wwPDB NMR Structure Validation Summary Report (i)

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PDB ID	:	1A1T
Title	:	STRUCTURE OF THE HIV-1 NUCLEOCAPSID PROTEIN BOUND TO THE SL3 PSI-RNA RECOGNITION ELEMENT, NMR, 25 STRUCTURES
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Deposited on	:	1997-12-15

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:

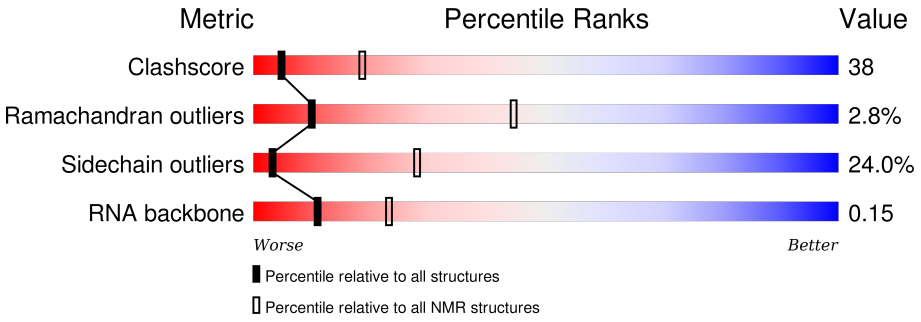
Cyrange	:	Kirchner and Güntert (2011)
NmrClust	:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Mogul	:	unknown
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	rb-20027457
Ideal 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

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

The overall completeness of chemical shifts assignment was not calculated.

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
RNA backbone	3027	600

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	B	20	5% 50% 45%
2	A	55	36% 42% 5% 16%

2 Ensemble composition and analysis

This entry contains 25 models. Model 1 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:5-A:50 (46)	0.20	1

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 3 clusters and 3 single-model clusters were found.

Cluster number	Models
1	1, 2, 3, 5, 6, 10, 11, 12, 13, 14, 16, 18, 19, 20, 22, 25
2	4, 8, 24
3	7, 9, 21
Single-model clusters	15; 17; 23

3 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 1516 atoms, of which 643 are hydrogens and 0 are deuteriums.

- Molecule 1 is a RNA chain called SL3 STEM-LOOP RNA.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	P	
1	B	20	649	192	217	81	139	20	0

- Molecule 2 is a protein called NUCLEOCAPSID PROTEIN.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
2	A	55	865	263	426	94	74	8	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	ILE	CONFLICT	UNP Q75677

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

Mol	Chain	Residues	Atoms	
			Total	Zn
3	A	2	2	2

4 Residue-property plots

4.1 Average score per residue in the NMR ensemble

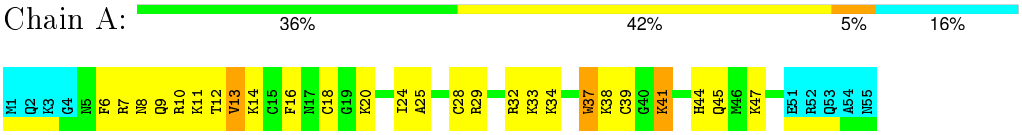
These plots are provided for all protein, RNA and DNA chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-coded according to the number of geometric quality criteria for which they contain 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: SL3 STEM-LOOP RNA

Chain B:

- Molecule 2: NUCLEOCAPSID PROTEIN

Chain A:



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

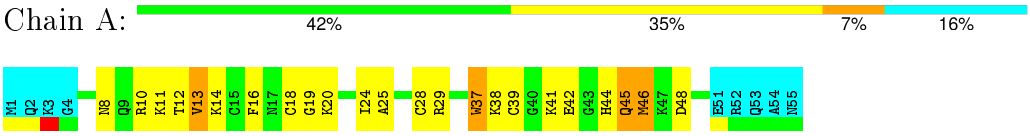
The representative model is number 1. Colouring as in section 4.1 above.

- Molecule 1: SL3 STEM-LOOP RNA

Chain B:

- Molecule 2: NUCLEOCAPSID PROTEIN

Chain A:



5 Refinement protocol and experimental data overview

The models were refined using the following method: *DISTANCE GEOMETRY*.

Of the 800 calculated structures, 25 were deposited, based on the following criterion: *LEAST TOTAL PENALTY*.

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

Software name	Classification	Version
DYANA	refinement	
NMRVIEW	structure solution	

No chemical shift data was provided. 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	B	3.14±0.23	15±2/483 (3.0±0.4%)	4.19±0.17	90±2/752 (11.9±0.3%)
2	A	0.69±0.00	0±0/374 (0.0±0.0%)	0.93±0.00	0±0/493 (0.0±0.0%)
All	All	2.40	365/21425 (1.7%)	3.31	2246/31125 (7.2%)

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	B	2.8±1.3	0.0±0.0
All	All	71	0

5 of 20 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	B	210	G	C4'-O4'	-29.15	1.07	1.45	16	25
1	B	208	C	C4'-O4'	-29.07	1.07	1.45	22	23
1	B	212	G	C4'-O4'	-28.94	1.07	1.45	24	22
1	B	204	C	C4'-O4'	-28.59	1.08	1.45	4	23
1	B	215	U	C4'-O4'	-28.33	1.08	1.45	22	25

5 of 106 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(^{o})	Ideal(^{o})	Models	
								Worst	Total
1	B	210	G	C5'-C4'-O4'	35.85	152.12	109.10	23	22
1	B	220	C	C5'-C4'-O4'	34.79	150.84	109.10	16	15

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})	Models	
								Worst	Total
1	B	219	C	C5'-C4'-O4'	32.99	148.68	109.10	15	18
1	B	211	A	C5'-C4'-O4'	31.52	146.93	109.10	15	25
1	B	209	G	C5'-C4'-O4'	30.14	145.26	109.10	19	24

5 of 11 unique chiral outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Models (Total)
1	B	211	A	C4'	17
1	B	210	G	C4'	16
1	B	209	G	C4'	8
1	B	215	U	C4'	8
1	B	208	C	C4'	6

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	B	432	217	218	35±5
2	A	367	356	366	35±4
All	All	20025	14325	14600	1333

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 38.

5 of 227 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:8:ASN:ND2	2:A:13:VAL:HG11	0.98	1.72	17	25
1:B:210:G:H4'	2:A:16:PHE:CE1	0.84	2.06	22	14
1:B:210:G:C4	2:A:37:TRP:CZ2	0.84	2.66	2	25
1:B:210:G:C5	2:A:37:TRP:CZ2	0.82	2.68	20	25
2:A:12:THR:HG23	2:A:12:THR:O	0.75	1.81	7	15

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
2	A	46/55 (84%)	37±1 (81±2%)	8±1 (17±2%)	1±0 (3±1%)	10 44
All	All	1150/1375 (84%)	926 (81%)	192 (17%)	32 (3%)	10 44

All 3 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
2	A	13	VAL	25
2	A	12	THR	6
2	A	32	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
2	A	39/46 (85%)	30±2 (76±6%)	9±2 (24±6%)	3 28
All	All	975/1150 (85%)	741 (76%)	234 (24%)	3 28

5 of 21 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)
2	A	37	TRP	25
2	A	38	LYS	21
2	A	14	LYS	18
2	A	41	LYS	16
2	A	29	ARG	16

6.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers	Suiteness
1	B	19/20 (95%)	8±2 (43±10%)	6±1 (33±7%)	0.15±0.04
All	All	487/500 (97%)	202 (41%)	158 (32%)	0.15

The overall RNA backbone suiteness is 0.15.

5 of 19 unique RNA backbone outliers are listed below:

Mol	Chain	Res	Type	Models (Total)
1	B	211	A	25
1	B	210	G	24
1	B	212	G	24
1	B	209	G	22
1	B	213	G	18

5 of 15 unique RNA pucker outliers are listed below:

Mol	Chain	Res	Type	Models (Total)
1	B	211	A	24
1	B	207	G	21
1	B	210	G	20
1	B	212	G	18
1	B	217	G	13

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

There are no carbohydrates in this entry.

6.6 Ligand geometry

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

6.7 Other polymers

There are no such molecules in this entry.

6.8 Polymer linkage issues

There are no chain breaks in this entry.

7 Chemical shift validation

No chemical shift data were provided