



Full wwPDB NMR Structure Validation Report ⓘ

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PDB ID : 1JBH
Title : Solution structure of cellular retinol binding protein type-I in the ligand-free state
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Deposited on : 2001-06-04

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

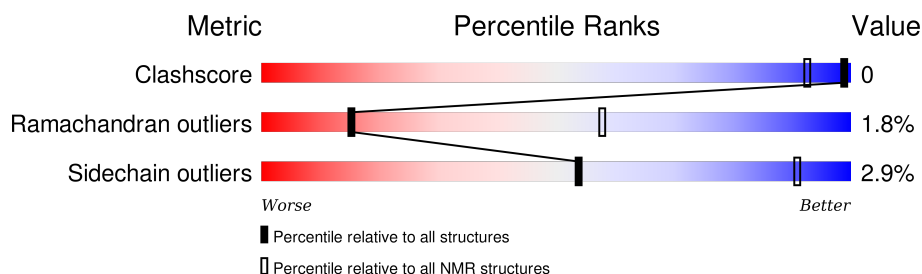
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 58%.

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	135	

2 Ensemble composition and analysis

This entry contains 20 models. Model 8 is the overall representative, medoid model (most similar to other models).

The following residues are included in the computation of the global validation metrics.

Well-defined (core) protein residues			
Well-defined core	Residue range (total)	Backbone RMSD (Å)	Medoid model
1	A:1-A:72, A:82-A:134 (125)	0.36	8

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 5 clusters and 4 single-model clusters were found.

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

3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 2208 atoms, of which 1098 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called CELLULAR RETINOL-BINDING PROTEIN TYPE I.

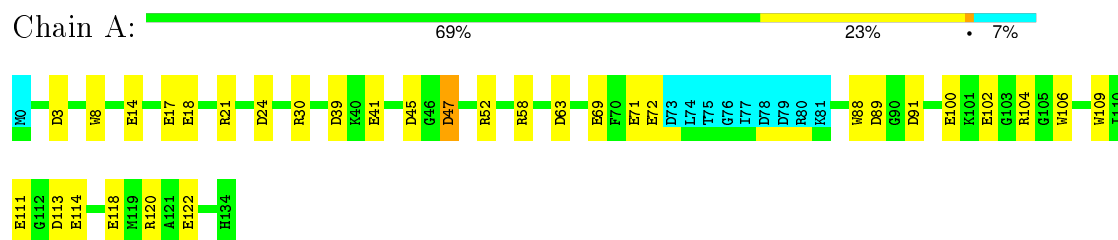
Mol	Chain	Residues	Atoms						Trace
1	A	135	Total	C	H	N	O	S	0
			2208	700	1098	190	211	9	

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: CELLULAR RETINOL-BINDING PROTEIN TYPE I

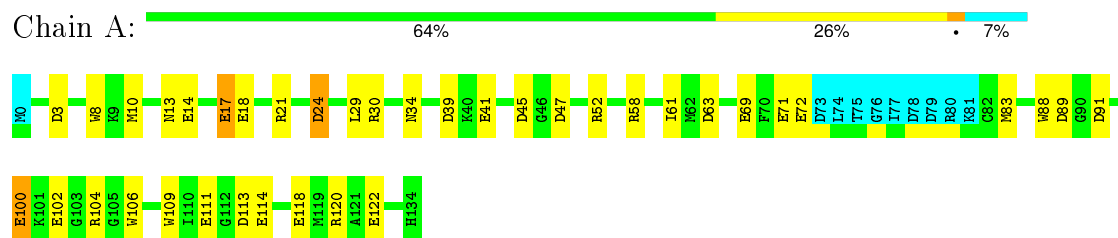


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

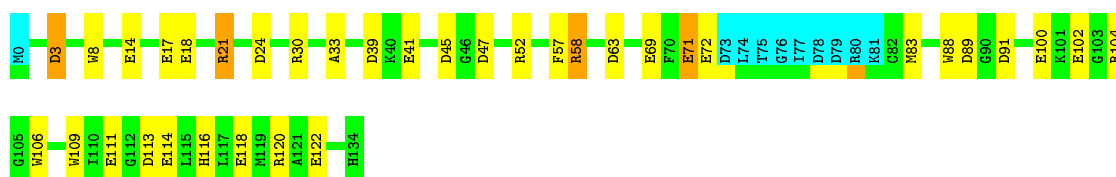
- Molecule 1: CELLULAR RETINOL-BINDING PROTEIN TYPE I



4.2.2 Score per residue for model 2

- Molecule 1: CELLULAR RETINOL-BINDING PROTEIN TYPE I

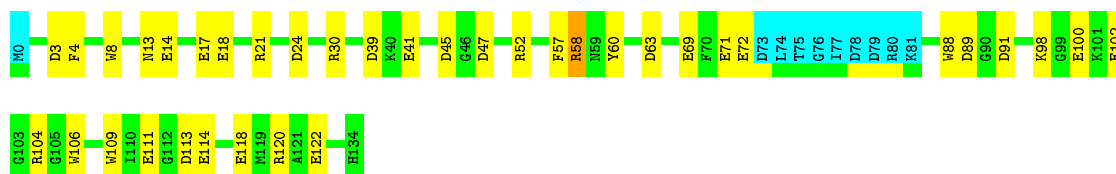




4.2.3 Score per residue for model 3

- Molecule 1: CELLULAR RETINOL-BINDING PROTEIN TYPE I

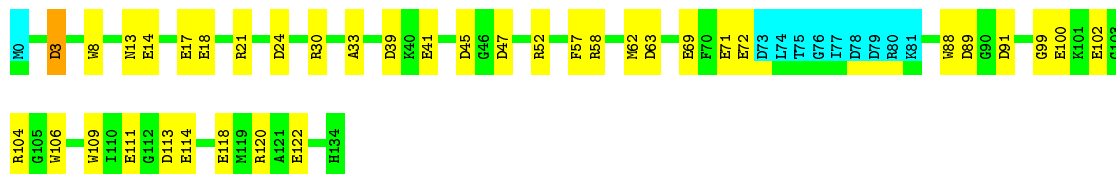
Chain A: 65% 27% 7%



4.2.4 Score per residue for model 4

- Molecule 1: CELLULAR RETINOL-BINDING PROTEIN TYPE I

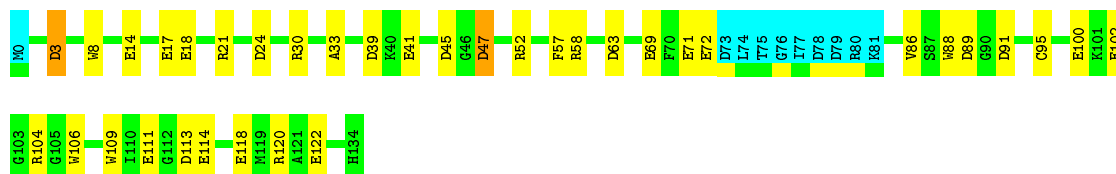
Chain A: 65% 27% 7%



4.2.5 Score per residue for model 5

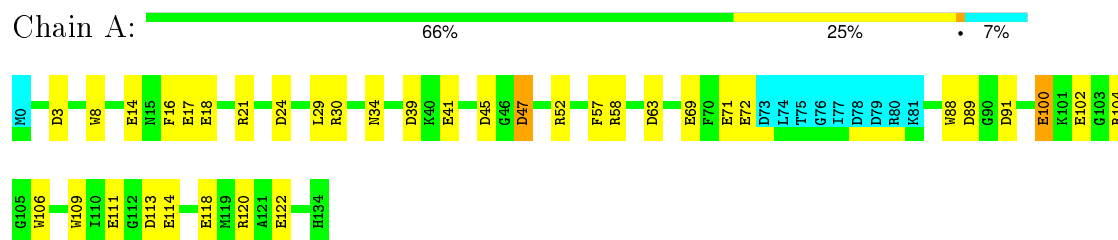
- Molecule 1: CELLULAR RETINOL-BINDING PROTEIN TYPE I

Chain A: 66% 25% 7%



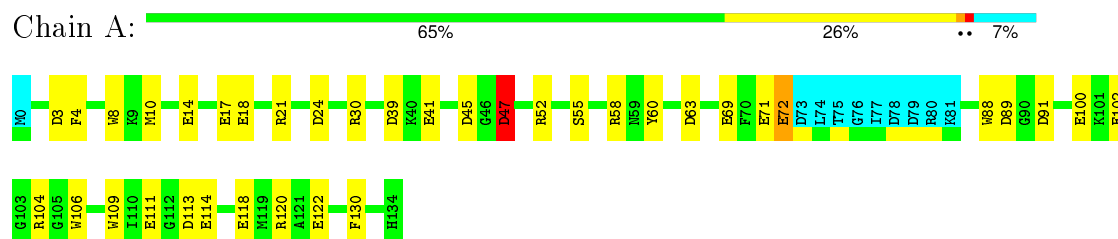
4.2.6 Score per residue for model 6

- Molecule 1: CELLULAR RETINOL-BINDING PROTEIN TYPE I



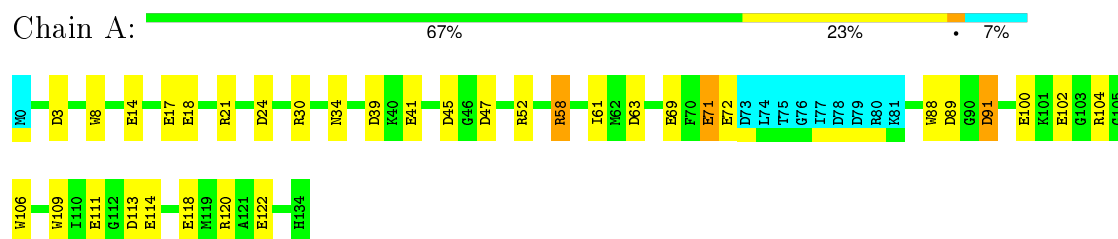
4.2.7 Score per residue for model 7

- Molecule 1: CELLULAR RETINOL-BINDING PROTEIN TYPE I



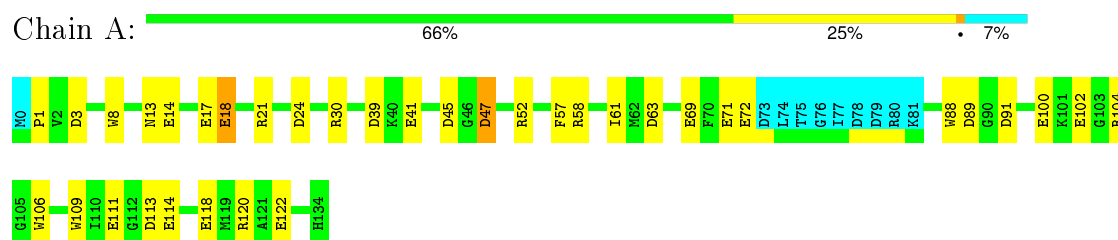
4.2.8 Score per residue for model 8 (medoid)

- Molecule 1: CELLULAR RETINOL-BINDING PROTEIN TYPE I



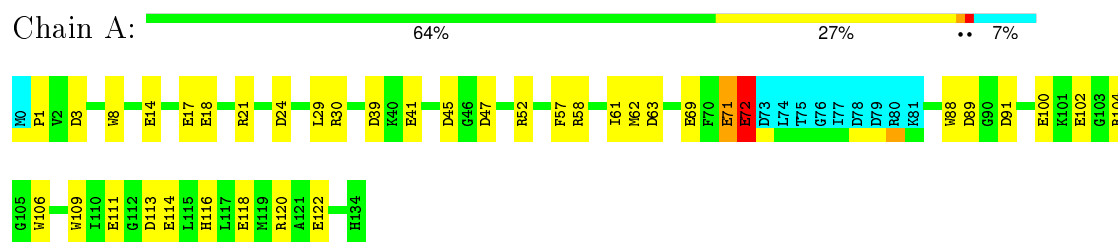
4.2.9 Score per residue for model 9

- Molecule 1: CELLULAR RETINOL-BINDING PROTEIN TYPE I



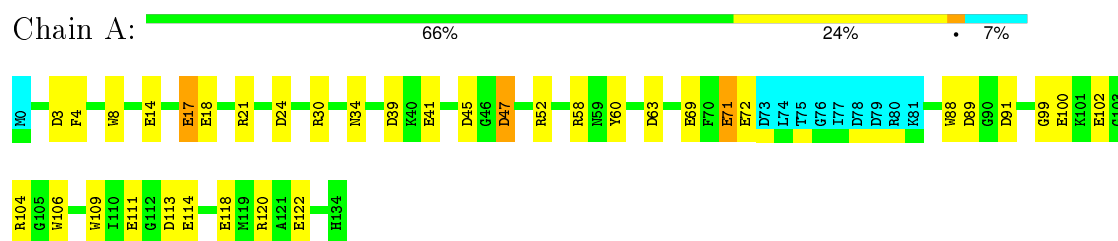
4.2.10 Score per residue for model 10

- Molecule 1: CELLULAR RETINOL-BINDING PROTEIN TYPE I



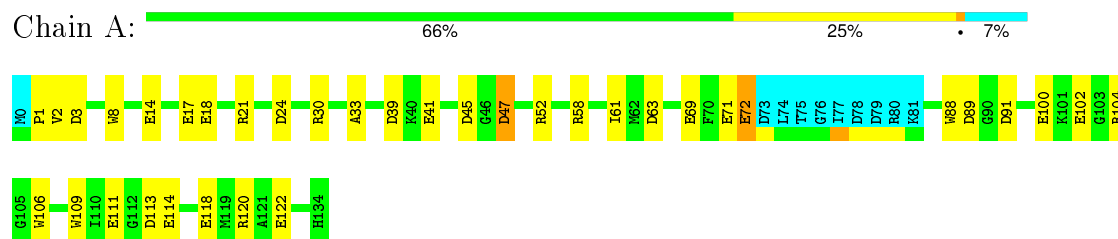
4.2.11 Score per residue for model 11

- Molecule 1: CELLULAR RETINOL-BINDING PROTEIN TYPE I



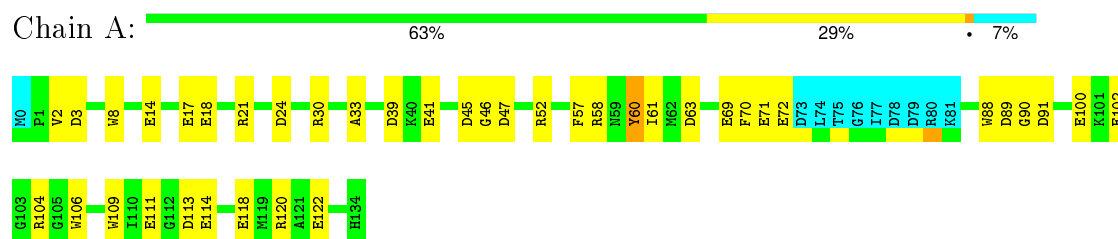
4.2.12 Score per residue for model 12

- Molecule 1: CELLULAR RETINOL-BINDING PROTEIN TYPE I



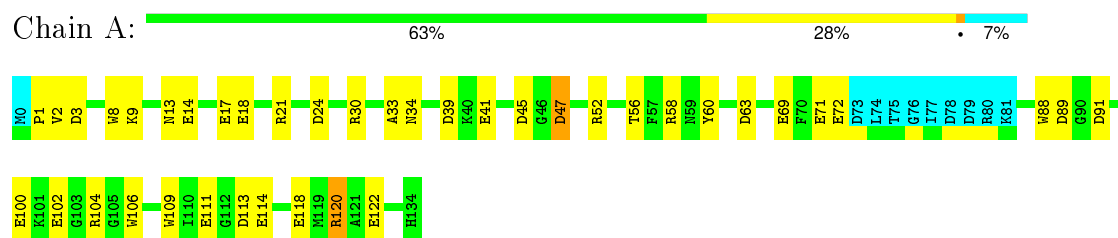
4.2.13 Score per residue for model 13

- Molecule 1: CELLULAR RETINOL-BINDING PROTEIN TYPE I



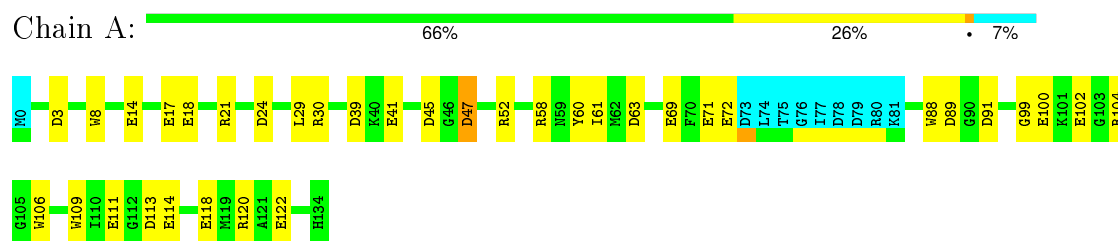
4.2.14 Score per residue for model 14

- Molecule 1: CELLULAR RETINOL-BINDING PROTEIN TYPE I



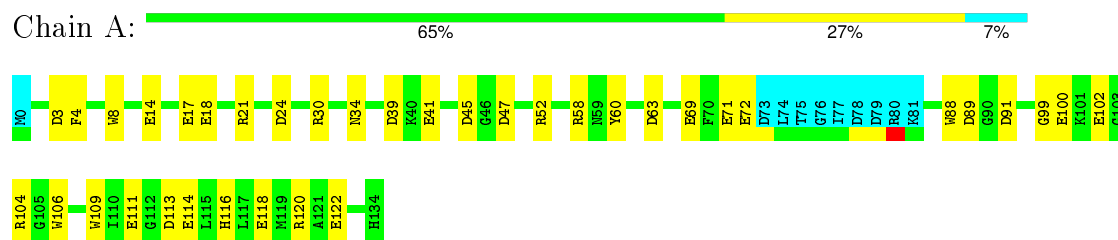
4.2.15 Score per residue for model 15

- Molecule 1: CELLULAR RETINOL-BINDING PROTEIN TYPE I



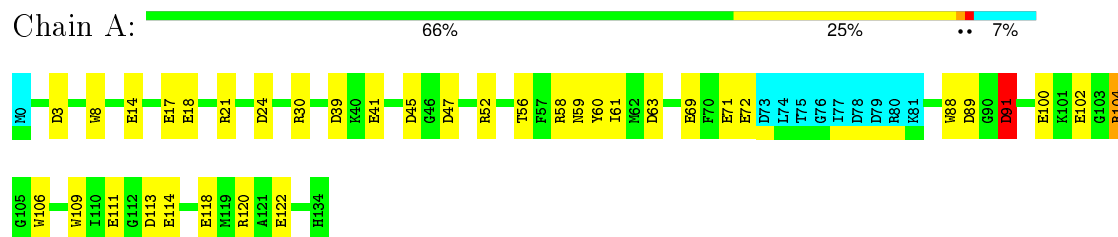
4.2.16 Score per residue for model 16

- Molecule 1: CELLULAR RETINOL-BINDING PROTEIN TYPE I



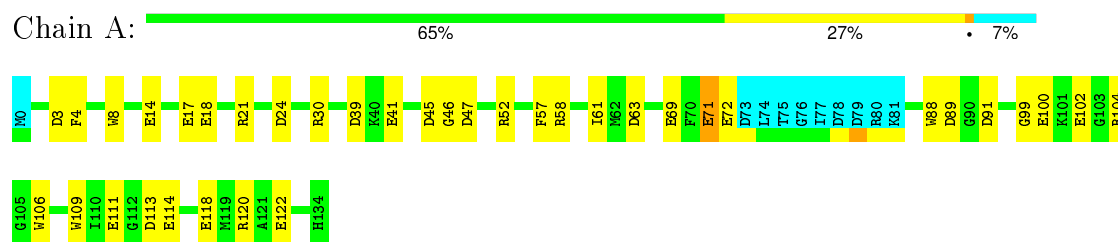
4.2.17 Score per residue for model 17

- Molecule 1: CELLULAR RETINOL-BINDING PROTEIN TYPE I



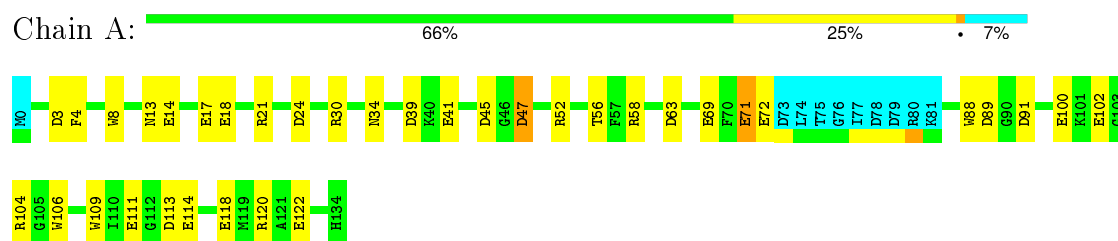
4.2.18 Score per residue for model 18

- Molecule 1: CELLULAR RETINOL-BINDING PROTEIN TYPE I



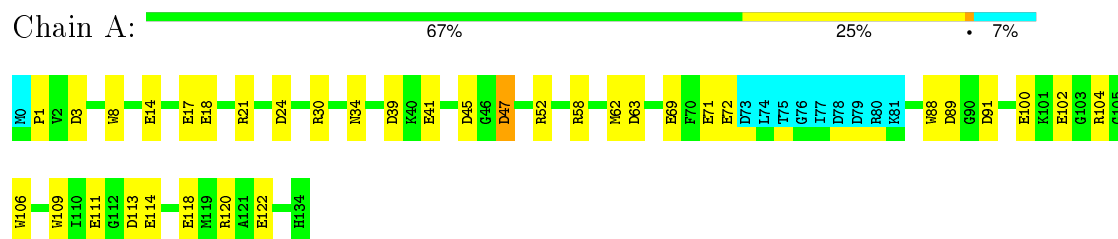
4.2.19 Score per residue for model 19

- Molecule 1: CELLULAR RETINOL-BINDING PROTEIN TYPE I



4.2.20 Score per residue for model 20

- Molecule 1: CELLULAR RETINOL-BINDING PROTEIN TYPE I



5 Refinement protocol and experimental data overview

The models were refined using the following method: *TORSION ANGLE DYNAMICS COMBINED WITH SIMULATED ANNEALING FOLLOWED BY ENERGY MINIMIZATION*.

Of the 100 calculated structures, 20 were deposited, based on the following criterion: *TARGET FUNCTION*.

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

Software name	Classification	Version
DISCOVER	refinement	97
XWINNMR	structure solution	1.3
AURELIA	structure solution	2.5.9
FELIX	structure solution	97
NMR2ST	structure solution	2.05
DYANA	structure solution	1.5

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)	BMRB entry 5319, BMRB entry 5048
Number of chemical shift lists	3
Total number of shifts	2320
Number of shifts mapped to atoms	2291
Number of unparsed shifts	0
Number of shifts with mapping errors	29
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	58%

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

6 Model quality i

6.1 Standard geometry i

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the (average) root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#Z>5	RMSZ	#Z>5
1	A	1.70±0.01	17±1/1052 (1.6±0.1%)	1.57±0.01	32±1/1412 (2.3±0.1%)
All	All	1.70	344/21040 (1.6%)	1.57	649/28240 (2.3%)

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	0.4±0.7
All	All	0	8

All unique bond 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(Å)	Ideal(Å)	Models	
								Worst	Total
1	A	114	GLU	CD-OE2	10.79	1.37	1.25	7	20
1	A	111	GLU	CD-OE2	10.78	1.37	1.25	17	20
1	A	102	GLU	CD-OE2	10.77	1.37	1.25	12	20
1	A	100	GLU	CD-OE2	10.63	1.37	1.25	14	20
1	A	69	GLU	CD-OE2	10.60	1.37	1.25	1	20
1	A	71	GLU	CD-OE2	10.58	1.37	1.25	2	20
1	A	41	GLU	CD-OE2	10.56	1.37	1.25	12	20
1	A	18	GLU	CD-OE2	10.55	1.37	1.25	3	20
1	A	122	GLU	CD-OE2	10.55	1.37	1.25	13	20
1	A	17	GLU	CD-OE2	10.50	1.37	1.25	7	20
1	A	72	GLU	CD-OE2	10.50	1.37	1.25	12	20
1	A	118	GLU	CD-OE2	10.45	1.37	1.25	5	20
1	A	14	GLU	CD-OE2	10.38	1.37	1.25	16	20
1	A	63	ASP	CG-OD2	5.38	1.37	1.25	14	11
1	A	89	ASP	CG-OD2	5.30	1.37	1.25	10	7
1	A	3	ASP	CG-OD2	5.29	1.37	1.25	9	13

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
1	A	47	ASP	CG-OD2	5.23	1.37	1.25	20	8
1	A	39	ASP	CG-OD2	5.23	1.37	1.25	15	10
1	A	91	ASP	CG-OD2	5.18	1.37	1.25	14	6
1	A	45	ASP	CG-OD2	5.15	1.37	1.25	12	10
1	A	24	ASP	CG-OD2	5.11	1.37	1.25	15	10
1	A	113	ASP	CG-OD2	5.11	1.37	1.25	8	9

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	104	ARG	NE-CZ-NH1	9.35	124.97	120.30	9	20
1	A	58	ARG	NE-CZ-NH1	9.33	124.97	120.30	7	20
1	A	30	ARG	NE-CZ-NH1	9.25	124.92	120.30	10	20
1	A	120	ARG	NE-CZ-NH1	9.13	124.86	120.30	4	20
1	A	21	ARG	NE-CZ-NH1	8.98	124.79	120.30	4	20
1	A	52	ARG	NE-CZ-NH1	8.88	124.74	120.30	14	20
1	A	47	ASP	CB-CG-OD2	-7.68	111.39	118.30	15	20
1	A	113	ASP	CB-CG-OD2	-7.68	111.39	118.30	15	20
1	A	91	ASP	CB-CG-OD2	-7.54	111.51	118.30	18	20
1	A	24	ASP	CB-CG-OD1	7.47	125.02	118.30	12	19
1	A	24	ASP	CB-CG-OD2	-7.46	111.58	118.30	12	20
1	A	63	ASP	CB-CG-OD2	-7.45	111.59	118.30	15	20
1	A	113	ASP	CB-CG-OD1	7.40	124.96	118.30	14	20
1	A	39	ASP	CB-CG-OD2	-7.13	111.89	118.30	14	19
1	A	3	ASP	CB-CG-OD2	-7.08	111.93	118.30	20	20
1	A	89	ASP	CB-CG-OD2	-7.05	111.96	118.30	2	20
1	A	60	TYR	CB-CG-CD2	-7.03	116.78	121.00	13	3
1	A	47	ASP	CB-CG-OD1	7.01	124.61	118.30	1	17
1	A	39	ASP	CB-CG-OD1	7.01	124.61	118.30	4	17
1	A	45	ASP	CB-CG-OD2	-7.00	112.00	118.30	2	20
1	A	89	ASP	CB-CG-OD1	6.89	124.50	118.30	2	19
1	A	91	ASP	CB-CG-OD1	6.81	124.43	118.30	18	17
1	A	63	ASP	CB-CG-OD1	6.80	124.42	118.30	15	12
1	A	3	ASP	CB-CG-OD1	6.66	124.29	118.30	16	19
1	A	45	ASP	CB-CG-OD1	6.44	124.09	118.30	14	20
1	A	104	ARG	NE-CZ-NH2	-6.17	117.22	120.30	4	12
1	A	30	ARG	NE-CZ-NH2	-6.04	117.28	120.30	10	19
1	A	88	TRP	CD1-NE1-CE2	-5.94	103.66	109.00	8	20
1	A	58	ARG	NE-CZ-NH2	-5.89	117.35	120.30	3	17
1	A	8	TRP	CD1-NE1-CE2	-5.89	103.70	109.00	19	20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	109	TRP	CD1-NE1-CE2	-5.89	103.70	109.00	3	20
1	A	60	TYR	CB-CG-CD1	5.86	124.51	121.00	13	1
1	A	106	TRP	CD1-NE1-CE2	-5.83	103.75	109.00	3	20
1	A	52	ARG	NE-CZ-NH2	-5.73	117.44	120.30	11	17
1	A	21	ARG	NE-CZ-NH2	-5.67	117.47	120.30	15	14
1	A	120	ARG	NE-CZ-NH2	-5.60	117.50	120.30	4	13
1	A	4	PHE	CB-CG-CD2	-5.40	117.02	120.80	7	6
1	A	4	PHE	CB-CG-CD1	5.08	124.36	120.80	7	4
1	A	116	HIS	CG-ND1-CE1	-5.08	99.10	105.70	10	3
1	A	16	PHE	CB-CG-CD2	-5.07	117.25	120.80	6	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)
1	A	60	TYR	Sidechain	3
1	A	104	ARG	Sidechain	1
1	A	72	GLU	Peptide	1
1	A	90	GLY	Peptide	1
1	A	70	PHE	Sidechain,Peptide	1

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	1031	1016	1005	0±0
All	All	20620	20320	20100	3

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:10:MET:SD	1:A:130:PHE:CZ	0.44	3.11	7	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:86:VAL:HG22	1:A:95:CYS:SG	0.41	2.56	5	1
1:A:10:MET:SD	1:A:13:ASN:OD1	0.41	2.78	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	124/135 (92%)	113±3 (91±2%)	9±2 (8±2%)	2±1 (2±1%)	15	58
All	All	2480/2700 (92%)	2250 (91%)	186 (8%)	44 (2%)	15	58

All 11 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	61	ILE	9
1	A	57	PHE	9
1	A	33	ALA	6
1	A	99	GLY	5
1	A	1	PRO	5
1	A	56	THR	3
1	A	2	VAL	2
1	A	46	GLY	2
1	A	91	ASP	1
1	A	47	ASP	1
1	A	58	ARG	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	112/121 (93%)	109±1 (97±1%)	3±1 (3±1%)	54	91
All	All	2240/2420 (93%)	2176 (97%)	64 (3%)	54	91

All 23 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	47	ASP	10
1	A	34	ASN	8
1	A	71	GLU	6
1	A	13	ASN	5
1	A	29	LEU	4
1	A	72	GLU	3
1	A	62	MET	3
1	A	3	ASP	3
1	A	60	TYR	3
1	A	58	ARG	2
1	A	83	MET	2
1	A	91	ASP	2
1	A	100	GLU	2
1	A	17	GLU	2
1	A	9	LYS	1
1	A	120	ARG	1
1	A	59	ASN	1
1	A	55	SER	1
1	A	98	LYS	1
1	A	2	VAL	1
1	A	21	ARG	1
1	A	18	GLU	1
1	A	24	ASP	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 [i](#)

The completeness of assignment taking into account all chemical shift lists is 58% for the well-defined parts and 58% for the entire structure.

7.1 Chemical shift list 1

File name: BMRB entry 5048

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	1122
Number of shifts mapped to atoms	1122
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	11

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
$^{13}\text{C}_\alpha$	0	—	—
$^{13}\text{C}_\beta$	0	—	—
$^{13}\text{C}'$	0	—	—
^{15}N	125	-1.30 ± 0.29	Should be applied

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 58%, i.e. 928 atoms were assigned a chemical shift out of a possible 1608. 0 out of 20 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	369/621 (59%)	247/248 (100%)	0/250 (0%)	122/123 (99%)
Sidechain	483/840 (58%)	463/491 (94%)	0/308 (0%)	20/41 (49%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	76/147 (52%)	72/78 (92%)	0/62 (0%)	4/7 (57%)
Overall	928/1608 (58%)	782/817 (96%)	0/620 (0%)	146/171 (85%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 56%, i.e. 962 atoms were assigned a chemical shift out of a possible 1731. 0 out of 21 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	381/671 (57%)	256/268 (96%)	0/270 (0%)	125/133 (94%)
Sidechain	505/913 (55%)	485/533 (91%)	0/335 (0%)	20/45 (44%)
Aromatic	76/147 (52%)	72/78 (92%)	0/62 (0%)	4/7 (57%)
Overall	962/1731 (56%)	813/879 (92%)	0/667 (0%)	149/185 (81%)

7.1.4 Statistically unusual chemical shifts ⓘ

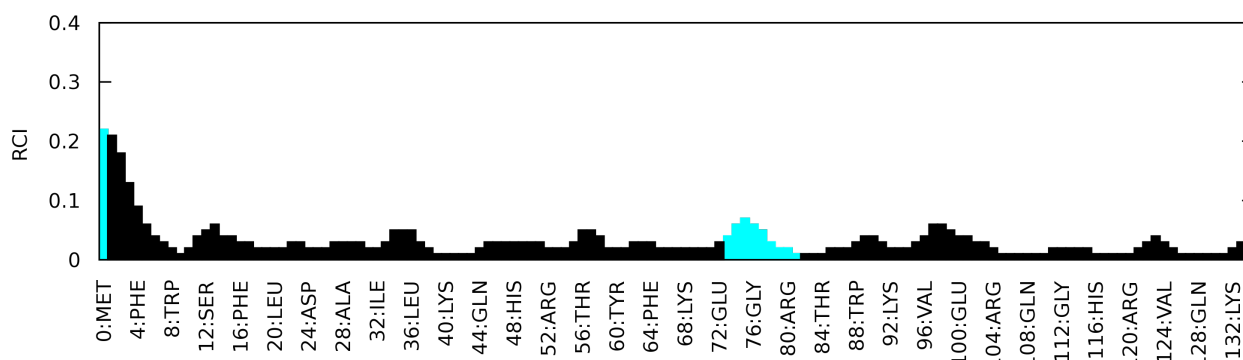
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

Mol	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	108	GLN	NE2	97.90	120.91 – 102.81	-7.7
1	A	108	GLN	HE22	3.66	9.27 – 4.77	-7.5
1	A	108	GLN	HE21	3.85	9.53 – 4.93	-7.3
1	A	95	CYS	HB2	-0.03	5.20 – 0.70	-6.6
1	A	116	HIS	HB3	0.60	5.00 – 1.10	-6.3
1	A	116	HIS	HB2	1.00	4.91 – 1.31	-5.9
1	A	13	ASN	HD22	4.43	9.59 – 4.69	-5.5
1	A	132	LYS	HG3	-0.17	2.76 – -0.04	-5.5
1	A	40	LYS	HD3	0.38	2.75 – 0.45	-5.3
1	A	95	CYS	HB3	0.48	5.25 – 0.55	-5.1
1	A	84	THR	HB	2.49	5.82 – 2.52	-5.1

7.1.5 Random Coil Index (RCI) plots ⓘ

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: BMRB entry 5319

Chemical shift list name: *assigned_chem_shift_list_1*

7.2.1 Bookkeeping [i](#)

The following table shows the results of parsing the chemical shift list and reports the number of nuclei with statistically unusual chemical shifts.

Total number of shifts	1169
Number of shifts mapped to atoms	1169
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	14

7.2.2 Chemical shift referencing [i](#)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	0	—	—
$^{13}\text{C}_\beta$	0	—	—
$^{13}\text{C}'$	0	—	—
^{15}N	132	-1.39 ± 0.55	Should be applied

7.2.3 Completeness of resonance assignments [i](#)

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 58%, i.e. 933 atoms were assigned a chemical shift out of a possible 1608. 0 out of 20 assigned methyl groups (LEU and VAL) were assigned

stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	371/621 (60%)	248/248 (100%)	0/250 (0%)	123/123 (100%)
Sidechain	486/840 (58%)	465/491 (95%)	0/308 (0%)	21/41 (51%)
Aromatic	76/147 (52%)	72/78 (92%)	0/62 (0%)	4/7 (57%)
Overall	933/1608 (58%)	785/817 (96%)	0/620 (0%)	148/171 (87%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 58%, i.e. 1001 atoms were assigned a chemical shift out of a possible 1731. 0 out of 21 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	399/671 (59%)	267/268 (100%)	0/270 (0%)	132/133 (99%)
Sidechain	526/913 (58%)	503/533 (94%)	0/335 (0%)	23/45 (51%)
Aromatic	76/147 (52%)	72/78 (92%)	0/62 (0%)	4/7 (57%)
Overall	1001/1731 (58%)	842/879 (96%)	0/667 (0%)	159/185 (86%)

7.2.4 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.

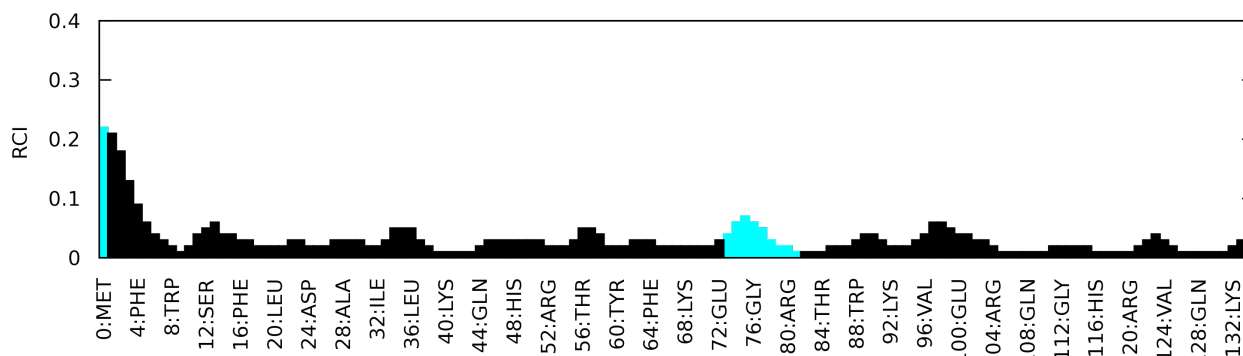
Mol	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	108	GLN	HE21	3.69	9.53 – 4.93	-7.7
1	A	108	GLN	NE2	98.70	120.91 – 102.81	-7.3
1	A	108	GLN	HE22	3.85	9.27 – 4.77	-7.0
1	A	95	CYS	HB2	-0.01	5.20 – 0.70	-6.6
1	A	116	HIS	HB3	0.55	5.00 – 1.10	-6.4
1	A	104	ARG	HH11	9.82	9.21 – 4.61	6.3
1	A	40	LYS	HE2	1.79	3.87 – 1.97	-5.9
1	A	116	HIS	HB2	0.98	4.91 – 1.31	-5.9
1	A	13	ASN	HD22	4.36	9.59 – 4.69	-5.7
1	A	40	LYS	HD3	0.31	2.75 – 0.45	-5.6
1	A	40	LYS	HG3	-0.21	2.76 – -0.04	-5.6
1	A	95	CYS	HB3	0.31	5.25 – 0.55	-5.5
1	A	132	LYS	HG3	-0.17	2.76 – -0.04	-5.5
1	A	84	THR	HB	2.44	5.82 – 2.52	-5.2

7.2.5 Random Coil Index (RCI) plots ⓘ

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:



7.3 Chemical shift list 3

File name: BMRB entry 5319

Chemical shift list name: *assigned_chem_shift_list_2*

7.3.1 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	29
Number of shifts mapped to atoms	0
Number of unparsed shifts	0
Number of shifts with mapping errors	29
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

The following assigned chemical shifts were not mapped to the molecules present in the coordinate file.

- Chain not found in structure. All 29 occurrences are reported below.

Chain	Res	Type	Atom	Shift Data		
				Value	Uncertainty	Ambiguity
UNMAPPED	1	RTL	H151	3.0	0.01	1
UNMAPPED	1	RTL	H31	2.07	0.01	9
UNMAPPED	1	RTL	H181	1.72	0.01	1

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Chain	Res	Type	Atom	Shift Data		
				Value	Uncertainty	Ambiguity
UNMAPPED	1	RTL	H8	6.38	0.01	1
UNMAPPED	1	RTL	H163	1.15	0.01	1
UNMAPPED	1	RTL	H203	0.91	0.01	1
UNMAPPED	1	RTL	H193	2.07	0.01	1
UNMAPPED	1	RTL	H14	5.26	0.01	1
UNMAPPED	1	RTL	H11	6.69	0.01	1
UNMAPPED	1	RTL	H12	6.41	0.01	1
UNMAPPED	1	RTL	H173	1.12	0.01	1
UNMAPPED	1	RTL	H152	2.17	0.01	1
UNMAPPED	1	RTL	H32	1.72	0.01	2
UNMAPPED	1	RTL	H22	1.73	0.01	1
UNMAPPED	1	RTL	H162	1.15	0.01	1
UNMAPPED	1	RTL	H183	1.72	0.01	1
UNMAPPED	1	RTL	H42	2.01	0.01	1
UNMAPPED	1	RTL	H161	1.15	0.01	1
UNMAPPED	1	RTL	H41	2.4	0.01	1
UNMAPPED	1	RTL	H201	0.91	0.01	1
UNMAPPED	1	RTL	H191	2.07	0.01	1
UNMAPPED	1	RTL	H21	1.49	0.01	1
UNMAPPED	1	RTL	H182	1.72	0.01	1
UNMAPPED	1	RTL	H7	6.63	0.01	1
UNMAPPED	1	RTL	H202	0.91	0.01	1
UNMAPPED	1	RTL	H192	2.07	0.01	1
UNMAPPED	1	RTL	H10	6.07	0.01	1
UNMAPPED	1	RTL	H171	1.12	0.01	1
UNMAPPED	1	RTL	H172	1.12	0.01	1

7.3.2 Chemical shift referencing [i](#)

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

7.3.3 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 0%, i.e. 0 atoms were assigned a chemical shift out of a possible 1608. 0 out of 20 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	0/621 (0%)	0/248 (0%)	0/250 (0%)	0/123 (0%)

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	Total	¹H	¹³C	¹⁵N
Sidechain	0/840 (0%)	0/491 (0%)	0/308 (0%)	0/41 (0%)
Aromatic	0/147 (0%)	0/78 (0%)	0/62 (0%)	0/7 (0%)
Overall	0/1608 (0%)	0/817 (0%)	0/620 (0%)	0/171 (0%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 0%, i.e. 0 atoms were assigned a chemical shift out of a possible 1731. 0 out of 21 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Backbone	0/671 (0%)	0/268 (0%)	0/270 (0%)	0/133 (0%)
Sidechain	0/913 (0%)	0/533 (0%)	0/335 (0%)	0/45 (0%)
Aromatic	0/147 (0%)	0/78 (0%)	0/62 (0%)	0/7 (0%)
Overall	0/1731 (0%)	0/879 (0%)	0/667 (0%)	0/185 (0%)

7.3.4 Statistically unusual chemical shifts [i](#)

There are no statistically unusual chemical shifts.

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

No *random coil index* (RCI) plot could be generated from the current chemical shift list (assigned_chem_shift_list_2). RCI is only applicable to proteins.