



Full wwPDB NMR Structure Validation Report ⓘ

Apr 27, 2016 – 04:50 AM BST

PDB ID : 2MZU
Title : Extending the eNOE data set of large proteins by evaluation of NOEs with unresolved diagonals
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Deposited on : 2015-02-24

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 ⓘ symbol.

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

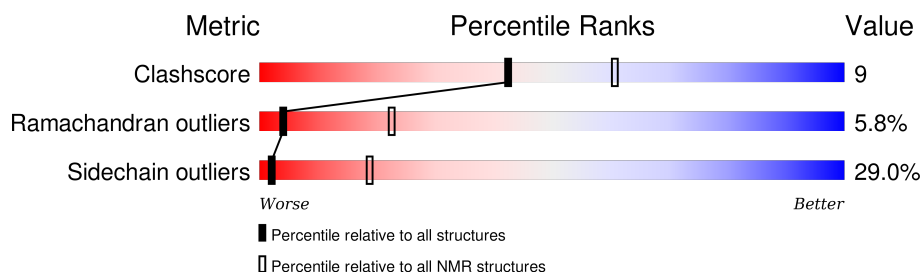
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 81%.

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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	165	

2 Ensemble composition and analysis

This entry contains 20 models. Model 2 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *closest to the average*.

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:2-A:64, A:78-A:165 (151)	0.43	2

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 2 single-model clusters were found.

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

3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 2500 atoms, of which 1235 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Peptidyl-prolyl cis-trans isomerase A.

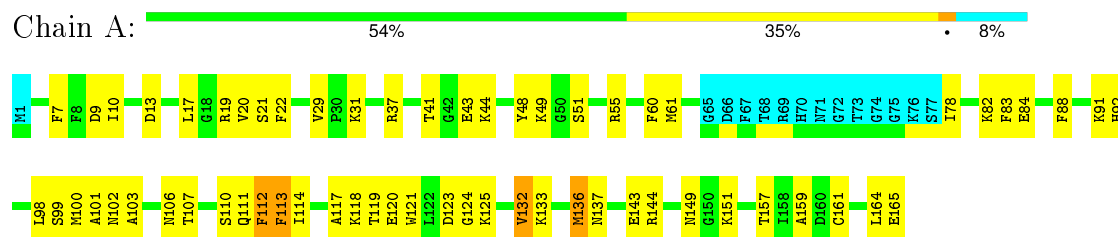
Mol	Chain	Residues	Atoms						Trace
1	A	165	Total	C	H	N	O	S	0
			2500	802	1235	218	236	9	

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: Peptidyl-prolyl cis-trans isomerase A

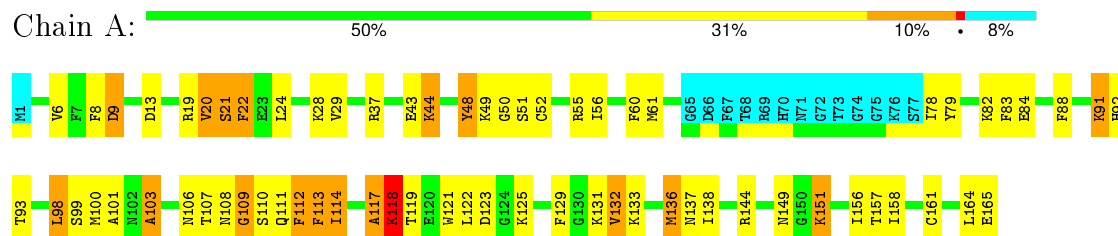


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

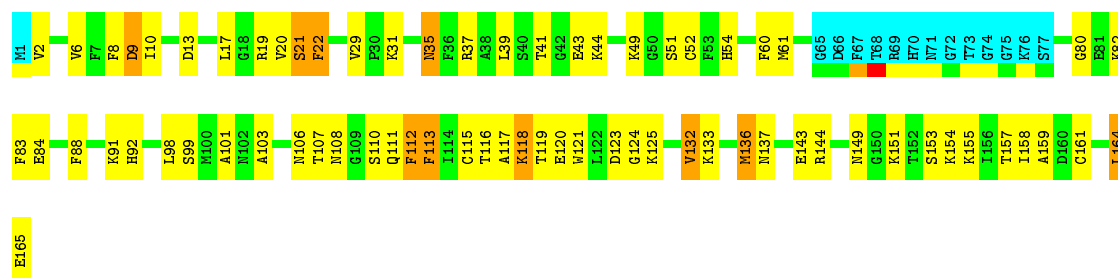
- Molecule 1: Peptidyl-prolyl cis-trans isomerase A



4.2.2 Score per residue for model 2 (medoid)

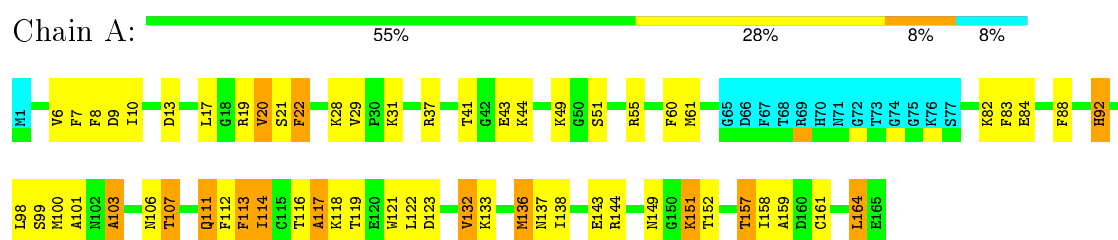
- Molecule 1: Peptidyl-prolyl cis-trans isomerase A





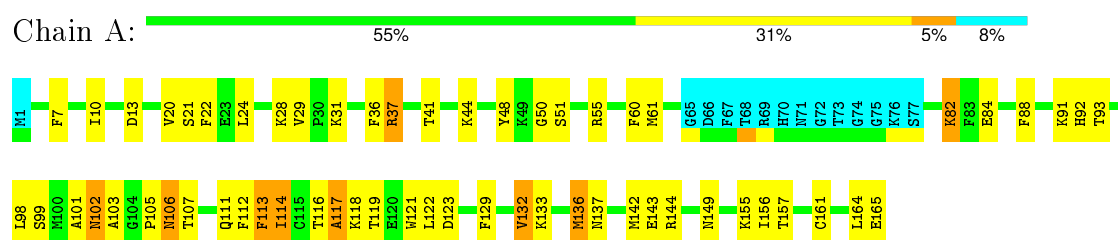
4.2.3 Score per residue for model 3

- Molecule 1: Peptidyl-prolyl cis-trans isomerase A



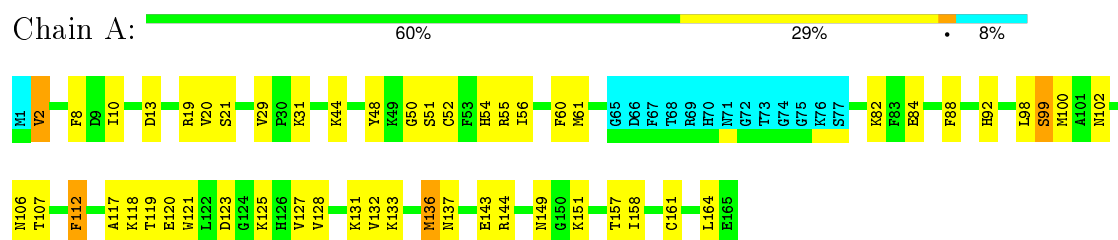
4.2.4 Score per residue for model 4

- Molecule 1: Peptidyl-prolyl cis-trans isomerase A



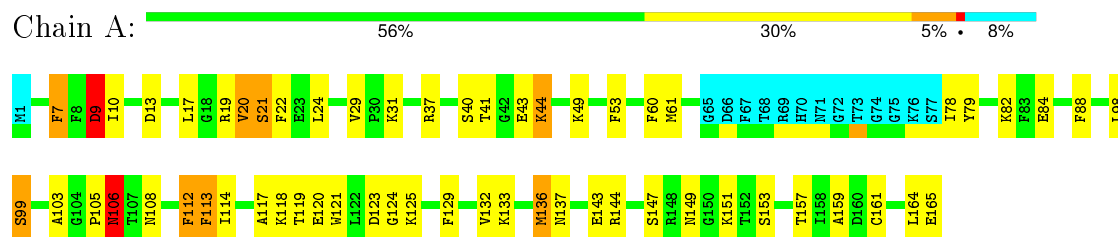
4.2.5 Score per residue for model 5

- Molecule 1: Peptidyl-prolyl cis-trans isomerase A



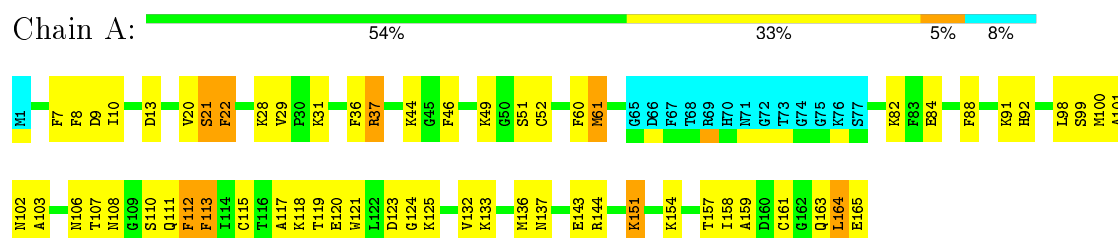
4.2.6 Score per residue for model 6

- Molecule 1: Peptidyl-prolyl cis-trans isomerase A



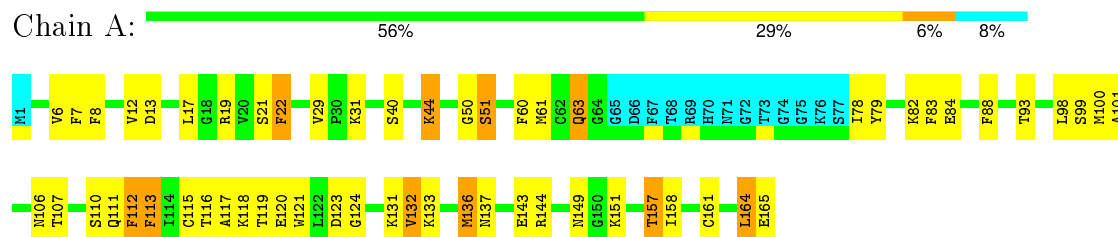
4.2.7 Score per residue for model 7

- Molecule 1: Peptidyl-prolyl cis-trans isomerase A



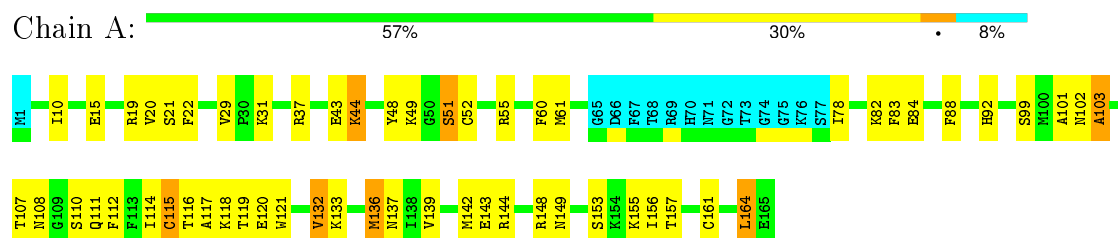
4.2.8 Score per residue for model 8

- Molecule 1: Peptidyl-prolyl cis-trans isomerase A



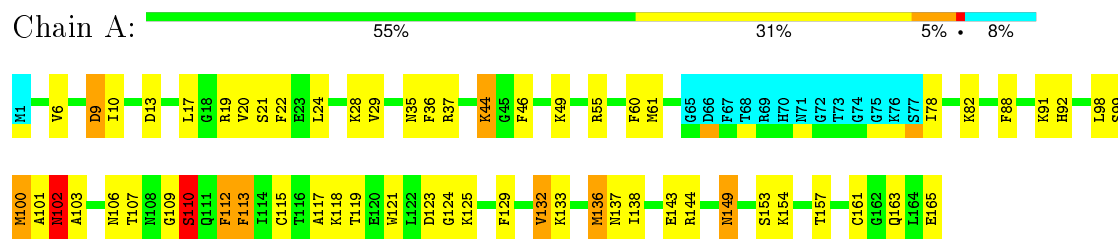
4.2.9 Score per residue for model 9

- Molecule 1: Peptidyl-prolyl cis-trans isomerase A



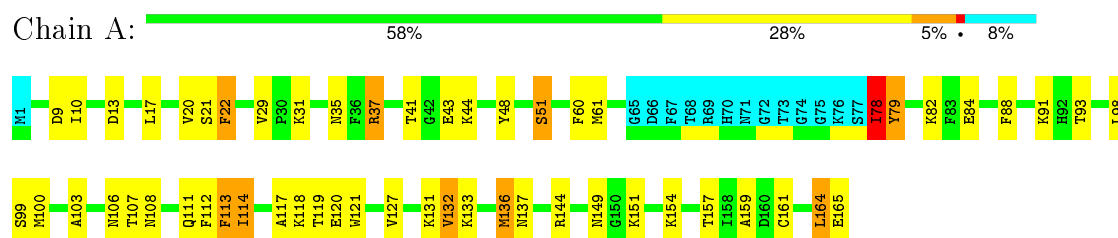
4.2.10 Score per residue for model 10

- Molecule 1: Peptidyl-prolyl cis-trans isomerase A



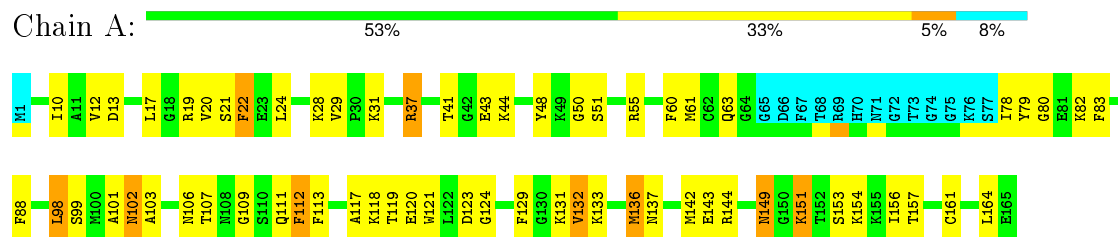
4.2.11 Score per residue for model 11

- Molecule 1: Peptidyl-prolyl cis-trans isomerase A



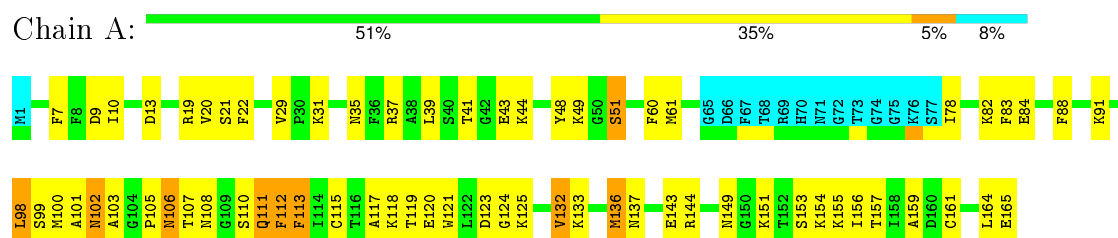
4.2.12 Score per residue for model 12

- Molecule 1: Peptidyl-prolyl cis-trans isomerase A



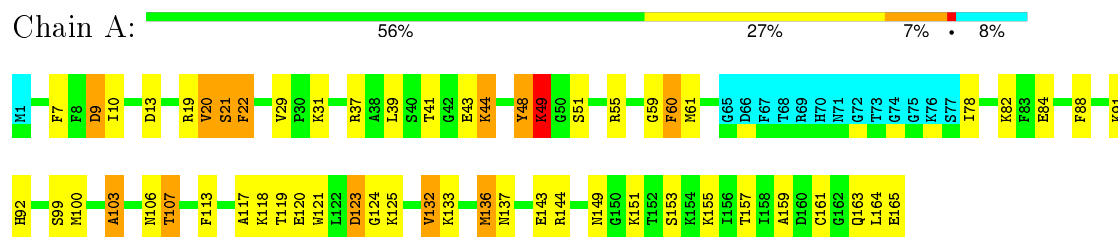
4.2.13 Score per residue for model 13

- Molecule 1: Peptidyl-prolyl cis-trans isomerase A



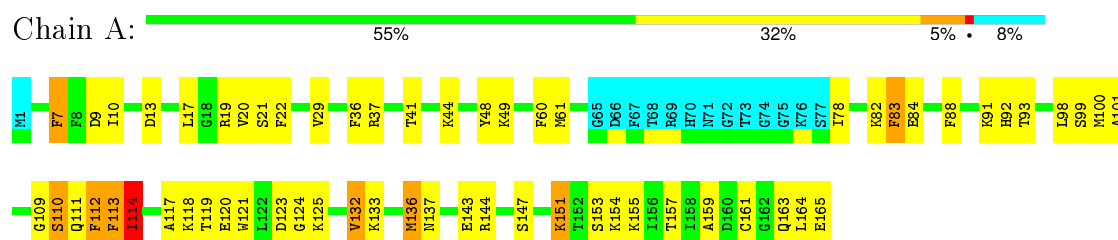
4.2.14 Score per residue for model 14

- Molecule 1: Peptidyl-prolyl cis-trans isomerase A



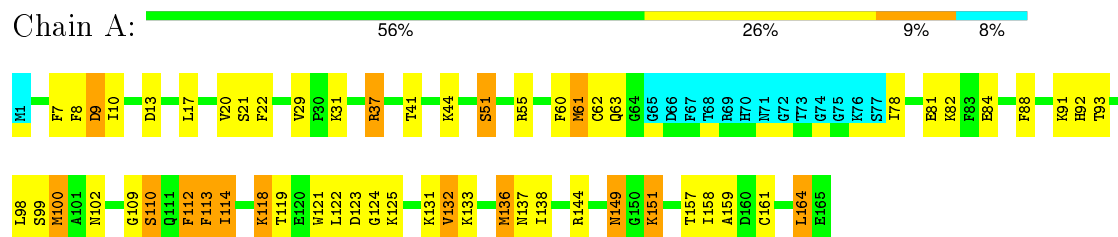
4.2.15 Score per residue for model 15

- Molecule 1: Peptidyl-prolyl cis-trans isomerase A



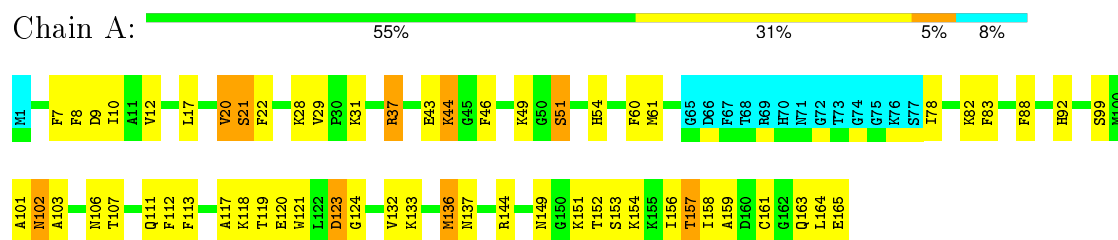
4.2.16 Score per residue for model 16

- Molecule 1: Peptidyl-prolyl cis-trans isomerase A



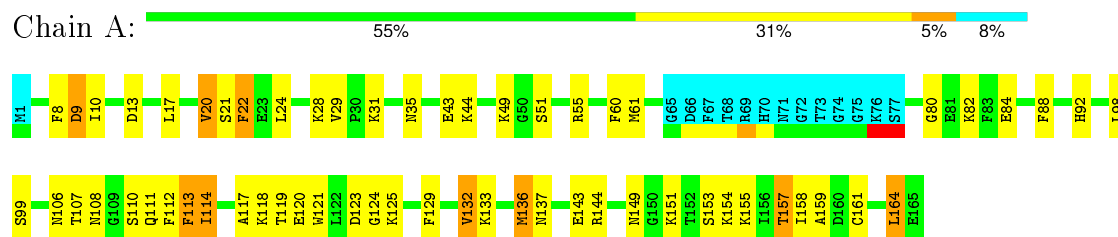
4.2.17 Score per residue for model 17

- Molecule 1: Peptidyl-prolyl cis-trans isomerase A



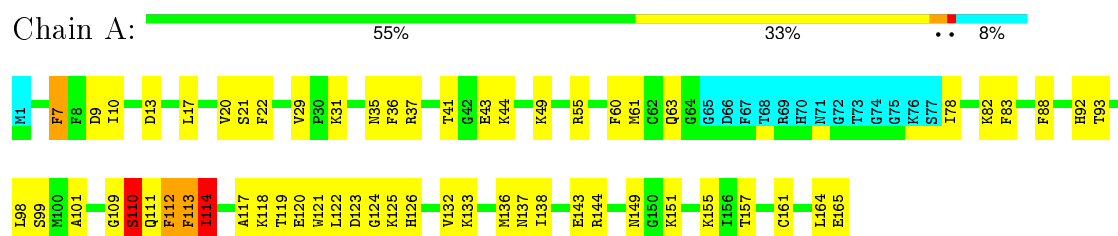
4.2.18 Score per residue for model 18

- Molecule 1: Peptidyl-prolyl cis-trans isomerase A



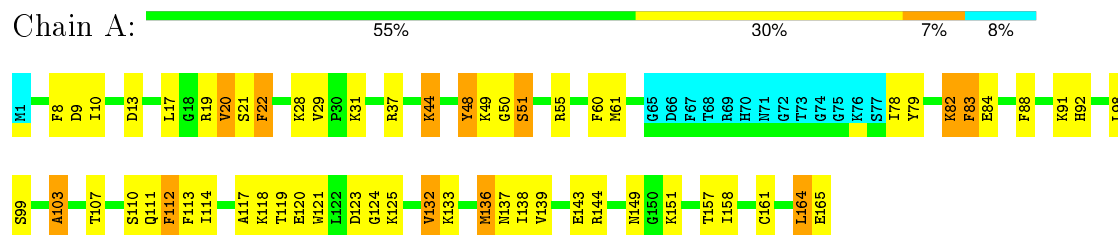
4.2.19 Score per residue for model 19

- Molecule 1: Peptidyl-prolyl cis-trans isomerase A



4.2.20 Score per residue for model 20

- Molecule 1: Peptidyl-prolyl cis-trans isomerase A



5 Refinement protocol and experimental data overview

The models were refined using the following method: *DGSA-distance geometry simulated annealing*.

Of the 20 calculated structures, 20 were deposited, based on the following criterion: *all calculated structures submitted*.

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

Software name	Classification	Version
CYANA	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)	2mzu_cs.str
Number of chemical shift lists	1
Total number of shifts	1786
Number of shifts mapped to atoms	1786
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	81%

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

6 Model quality ⓘ

6.1 Standard geometry ⓘ

There are no covalent bond-length or bond-angle outliers.

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no planarity outliers.

6.2 Too-close contacts ⓘ

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	1164	1143	1143	20±3
All	All	23280	22860	22860	403

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 9.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:101:ALA:HB2	1:A:113:PHE:HB3	0.77	1.55	8	6
1:A:119:THR:HG22	1:A:121:TRP:CZ2	0.75	2.16	1	20
1:A:103:ALA:HB3	1:A:107:THR:OG1	0.73	1.82	10	11
1:A:98:LEU:HD11	1:A:112:PHE:CE2	0.70	2.21	13	1
1:A:117:ALA:O	1:A:119:THR:HG23	0.69	1.86	13	16
1:A:10:ILE:HG23	1:A:156:ILE:HG23	0.69	1.63	13	5
1:A:101:ALA:HB3	1:A:111:GLN:CG	0.69	2.18	19	2
1:A:101:ALA:HB3	1:A:111:GLN:O	0.69	1.88	1	6
1:A:39:LEU:HD21	1:A:78:ILE:HG22	0.69	1.64	14	1
1:A:111:GLN:O	1:A:112:PHE:CB	0.69	2.41	13	1
1:A:48:TYR:O	1:A:49:LYS:C	0.67	2.33	14	1
1:A:10:ILE:HG22	1:A:17:LEU:HD12	0.66	1.67	19	9
1:A:44:LYS:HD2	1:A:78:ILE:HG22	0.65	1.69	8	8
1:A:8:PHE:CD2	1:A:158:ILE:HD13	0.63	2.29	20	8

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:7:PHE:HB3	1:A:164:LEU:HD21	0.63	1.71	14	6
1:A:101:ALA:HB2	1:A:113:PHE:CE2	0.62	2.29	1	1
1:A:112:PHE:CD1	1:A:112:PHE:C	0.61	2.74	15	2
1:A:101:ALA:HB3	1:A:111:GLN:HG2	0.61	1.72	19	2
1:A:41:THR:HG22	1:A:163:GLN:HG3	0.61	1.71	14	1
1:A:91:LYS:O	1:A:93:THR:HG23	0.61	1.95	16	4
1:A:8:PHE:CE2	1:A:158:ILE:HD13	0.60	2.31	5	10
1:A:51:SER:O	1:A:157:THR:HG22	0.60	1.96	17	4
1:A:122:LEU:HD22	1:A:126:HIS:NE2	0.59	2.12	19	1
1:A:9:ASP:HB3	1:A:159:ALA:HB3	0.59	1.75	7	11
1:A:56:ILE:CD1	1:A:156:ILE:HD13	0.59	2.27	1	1
1:A:113:PHE:CD1	1:A:113:PHE:O	0.59	2.56	19	4
1:A:119:THR:OG1	1:A:122:LEU:HD12	0.58	1.98	1	3
1:A:103:ALA:HB3	1:A:107:THR:CB	0.57	2.29	1	4
1:A:35:ASN:O	1:A:39:LEU:HD12	0.57	1.99	13	2
1:A:112:PHE:C	1:A:112:PHE:CD1	0.57	2.77	16	3
1:A:122:LEU:HD13	1:A:126:HIS:CD2	0.57	2.35	19	1
1:A:113:PHE:O	1:A:114:ILE:C	0.56	2.44	15	7
1:A:132:VAL:HG11	1:A:136:MET:HG2	0.56	1.77	17	18
1:A:111:GLN:O	1:A:112:PHE:HB3	0.56	2.00	13	2
1:A:113:PHE:CD1	1:A:113:PHE:C	0.55	2.79	2	6
1:A:113:PHE:O	1:A:113:PHE:CD1	0.55	2.59	15	3
1:A:113:PHE:C	1:A:113:PHE:CD1	0.55	2.78	10	3
1:A:101:ALA:HB2	1:A:113:PHE:CB	0.55	2.32	13	3
1:A:10:ILE:CG2	1:A:17:LEU:HD12	0.55	2.32	15	10
1:A:61:MET:HE3	1:A:62:CYS:O	0.54	2.02	16	1
1:A:113:PHE:N	1:A:113:PHE:CD1	0.54	2.73	1	4
1:A:109:GLY:O	1:A:110:SER:CB	0.53	2.56	10	4
1:A:113:PHE:CD1	1:A:113:PHE:N	0.53	2.75	16	5
1:A:24:LEU:HD23	1:A:129:PHE:O	0.52	2.03	1	6
1:A:113:PHE:CG	1:A:113:PHE:O	0.51	2.63	13	2
1:A:106:ASN:C	1:A:107:THR:HG23	0.50	2.26	8	9
1:A:2:VAL:O	1:A:2:VAL:HG22	0.50	2.07	5	1
1:A:12:VAL:HG23	1:A:17:LEU:HD13	0.50	1.83	12	3
1:A:117:ALA:O	1:A:118:LYS:C	0.49	2.50	1	3
1:A:56:ILE:HD12	1:A:156:ILE:HD13	0.48	1.84	1	1
1:A:12:VAL:CG2	1:A:17:LEU:HD13	0.48	2.38	8	3
1:A:164:LEU:CD2	1:A:164:LEU:N	0.48	2.77	7	9
1:A:101:ALA:HB3	1:A:111:GLN:HB3	0.48	1.84	8	2
1:A:119:THR:HG22	1:A:121:TRP:HZ2	0.48	1.68	3	2
1:A:108:ASN:O	1:A:109:GLY:C	0.48	2.51	1	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:37:ARG:O	1:A:41:THR:HG23	0.48	2.09	19	10
1:A:102:ASN:CG	1:A:109:GLY:HA3	0.48	2.29	10	1
1:A:98:LEU:HD22	1:A:112:PHE:HB2	0.47	1.85	6	1
1:A:131:LYS:O	1:A:132:VAL:C	0.47	2.53	8	5
1:A:78:ILE:O	1:A:78:ILE:HD12	0.47	2.09	12	2
1:A:142:MET:SD	1:A:156:ILE:HG21	0.47	2.49	12	3
1:A:114:ILE:HG21	1:A:139:VAL:CG1	0.47	2.39	20	1
1:A:98:LEU:HD22	1:A:112:PHE:CG	0.46	2.45	5	2
1:A:82:LYS:HD2	1:A:82:LYS:C	0.46	2.31	20	1
1:A:22:PHE:CZ	1:A:114:ILE:HD11	0.46	2.46	19	1
1:A:8:PHE:CD2	1:A:158:ILE:HG21	0.46	2.46	5	2
1:A:63:GLN:CG	1:A:101:ALA:HB1	0.46	2.40	8	1
1:A:164:LEU:N	1:A:164:LEU:CD2	0.46	2.79	1	4
1:A:101:ALA:HB3	1:A:111:GLN:HG3	0.46	1.87	19	1
1:A:21:SER:OG	1:A:22:PHE:N	0.46	2.49	8	18
1:A:113:PHE:O	1:A:113:PHE:CG	0.45	2.69	2	2
1:A:101:ALA:O	1:A:102:ASN:CB	0.45	2.64	17	1
1:A:114:ILE:HG22	1:A:114:ILE:O	0.45	2.10	6	2
1:A:20:VAL:CG2	1:A:138:ILE:HG21	0.45	2.42	1	3
1:A:106:ASN:O	1:A:107:THR:HG23	0.45	2.12	13	2
1:A:98:LEU:HD21	1:A:112:PHE:CD1	0.45	2.47	1	3
1:A:122:LEU:HD13	1:A:126:HIS:HD2	0.45	1.72	19	1
1:A:116:THR:HG22	1:A:139:VAL:CG1	0.45	2.41	9	1
1:A:102:ASN:HB3	1:A:107:THR:O	0.44	2.12	10	1
1:A:17:LEU:HB3	1:A:138:ILE:HD12	0.44	1.89	19	4
1:A:44:LYS:CD	1:A:78:ILE:HG22	0.44	2.41	1	2
1:A:116:THR:O	1:A:117:ALA:HB2	0.44	2.11	3	4
1:A:99:SER:O	1:A:112:PHE:HB3	0.44	2.13	5	1
1:A:92:HIS:CE1	1:A:122:LEU:HD12	0.44	2.48	16	1
1:A:10:ILE:HG13	1:A:20:VAL:HG21	0.44	1.89	15	7
1:A:112:PHE:CZ	1:A:114:ILE:HD12	0.44	2.48	16	1
1:A:111:GLN:O	1:A:111:GLN:CG	0.44	2.65	20	1
1:A:78:ILE:HD12	1:A:78:ILE:O	0.44	2.12	15	1
1:A:10:ILE:CG1	1:A:20:VAL:HG21	0.44	2.43	6	5
1:A:82:LYS:C	1:A:82:LYS:HD2	0.43	2.34	4	1
1:A:98:LEU:HD23	1:A:113:PHE:O	0.43	2.13	6	1
1:A:37:ARG:NH2	1:A:163:GLN:HG2	0.43	2.28	7	2
1:A:105:PRO:O	1:A:107:THR:HG23	0.43	2.13	4	1
1:A:83:PHE:CD1	1:A:83:PHE:N	0.43	2.84	20	2
1:A:105:PRO:O	1:A:106:ASN:CB	0.43	2.67	6	1
1:A:78:ILE:HG13	1:A:79:TYR:CD2	0.43	2.49	11	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:22:PHE:N	1:A:22:PHE:CD1	0.43	2.86	8	3
1:A:123:ASP:O	1:A:124:GLY:C	0.42	2.57	20	14
1:A:7:PHE:HA	1:A:21:SER:HA	0.42	1.91	17	6
1:A:41:THR:HG22	1:A:163:GLN:CG	0.42	2.42	14	1
1:A:143:GLU:HA	1:A:143:GLU:OE1	0.42	2.14	20	1
1:A:105:PRO:O	1:A:106:ASN:C	0.42	2.58	4	2
1:A:100:MET:HE2	1:A:127:VAL:HB	0.42	1.92	11	2
1:A:39:LEU:CD2	1:A:78:ILE:HG22	0.41	2.42	14	1
1:A:100:MET:HE2	1:A:110:SER:HA	0.40	1.93	10	1
1:A:98:LEU:O	1:A:128:VAL:HG22	0.40	2.16	5	1
1:A:56:ILE:HG22	1:A:56:ILE:O	0.40	2.16	5	1
1:A:101:ALA:CB	1:A:111:GLN:O	0.40	2.69	4	1
1:A:44:LYS:CE	1:A:78:ILE:HG22	0.40	2.46	1	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	150/165 (91%)	107±3 (71±2%)	34±3 (23±2%)	9±3 (6±2%)	4	22
All	All	3000/3300 (91%)	2137 (71%)	689 (23%)	174 (6%)	4	22

All 35 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	118	LYS	17
1	A	132	VAL	17
1	A	149	ASN	17
1	A	92	HIS	14
1	A	112	PHE	11
1	A	103	ALA	8
1	A	110	SER	8
1	A	114	ILE	8
1	A	51	SER	8

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Mol	Chain	Res	Type	Models (Total)
1	A	151	LYS	7
1	A	50	GLY	6
1	A	102	ASN	6
1	A	99	SER	5
1	A	9	ASP	5
1	A	123	ASP	3
1	A	80	GLY	3
1	A	46	PHE	3
1	A	117	ALA	3
1	A	79	TYR	3
1	A	52	CYS	2
1	A	2	VAL	2
1	A	48	TYR	2
1	A	55	ARG	2
1	A	109	GLY	2
1	A	111	GLN	2
1	A	49	LYS	1
1	A	106	ASN	1
1	A	115	CYS	1
1	A	61	MET	1
1	A	78	ILE	1
1	A	60	PHE	1
1	A	59	GLY	1
1	A	63	GLN	1
1	A	100	MET	1
1	A	148	ARG	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	123/133 (92%)	87±4 (71±3%)	36±4 (29±3%)	2	19
All	All	2460/2660 (92%)	1747 (71%)	713 (29%)	2	19

All 73 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	88	PHE	20
1	A	144	ARG	20
1	A	82	LYS	20
1	A	133	LYS	20
1	A	161	CYS	20
1	A	61	MET	20
1	A	44	LYS	20
1	A	29	VAL	20
1	A	60	PHE	20
1	A	157	THR	20
1	A	136	MET	20
1	A	137	ASN	20
1	A	13	ASP	18
1	A	113	PHE	18
1	A	31	LYS	17
1	A	151	LYS	16
1	A	99	SER	16
1	A	84	GLU	16
1	A	143	GLU	15
1	A	120	GLU	15
1	A	20	VAL	14
1	A	49	LYS	14
1	A	98	LEU	14
1	A	165	GLU	14
1	A	19	ARG	13
1	A	125	LYS	13
1	A	43	GLU	12
1	A	83	PHE	11
1	A	37	ARG	11
1	A	51	SER	11
1	A	22	PHE	11
1	A	55	ARG	10
1	A	48	TYR	10
1	A	153	SER	10
1	A	112	PHE	10
1	A	164	LEU	9
1	A	154	LYS	9
1	A	28	LYS	9
1	A	100	MET	9
1	A	91	LYS	8
1	A	155	LYS	8
1	A	108	ASN	7
1	A	21	SER	7

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Mol	Chain	Res	Type	Models (Total)
1	A	102	ASN	7
1	A	9	ASP	7
1	A	115	CYS	6
1	A	110	SER	6
1	A	106	ASN	5
1	A	35	ASN	5
1	A	6	VAL	5
1	A	36	PHE	5
1	A	118	LYS	4
1	A	149	ASN	4
1	A	52	CYS	3
1	A	123	ASP	3
1	A	93	THR	3
1	A	54	HIS	3
1	A	63	GLN	3
1	A	7	PHE	3
1	A	111	GLN	3
1	A	114	ILE	3
1	A	79	TYR	3
1	A	107	THR	2
1	A	78	ILE	2
1	A	163	GLN	2
1	A	152	THR	2
1	A	40	SER	2
1	A	147	SER	2
1	A	53	PHE	1
1	A	15	GLU	1
1	A	81	GLU	1
1	A	92	HIS	1
1	A	131	LYS	1

6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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 [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 81% for the well-defined parts and 80% for the entire structure.

7.1 Chemical shift list 1

File name: 2mzu_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	1786
Number of shifts mapped to atoms	1786
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	81

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	164	0.11 ± 0.14	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	138	0.46 ± 0.19	None needed (< 0.5 ppm)
$^{13}\text{C}'$	0	—	—
^{15}N	156	1.10 ± 0.33	Should be applied

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 81%, i.e. 1463 atoms were assigned a chemical shift out of a possible 1811. 10 out of 16 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	588/743 (79%)	295/296 (100%)	150/302 (50%)	143/145 (99%)
Sidechain	772/893 (86%)	496/526 (94%)	261/328 (80%)	15/39 (38%)

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	Total	¹H	¹³C	¹⁵N
Aromatic	103/175 (59%)	78/96 (81%)	24/75 (32%)	1/4 (25%)
Overall	1463/1811 (81%)	869/918 (95%)	435/705 (62%)	159/188 (85%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 80%, i.e. 1574 atoms were assigned a chemical shift out of a possible 1964. 10 out of 16 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Backbone	641/813 (79%)	321/324 (99%)	164/330 (50%)	156/159 (98%)
Sidechain	823/960 (86%)	529/566 (93%)	278/350 (79%)	16/44 (36%)
Aromatic	110/191 (58%)	84/105 (80%)	25/81 (31%)	1/5 (20%)
Overall	1574/1964 (80%)	934/995 (94%)	467/761 (61%)	173/208 (83%)

7.1.4 Statistically unusual chemical shifts ⓘ

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	8	PHE	CD2	2.87	137.34 – 125.84	-111.9
1	A	22	PHE	CD2	8.19	137.34 – 125.84	-107.3
1	A	53	PHE	CE2	1.01	136.81 – 124.71	-107.2
1	A	46	PHE	CE2	1.27	136.81 – 124.71	-107.0
1	A	129	PHE	CE2	2.81	136.81 – 124.71	-105.7
1	A	8	PHE	CD1	2.87	137.63 – 125.43	-105.5
1	A	8	PHE	CE2	5.54	136.81 – 124.71	-103.5
1	A	22	PHE	CD1	8.19	137.63 – 125.43	-101.1
1	A	79	TYR	CE1	2.02	124.14 – 111.74	-93.5
1	A	53	PHE	CE1	1.01	137.92 – 123.42	-89.4
1	A	46	PHE	CE1	1.27	137.92 – 123.42	-89.2
1	A	8	PHE	CE1	5.54	137.92 – 123.42	-86.3
1	A	79	TYR	CE2	2.02	124.68 – 111.18	-85.9
1	A	25	PHE	CZ	2.71	137.04 – 121.44	-81.1
1	A	67	PHE	CZ	3.15	137.04 – 121.44	-80.8
1	A	88	PHE	CZ	8.01	137.04 – 121.44	-77.7
1	A	7	PHE	CD2	42.95	137.34 – 125.84	-77.1
1	A	8	PHE	CZ	9.27	137.04 – 121.44	-76.9
1	A	46	PHE	CD2	43.35	137.34 – 125.84	-76.7
1	A	22	PHE	CE2	41.07	136.81 – 124.71	-74.1
1	A	7	PHE	CD1	42.95	137.63 – 125.43	-72.6
1	A	46	PHE	CD1	43.35	137.63 – 125.43	-72.3

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Mol	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	7	PHE	CE2	53.44	136.81 – 124.71	-63.9
1	A	22	PHE	CE1	41.07	137.92 – 123.42	-61.8
1	A	53	PHE	CZ	41.16	137.04 – 121.44	-56.5
1	A	92	HIS	CE1	5.32	149.70 – 125.30	-54.2
1	A	7	PHE	CE1	53.44	137.92 – 123.42	-53.3
1	A	70	HIS	CD2	2.17	137.40 – 103.40	-34.8
1	A	92	HIS	CD2	8.29	137.40 – 103.40	-33.0
1	A	54	HIS	CD2	8.73	137.40 – 103.40	-32.8
1	A	31	LYS	CG	59.57	30.67 – 19.17	30.1
1	A	68	THR	CG2	52.78	27.15 – 15.95	27.9
1	A	93	THR	CG2	52.57	27.15 – 15.95	27.7
1	A	95	PRO	CG	57.29	32.66 – 21.76	27.6
1	A	32	THR	CG2	52.17	27.15 – 15.95	27.3
1	A	5	THR	CG2	52.13	27.15 – 15.95	27.3
1	A	41	THR	CG2	52.06	27.15 – 15.95	27.2
1	A	31	LYS	CD	59.57	34.86 – 23.06	25.9
1	A	73	THR	CG2	50.55	27.15 – 15.95	25.9
1	A	76	LYS	CD	59.27	34.86 – 23.06	25.7
1	A	55	ARG	CG	58.00	33.23 – 21.23	25.6
1	A	16	PRO	CB	62.11	37.79 – 25.89	25.4
1	A	95	PRO	CB	61.95	37.79 – 25.89	25.3
1	A	100	MET	CG	61.92	38.33 – 25.73	23.7
1	A	56	ILE	CG2	47.56	24.63 – 10.43	21.2
1	A	11	ALA	CB	52.56	28.03 – 9.93	18.6
1	A	32	THR	CB	38.88	78.10 – 61.30	-18.3
1	A	56	ILE	CD1	44.28	21.91 – 5.01	18.2
1	A	107	THR	CB	39.20	78.10 – 61.30	-18.2
1	A	21	SER	CB	36.77	71.24 – 56.34	-18.1
1	A	78	ILE	CD1	44.02	21.91 – 5.01	18.1
1	A	73	THR	CB	40.76	78.10 – 61.30	-17.2
1	A	5	THR	CB	41.14	78.10 – 61.30	-17.0
1	A	69	ARG	CB	61.53	39.81 – 21.51	16.9
1	A	57	ILE	CG1	57.09	36.54 – 18.94	16.7
1	A	77	SER	CB	38.96	71.24 – 56.34	-16.7
1	A	10	ILE	CD1	41.27	21.91 – 5.01	16.5
1	A	34	GLU	CB	57.90	38.65 – 21.35	16.1
1	A	37	ARG	CG	45.21	33.23 – 21.23	15.0
1	A	29	VAL	CG1	40.20	28.40 – 14.60	13.6
1	A	70	HIS	CB	58.43	40.69 – 19.69	13.4
1	A	20	VAL	CG1	37.22	28.40 – 14.60	11.4
1	A	6	VAL	CG1	36.66	28.40 – 14.60	11.0
1	A	12	VAL	CG1	36.14	28.40 – 14.60	10.6

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Mol	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	90	LEU	CD1	41.73	32.77 – 16.57	10.5
1	A	2	VAL	CG1	35.83	28.40 – 14.60	10.4
1	A	20	VAL	CG2	36.85	29.20 – 13.40	9.8
1	A	39	LEU	CD1	40.37	32.77 – 16.57	9.7
1	A	12	VAL	CG2	36.53	29.20 – 13.40	9.6
1	A	24	LEU	CD1	39.82	32.77 – 16.57	9.3
1	A	32	THR	CA	37.68	75.37 – 49.07	-9.3
1	A	98	LEU	CD1	39.58	32.77 – 16.57	9.2
1	A	98	LEU	CD2	39.53	32.60 – 15.60	9.1
1	A	6	VAL	CG2	35.60	29.20 – 13.40	9.0
1	A	29	VAL	CG2	35.55	29.20 – 13.40	9.0
1	A	17	LEU	CD2	39.12	32.60 – 15.60	8.8
1	A	90	LEU	CD2	37.46	32.60 – 15.60	7.9
1	A	76	LYS	HE3	1.51	3.86 – 1.96	-7.4
1	A	108	ASN	HB3	0.92	4.41 – 1.11	-5.6
1	A	31	LYS	HE3	1.86	3.86 – 1.96	-5.5
1	A	39	LEU	HB3	-0.33	3.34 – -0.26	-5.2

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:

