wwPDB NMR Structure Validation Summary Report (i)

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PDB ID	:	2KHC
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This is a wwPDB NMR Structure Validation Summary Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
http://wwpdb.org/validation/2016/NMRValidationReportHelp
with specific help available everywhere you see the (i) symbol.

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

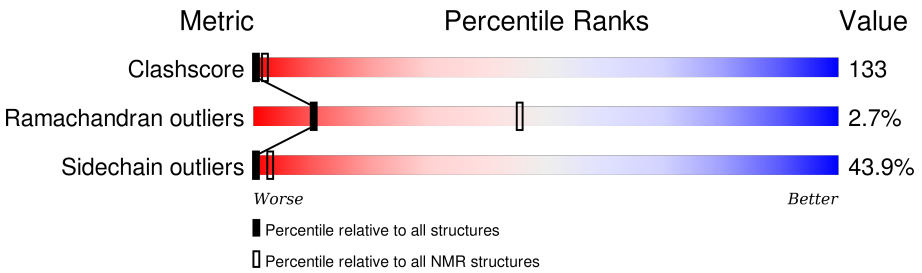
Cyrange	:	Kirchner and Güntert (2011)
NmrClust	:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Mogul	:	unknown
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	rb-20027457
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20027457

1 Overall quality at a glance (i)

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

The overall completeness of chemical shifts assignment is 89%.

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 <=5%

Mol	Chain	Length	Quality of chain
1	A	118	13% 36% 22% 29%

2 Ensemble composition and analysis (i)

This entry contains 10 models. Model 5 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:487-A:497 (11)	0.74	9
2	A:517-A:552, A:561-A:597 (73)	0.29	5

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. No single-model clusters were found.

Cluster number	Models
1	1, 2, 3, 4, 5, 6, 7, 8, 9, 10

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 1737 atoms, of which 873 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Testis-specific RNP-type RNA binding protein.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	118	1737	555	873	143	163	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 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: Testis-specific RNP-type RNA binding protein

Chain A: 13% 36% 22% 29%

A480 A481 G482 L483 P484 Q485 F486 L492 L497 A498 S499 V500 A501 L502 S503 A504 A505 A506 A507 A508 A509 A510 G511 K512 Q513 I514 E515 G516 G519 C520 N521 L522 F523 I524 Y525 H526 L527 P528 Q529 E530 F531 T532 D533 T534 D535 L536 A537 S538 T539 F540 L541 P542 F543 G544 N545 V546 I547

S548 A549 K550 V551 F552 I553 D554 K555 Q556 T557 S558 L559 S560 K561 C562 F563 G564 F565 V566 S567 F568 D569 N570 P571 D572 S573 A574 Q575 V576 A577 I578 K579 A580 M581 N582 G583 F584 Q585 V586 G587 T588 K589 R590 L591 K592 V593 Q594 L595 K596 K597

4.2 Residue scores for the representative (medoid) model from the NMR ensemble

The representative model is number 5. Colouring as in section 4.1 above.

- Molecule 1: Testis-specific RNP-type RNA binding protein

Chain A: 18% 31% 22% • 29%

A480 A481 G482 L483 P484 Q485 F486 S490 A491 L492 A498 S499 V500 A501 L502 S503 A504 A505 A506 A507 A508 A509 A510 G511 K512 Q513 I514 E515 G516 P517 E518 G519 C520 N521 L522 F523 I524 Y525 H526 L527 P528 Q529 E530 F531 T532 D533 T534 D535 L536 A537 S538 T539 F540 L541 P542 F543 G544 N545

V546 I547 S548 V551 F552 I553 D554 K555 Q556 T557 S558 L559 S560 K561 C562 F563 G564 F565 V566 S567 F568 D569 N570 P571 D572 S573 A574 Q575 V576 A577 I578 K579 A580 M581 N582 G583 F584 Q585 V586 G587 T588 K589 R590 L591 K592 V593 Q594 L595 K596 K597

5 Refinement protocol and experimental data overview (i)

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 least restraint violations*.

The authors did not provide any information on software used for structure solution, optimization or 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)	BMRB entry 16236
Number of chemical shift lists	1
Total number of shifts	1331
Number of shifts mapped to atoms	1331
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	89%

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)

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 (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	639	643	642	171±15
All	All	6390	6430	6420	1708

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 133.

5 of 729 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:522:LEU:HD21	1:A:524:ILE:HG23	1.12	1.13	1	3
1:A:522:LEU:HD12	1:A:578:ILE:HG23	1.12	1.22	4	2
1:A:543:PHE:CD1	1:A:544:GLY:N	1.07	2.22	4	3
1:A:526:HIS:HB2	1:A:591:LEU:HA	1.04	1.27	2	10
1:A:522:LEU:HD12	1:A:524:ILE:HG23	1.04	1.30	8	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	83/118 (70%)	71±2 (85±2%)	10±1 (12±2%)	2±1 (3±2%)	10 45
All	All	830/1180 (70%)	705 (85%)	103 (12%)	22 (3%)	10 45

5 of 8 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	544	GLY	6
1	A	543	PHE	6
1	A	542	PRO	3
1	A	561	LYS	2
1	A	571	PRO	2

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	71/91 (78%)	40±3 (56±4%)	31±3 (44±4%)	0 3
All	All	710/910 (78%)	398 (56%)	312 (44%)	0 3

5 of 58 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	536	LEU	10
1	A	585	GLN	10
1	A	592	LYS	10
1	A	563	PHE	10
1	A	579	LYS	10

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)

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 89% for the well-defined parts and 88% for the entire structure.

7.1 Chemical shift list 1

File name: BMRB entry 16236

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	1331
Number of shifts mapped to atoms	1331
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	5

7.1.2 Chemical shift referencing (i)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	112	-0.21 ± 0.12	None needed (< 0.5 ppm)
$^{13}C_{\beta}$	104	0.01 ± 0.15	None needed (< 0.5 ppm)
$^{13}C'$	109	0.89 ± 0.16	Should be applied
^{15}N	106	-0.79 ± 0.59	None needed (imprecise)

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 89%, i.e. 887 atoms were assigned a chemical shift out of a possible 999. 10 out of 14 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	401/410 (98%)	160/163 (98%)	163/168 (97%)	78/79 (99%)
Sidechain	433/492 (88%)	274/290 (94%)	151/184 (82%)	8/18 (44%)

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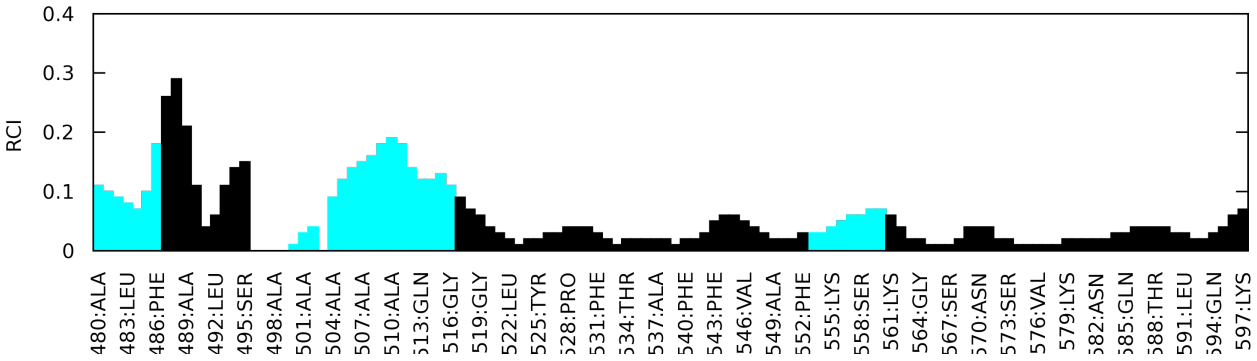
	Total	^{1}H	^{13}C	^{15}N
Aromatic	53/97 (55%)	53/53 (100%)	0/42 (0%)	0/2 (0%)
Overall	887/999 (89%)	487/506 (96%)	314/394 (80%)	86/99 (87%)

7.1.4 Statistically unusual chemical shifts (i)

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

Mol	Chain	Res	Type	Atom	Shift, *ppm*	Expected range, *ppm*	Z-score
1	A	561	LYS	CE	36.32	46.00 – 37.80	-6.8
1	A	555	LYS	CE	36.51	46.00 – 37.80	-6.6
1	A	542	PRO	HB2	0.17	3.82 – 0.32	-5.4
1	A	542	PRO	HD3	1.60	5.52 – 1.72	-5.3
1	A	542	PRO	HB3	0.17	3.81 – 0.21	-5.1

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: