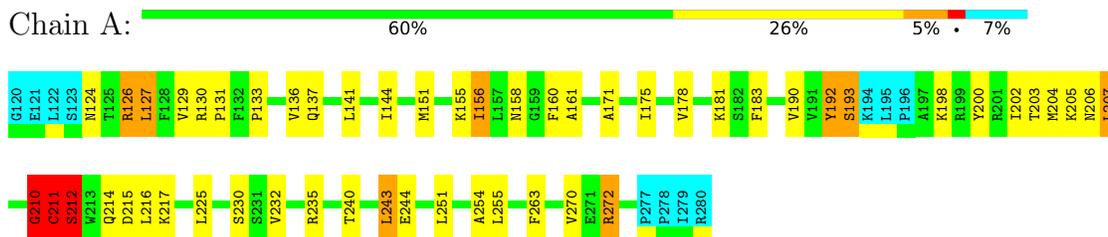
4.2.7 Score per residue for model 7

- Molecule 1: Serine/arginine (SR)-type shuttling mRNA binding protein NPL3



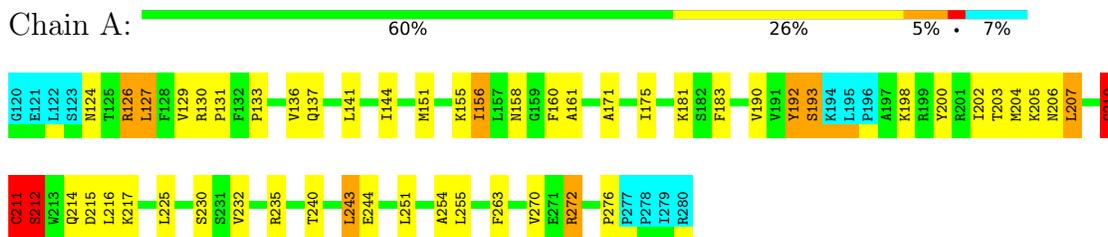
4.2.8 Score per residue for model 8

- Molecule 1: Serine/arginine (SR)-type shuttling mRNA binding protein NPL3



4.2.9 Score per residue for model 9

- Molecule 1: Serine/arginine (SR)-type shuttling mRNA binding protein NPL3



4.2.10 Score per residue for model 10

- Molecule 1: Serine/arginine (SR)-type shuttling mRNA binding protein NPL3



5 Refinement protocol and experimental data overview

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
CNS	refinement	1.21

The following table shows chemical shift validation statistics as aggregates over all chemical shift files. Detailed validation can be found in section 7 of this report.

Chemical shift file(s)	working_cs.cif
Number of chemical shift lists	1
Total number of shifts	1610
Number of shifts mapped to atoms	1610
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	74%

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	0.29±0.01	0±0/1225 (0.0± 0.0%)	0.43±0.00	2±0/1659 (0.1± 0.0%)
All	All	0.29	0/12250 (0.0%)	0.43	20/16590 (0.1%)

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	1.0±0.0
All	All	0	10

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(°)	Ideal(°)	Models	
								Worst	Total
1	A	211	CYS	C-N-CA	7.35	140.06	121.70	2	10
1	A	210	GLY	O-C-N	-5.45	113.98	122.70	2	10

There are no chirality outliers.

All unique planar outliers are listed below.

Mol	Chain	Res	Type	Group	Models (Total)
1	A	210	GLY	Mainchain	10

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	1200	1161	1160	40±1
All	All	12000	11610	11600	405

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 17.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:127:LEU:HD21	1:A:171:ALA:HB1	0.93	1.40	2	10
1:A:210:GLY:O	1:A:211:CYS:C	0.90	2.09	10	10
1:A:216:LEU:HD13	1:A:243:LEU:HD23	0.88	1.46	4	10
1:A:225:LEU:HD22	1:A:254:ALA:HB2	0.76	1.57	1	10
1:A:211:CYS:O	1:A:215:ASP:OD2	0.76	2.04	9	10
1:A:127:LEU:HD22	1:A:175:ILE:HD11	0.70	1.63	1	10
1:A:141:LEU:HD11	1:A:156:ILE:HG23	0.70	1.64	5	10
1:A:211:CYS:C	1:A:215:ASP:OD2	0.65	2.35	7	10
1:A:200:TYR:C	1:A:251:LEU:HD13	0.63	2.14	6	10
1:A:202:ILE:HG21	1:A:255:LEU:HD12	0.62	1.71	10	10
1:A:210:GLY:O	1:A:211:CYS:O	0.61	2.19	7	10
1:A:202:ILE:HG22	1:A:272:ARG:CA	0.59	2.28	8	10
1:A:211:CYS:O	1:A:212:SER:OG	0.59	2.19	3	10
1:A:127:LEU:HD22	1:A:175:ILE:CD1	0.59	2.28	10	10
1:A:192:TYR:O	1:A:193:SER:C	0.59	2.40	10	7
1:A:126:ARG:HB3	1:A:193:SER:HB2	0.58	1.74	8	3
1:A:129:VAL:HB	1:A:161:ALA:HB3	0.57	1.76	7	10
1:A:204:MET:HG2	1:A:270:VAL:HG12	0.57	1.77	4	10
1:A:127:LEU:HD21	1:A:171:ALA:CB	0.56	2.26	4	10
1:A:216:LEU:HD11	1:A:230:SER:HB2	0.56	1.78	8	10
1:A:126:ARG:C	1:A:127:LEU:HD23	0.55	2.23	1	10
1:A:129:VAL:HG13	1:A:190:VAL:HG22	0.54	1.79	7	10
1:A:216:LEU:HD13	1:A:243:LEU:CD2	0.53	2.30	9	10
1:A:200:TYR:HA	1:A:251:LEU:HD22	0.53	1.81	7	10
1:A:205:LYS:HD2	1:A:240:THR:HG22	0.53	1.81	1	10
1:A:126:ARG:HB3	1:A:193:SER:HB3	0.52	1.81	9	3
1:A:202:ILE:HG22	1:A:272:ARG:HA	0.52	1.82	9	10
1:A:127:LEU:HD22	1:A:175:ILE:CG1	0.52	2.35	1	10
1:A:175:ILE:HD13	1:A:192:TYR:CD2	0.49	2.42	7	10
1:A:144:ILE:HD11	1:A:183:PHE:CE2	0.49	2.43	3	10
1:A:141:LEU:CD1	1:A:156:ILE:HG23	0.49	2.37	4	10

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:216:LEU:HD12	1:A:217:LYS:N	0.49	2.23	3	10
1:A:136:VAL:O	1:A:136:VAL:HG13	0.47	2.10	9	10
1:A:202:ILE:HD12	1:A:202:ILE:O	0.46	2.11	5	10
1:A:216:LEU:HD11	1:A:230:SER:CB	0.45	2.42	6	10
1:A:207:LEU:HD21	1:A:240:THR:HA	0.44	1.89	3	10
1:A:127:LEU:CD2	1:A:175:ILE:HD11	0.44	2.41	8	9
1:A:144:ILE:HG23	1:A:181:LYS:NZ	0.44	2.28	7	10
1:A:255:LEU:HA	1:A:270:VAL:HG21	0.44	1.90	4	10
1:A:204:MET:HB3	1:A:207:LEU:HD22	0.43	1.91	8	10
1:A:130:ARG:CB	1:A:131:PRO:HD2	0.43	2.44	9	10
1:A:178:VAL:CG1	1:A:190:VAL:HG21	0.41	2.46	7	7
1:A:202:ILE:CD1	1:A:243:LEU:HD12	0.40	2.47	2	5
1:A:258:LEU:O	1:A:261:ILE:HG23	0.40	2.17	4	1

6.3 Torsion angles [i](#)

6.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all NMR entries. The Analysed column shows the number of residues for which the backbone conformation was analysed and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	150/161 (93%)	131±1 (87±1%)	12±1 (8±1%)	7±1 (5±1%)	4	26
All	All	1500/1610 (93%)	1310 (87%)	117 (8%)	73 (5%)	4	26

All 9 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	126	ARG	10
1	A	133	PRO	10
1	A	158	ASN	10
1	A	193	SER	10
1	A	211	CYS	10
1	A	212	SER	10
1	A	198	LYS	7
1	A	124	ASN	5
1	A	276	PRO	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	132/142 (93%)	112±1 (85±1%)	20±1 (15±1%)	6	44
All	All	1320/1420 (93%)	1123 (85%)	197 (15%)	6	44

All 22 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	124	ASN	10
1	A	127	LEU	10
1	A	137	GLN	10
1	A	151	MET	10
1	A	155	LYS	10
1	A	156	ILE	10
1	A	160	PHE	10
1	A	192	TYR	10
1	A	203	THR	10
1	A	206	ASN	10
1	A	207	LEU	10
1	A	212	SER	10
1	A	214	GLN	10
1	A	232	VAL	10
1	A	235	ARG	10
1	A	243	LEU	10
1	A	244	GLU	10
1	A	263	PHE	10
1	A	272	ARG	10
1	A	152	LYS	3
1	A	198	LYS	2
1	A	193	SER	2

6.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

6.5 Carbohydrates [i](#)

There are no 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 74% for the well-defined parts and 73% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *assigned_chemical_shifts_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	1610
Number of shifts mapped to atoms	1610
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 [i](#)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	157	-0.03 ± 0.13	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	148	-0.27 ± 0.13	None needed (< 0.5 ppm)
$^{13}\text{C}'$	147	0.34 ± 0.10	None needed (< 0.5 ppm)
^{15}N	149	0.17 ± 0.31	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 74%, i.e. 1520 atoms were assigned a chemical shift out of a possible 2053. 0 out of 24 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	723/742 (97%)	292/300 (97%)	289/300 (96%)	142/142 (100%)
Sidechain	794/1153 (69%)	641/742 (86%)	140/364 (38%)	13/47 (28%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	3/158 (2%)	2/78 (3%)	0/77 (0%)	1/3 (33%)
Overall	1520/2053 (74%)	935/1120 (83%)	429/741 (58%)	156/192 (81%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 73%, i.e. 1609 atoms were assigned a chemical shift out of a possible 2210. 0 out of 26 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	759/792 (96%)	306/320 (96%)	304/322 (94%)	149/150 (99%)
Sidechain	847/1260 (67%)	686/812 (84%)	148/397 (37%)	13/51 (25%)
Aromatic	3/158 (2%)	2/78 (3%)	0/77 (0%)	1/3 (33%)
Overall	1609/2210 (73%)	994/1210 (82%)	452/796 (57%)	163/204 (80%)

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. 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:

