



Full wwPDB NMR Structure Validation Report ⓘ

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PDB ID : 1R8U
Title : NMR structure of CBP TAZ1/CITED2 complex
Authors : De Guzman, R.N.; Martinez-Yamout, M.; Dyson, H.J.; Wright, P.E.
Deposited on : 2003-10-28

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

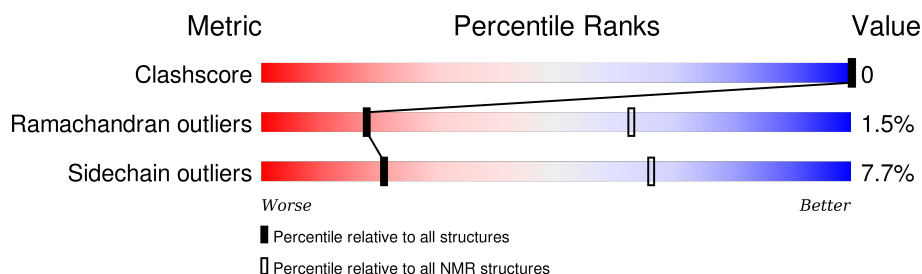
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR



The overall completeness of chemical shifts assignment is 80%.

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	50	 <div>60% • • 34%</div>
2	B	100	 <div>63% 7% 30%</div>

2 Ensemble composition and analysis ⓘ

This entry contains 20 models. Model 18 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:223-A:255, B:348-B:366, B:383-B:421, B:426-B:437 (103)	0.24	18

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 5 single-model clusters were found.

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

3 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 2382 atoms, of which 1187 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Cbp/p300-interacting transactivator 2.

Mol	Chain	Residues	Atoms						Trace
1	A	50	Total	C	H	N	O	S	0
			813	263	402	63	81	4	

- Molecule 2 is a protein called CREB-binding protein.

Mol	Chain	Residues	Atoms						Trace
2	B	100	Total	C	H	N	O	S	0
			1566	472	785	162	136	11	

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	
3	B	3	Total	Zn
			3	3

4 Residue-property plots

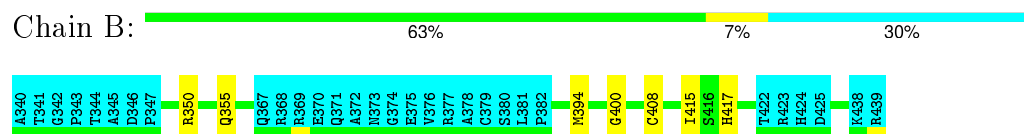
4.1 Average score per residue in the NMR ensemble

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: Cbp/p300-interacting transactivator 2



- Molecule 2: CREB-binding protein



4.2 Scores per residue for each member of the ensemble

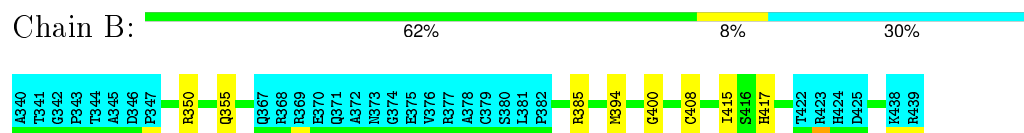
Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

- Molecule 1: Cbp/p300-interacting transactivator 2

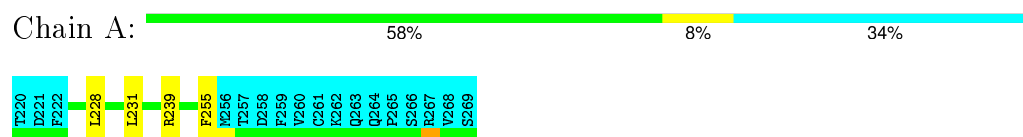


- Molecule 2: CREB-binding protein

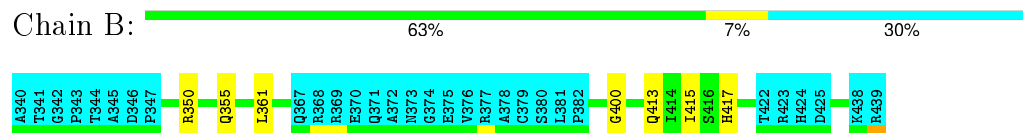


4.2.2 Score per residue for model 2

- Molecule 1: Cbp/p300-interacting transactivator 2



- Molecule 2: CREB-binding protein

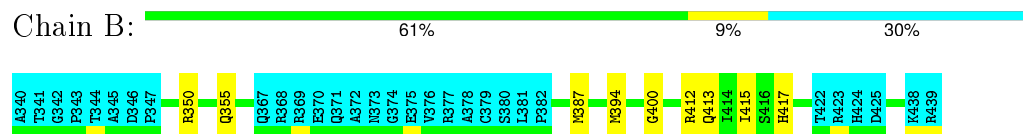


4.2.3 Score per residue for model 3

- Molecule 1: Cbp/p300-interacting transactivator 2



- Molecule 2: CREB-binding protein

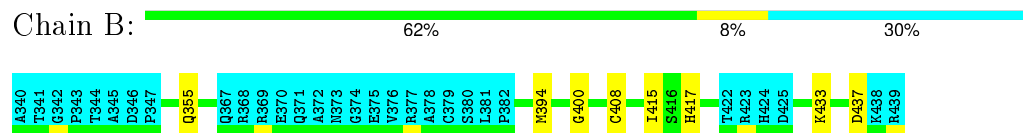


4.2.4 Score per residue for model 4

- Molecule 1: Cbp/p300-interacting transactivator 2

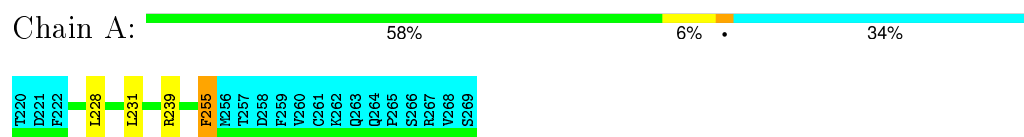


- Molecule 2: CREB-binding protein

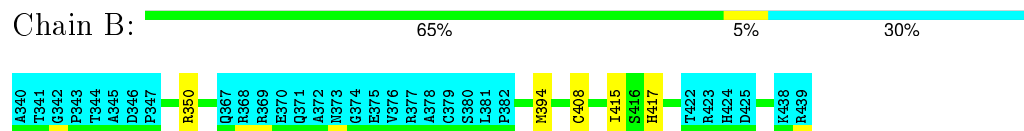


4.2.5 Score per residue for model 5

- Molecule 1: Cbp/p300-interacting transactivator 2



- Molecule 2: CREB-binding protein

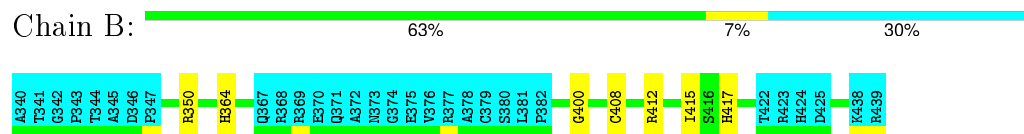


4.2.6 Score per residue for model 6

- Molecule 1: Cbp/p300-interacting transactivator 2

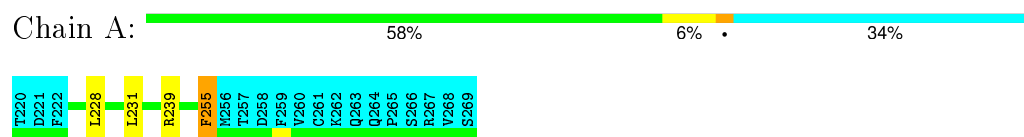


- Molecule 2: CREB-binding protein

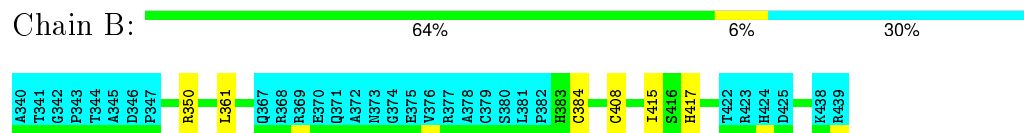


4.2.7 Score per residue for model 7

- Molecule 1: Cbp/p300-interacting transactivator 2

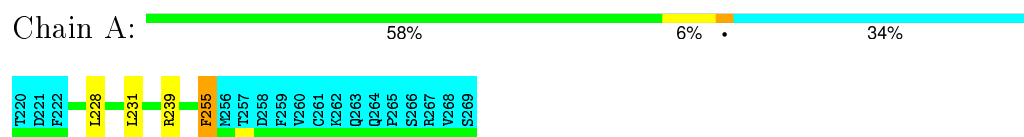


- Molecule 2: CREB-binding protein

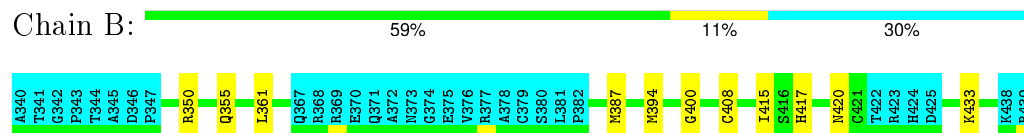


4.2.8 Score per residue for model 8

- Molecule 1: Cbp/p300-interacting transactivator 2



- Molecule 2: CREB-binding protein

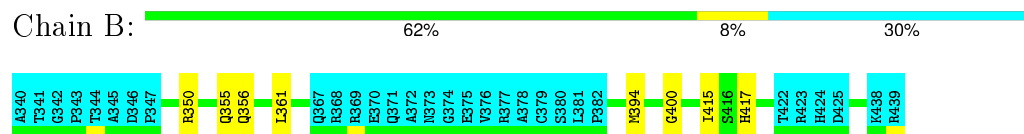


4.2.9 Score per residue for model 9

- Molecule 1: Cbp/p300-interacting transactivator 2



- Molecule 2: CREB-binding protein

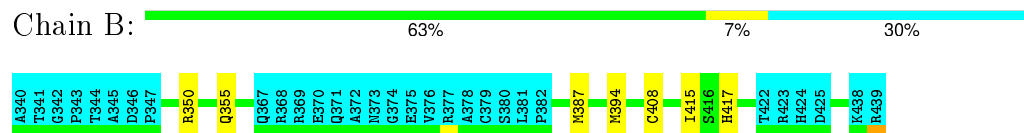


4.2.10 Score per residue for model 10

- Molecule 1: Cbp/p300-interacting transactivator 2

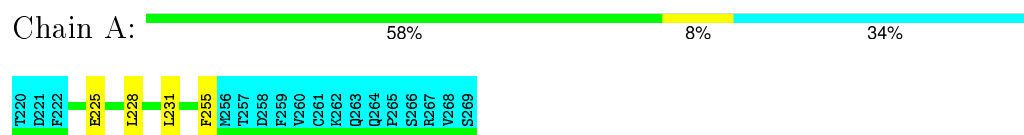


- Molecule 2: CREB-binding protein

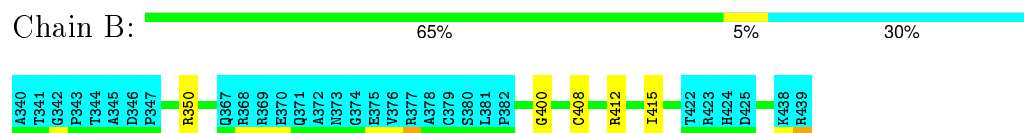


4.2.11 Score per residue for model 11

- Molecule 1: Cbp/p300-interacting transactivator 2

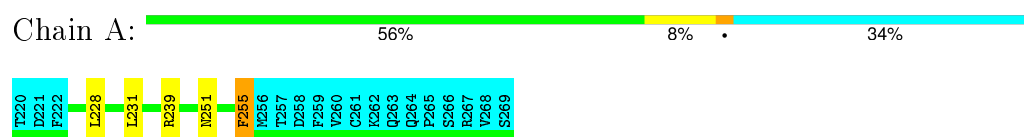


- Molecule 2: CREB-binding protein

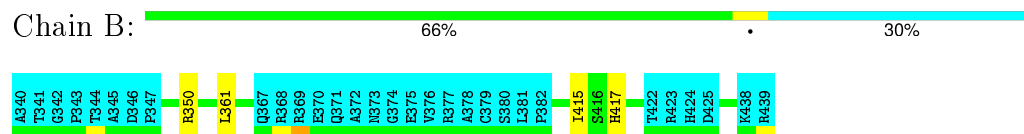


4.2.12 Score per residue for model 12

- Molecule 1: Cbp/p300-interacting transactivator 2

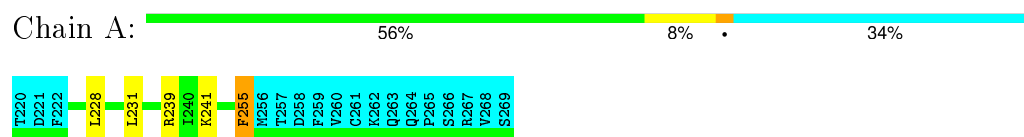


- Molecule 2: CREB-binding protein

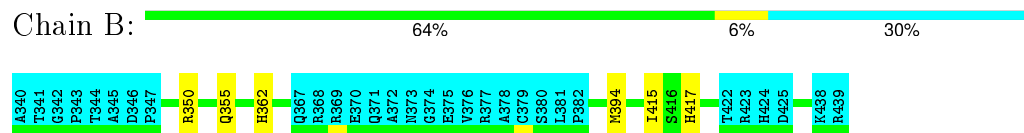


4.2.13 Score per residue for model 13

- Molecule 1: Cbp/p300-interacting transactivator 2



- Molecule 2: CREB-binding protein

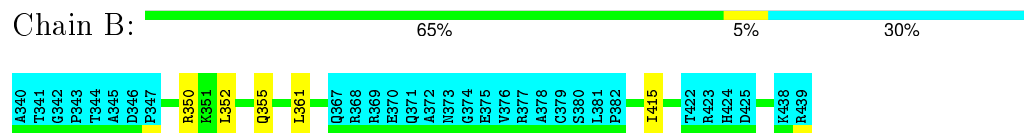


4.2.14 Score per residue for model 14

- Molecule 1: Cbp/p300-interacting transactivator 2



- Molecule 2: CREB-binding protein

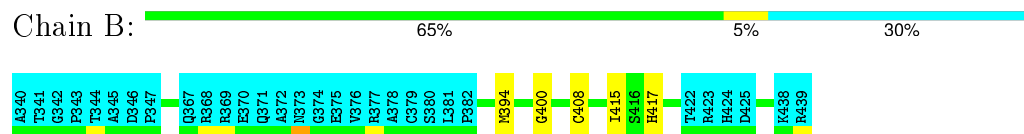


4.2.15 Score per residue for model 15

- Molecule 1: Cbp/p300-interacting transactivator 2

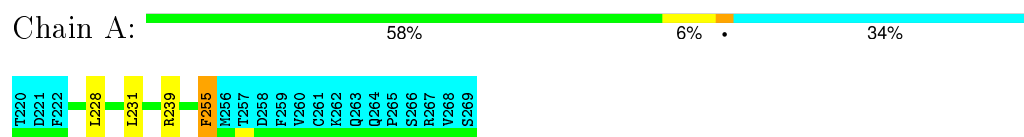


- Molecule 2: CREB-binding protein

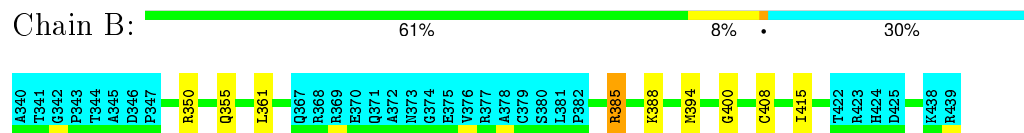


4.2.16 Score per residue for model 16

- Molecule 1: Cbp/p300-interacting transactivator 2

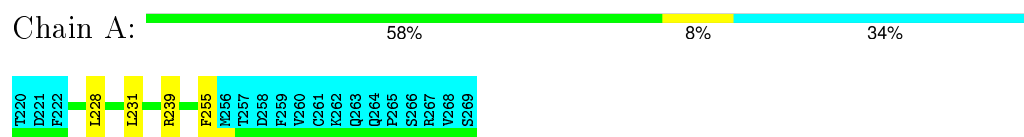


- Molecule 2: CREB-binding protein

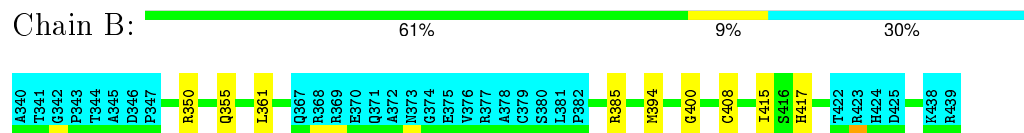


4.2.17 Score per residue for model 17

- Molecule 1: Cbp/p300-interacting transactivator 2



- Molecule 2: CREB-binding protein

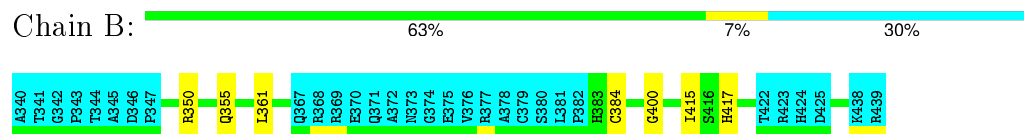


4.2.18 Score per residue for model 18 (medoid)

- Molecule 1: Cbp/p300-interacting transactivator 2

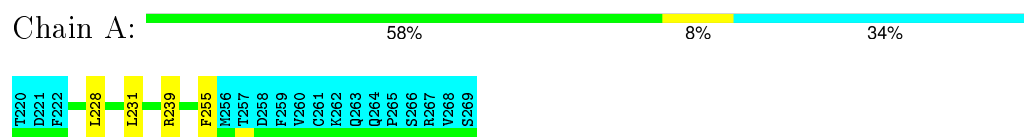


- Molecule 2: CREB-binding protein

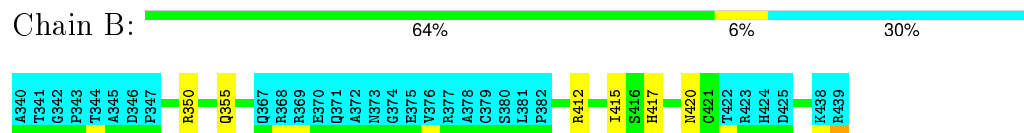


4.2.19 Score per residue for model 19

- Molecule 1: Cbp/p300-interacting transactivator 2

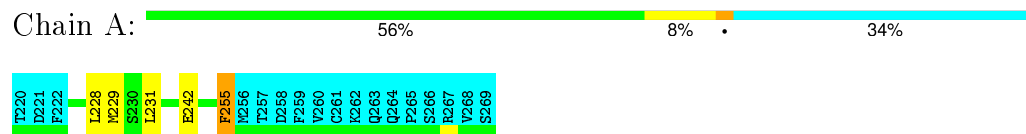


- Molecule 2: CREB-binding protein

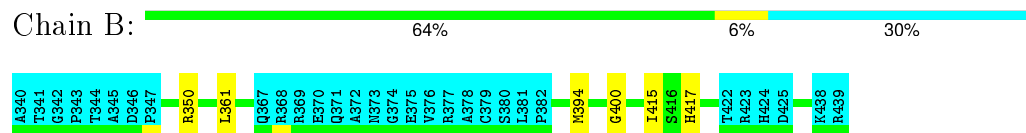


4.2.20 Score per residue for model 20

- Molecule 1: Cbp/p300-interacting transactivator 2



- Molecule 2: CREB-binding protein



5 Refinement protocol and experimental data overview

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

Of the 50 calculated structures, 20 were deposited, based on the following criterion: *structures with acceptable covalent geometry*.

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

Software name	Classification	Version
DYANA	structure solution	1.5
AMBER	refinement	7.0

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 5987
Number of chemical shift lists	2
Total number of shifts	1549
Number of shifts mapped to atoms	1539
Number of unparsed shifts	0
Number of shifts with mapping errors	10
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	80%

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

6 Model quality

6.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN

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	0.71±0.01	0±0/279 (0.0±0.0%)	1.01±0.03	0±0/377 (0.1±0.1%)
2	B	0.56±0.00	0±0/560 (0.0±0.0%)	1.03±0.02	1±1/754 (0.1±0.1%)
All	All	0.62	0/16780 (0.0%)	1.02	31/22620 (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
2	B	0.0±0.0	1.0±0.5
All	All	0	20

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
2	B	350	ARG	NE-CZ-NH1	7.04	123.82	120.30	11	16
1	A	239	ARG	NE-CZ-NH1	6.98	123.79	120.30	13	9
2	B	412	ARG	NE-CZ-NH1	6.43	123.52	120.30	11	3
2	B	385	ARG	NE-CZ-NH1	6.39	123.49	120.30	17	3

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)
2	B	417	HIS	Sidechain	17

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Mol	Chain	Res	Type	Group	Models (Total)
2	B	350	ARG	Sidechain	1
2	B	412	ARG	Sidechain	1
2	B	362	HIS	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
All	All	16520	16560	16560	-

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 -.

There are no clashes.

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	33/50 (66%)	29±1 (87±3%)	3±1 (10±3%)	1±0 (3±1%)	11	47
2	B	70/100 (70%)	67±1 (95±1%)	3±1 (4±1%)	1±1 (1±1%)	24	71
All	All	2060/3000 (69%)	1904 (92%)	125 (6%)	31 (2%)	18	63

All 4 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	255	PHE	16
2	B	400	GLY	13
1	A	242	GLU	1

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Mol	Chain	Res	Type	Models (Total)
2	B	437	ASP	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	31/48 (65%)	28±1 (90±2%)	3±1 (10±2%)	14	59
2	B	63/87 (72%)	59±2 (93±3%)	4±2 (7±3%)	25	71
All	All	1880/2700 (70%)	1736 (92%)	144 (8%)	21	66

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	228	LEU	20
1	A	231	LEU	20
2	B	415	ILE	20
1	A	255	PHE	17
2	B	355	GLN	13
2	B	394	MET	12
2	B	408	CYS	11
2	B	361	LEU	10
2	B	387	MET	3
2	B	413	GLN	2
2	B	384	CYS	2
2	B	433	LYS	2
2	B	420	ASN	2
2	B	364	HIS	1
1	A	251	ASN	1
2	B	356	GLN	1
2	B	385	ARG	1
2	B	388	LYS	1
1	A	229	MET	1
2	B	352	LEU	1
2	B	350	ARG	1
1	A	241	LYS	1
1	A	225	GLU	1

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 carbohydrates in this entry.

6.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

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 80% for the well-defined parts and 76% for the entire structure.

7.1 Chemical shift list 1

File name: BMRB entry 5987

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	553
Number of shifts mapped to atoms	543
Number of unparsed shifts	0
Number of shifts with mapping errors	10
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.

- Residue not found in structure. All 10 occurrences are reported below.

Chain	Res	Type	Atom	Shift Data		
				Value	Uncertainty	Ambiguity
A	1	MET	CB	32.59	0.1	1
A	1	MET	HA	4.04	0.02	1
A	1	MET	HE1	1.955	0.02	1
A	1	MET	HE3	1.955	0.02	1
A	1	MET	CG	30.551	0.1	1
A	1	MET	CA	54.516	0.1	1
A	1	MET	HG2	2.423	0.02	2
A	1	MET	HE2	1.955	0.02	1
A	1	MET	HB2	1.943	0.02	2
A	1	MET	CE	16.543	0.1	1

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	51	0.32 ± 0.36	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	47	0.65 ± 0.16	Should be applied
$^{13}\text{C}'$	0	—	—
^{15}N	45	-0.06 ± 0.57	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 27%, i.e. 354 atoms were assigned a chemical shift out of a possible 1313. 0 out of 20 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	128/509 (25%)	64/203 (32%)	33/206 (16%)	31/100 (31%)
Sidechain	202/713 (28%)	123/420 (29%)	77/261 (30%)	2/32 (6%)
Aromatic	24/91 (26%)	12/50 (24%)	11/32 (34%)	1/9 (11%)
Overall	354/1313 (27%)	199/673 (30%)	121/499 (24%)	34/141 (24%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 27%, i.e. 515 atoms were assigned a chemical shift out of a possible 1899. 0 out of 24 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	190/736 (26%)	95/293 (32%)	50/300 (17%)	45/143 (31%)
Sidechain	289/1047 (28%)	178/619 (29%)	107/371 (29%)	4/57 (7%)
Aromatic	36/116 (31%)	18/64 (28%)	17/42 (40%)	1/10 (10%)
Overall	515/1899 (27%)	291/976 (30%)	174/713 (24%)	50/210 (24%)

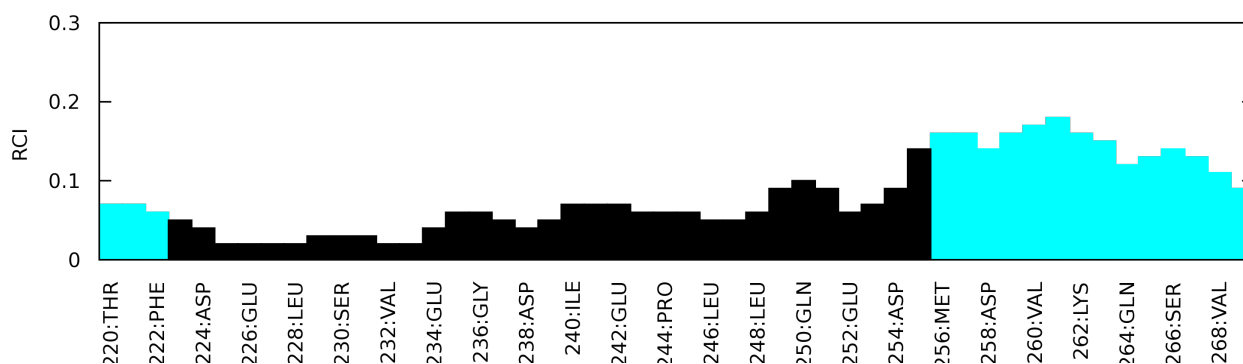
7.1.4 Statistically unusual chemical shifts [i](#)

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.

Random coil index (RCI) for chain A:



7.2 Chemical shift list 2

File name: BMRB entry 5987

Chemical shift list name: *assigned_chem_shift_list_2*

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	996
Number of shifts mapped to atoms	996
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

7.2.2 Chemical shift referencing [i](#)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	96	-0.59 ± 0.13	Should be applied
$^{13}\text{C}_\beta$	92	0.41 ± 0.16	None needed (< 0.5 ppm)
$^{13}\text{C}'$	0	—	—
^{15}N	84	-0.78 ± 0.46	None needed (imprecise)

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 53%, i.e. 691 atoms were assigned a chemical shift out of a possible 1313. 0 out of 20 assigned methyl groups (LEU and VAL) were assigned

stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	266/509 (52%)	133/203 (66%)	67/206 (33%)	66/100 (66%)
Sidechain	379/713 (53%)	233/420 (55%)	138/261 (53%)	8/32 (25%)
Aromatic	46/91 (51%)	27/50 (54%)	18/32 (56%)	1/9 (11%)
Overall	691/1313 (53%)	393/673 (58%)	223/499 (45%)	75/141 (53%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 49%, i.e. 937 atoms were assigned a chemical shift out of a possible 1899. 0 out of 24 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	361/736 (49%)	181/293 (62%)	96/300 (32%)	84/143 (59%)
Sidechain	525/1047 (50%)	326/619 (53%)	189/371 (51%)	10/57 (18%)
Aromatic	51/116 (44%)	30/64 (47%)	20/42 (48%)	1/10 (10%)
Overall	937/1899 (49%)	537/976 (55%)	305/713 (43%)	95/210 (45%)

7.2.4 Statistically unusual chemical shifts [i](#)

There are no statistically unusual chemical shifts.

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:

