Full wwPDB NMR Structure Validation Report (i)

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PDB ID	:	1ZUE
Title	:	Revised Solution Structure of DLP-2
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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 (i) symbol.

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

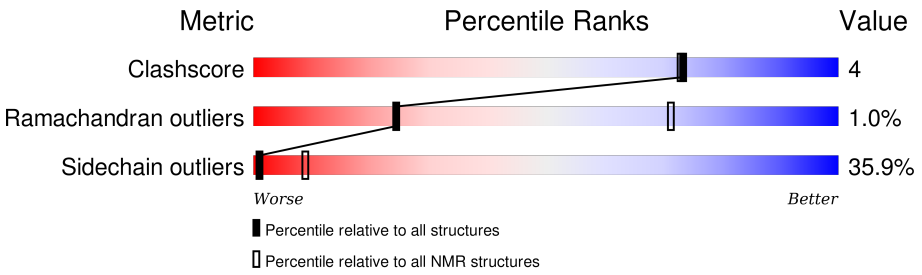
Cyrange	:	Kirchner and Güntert (2011)
NmrClust	:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Mogul	:	1.7.1 (RC1), CSD as537be (2016)
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	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 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

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	42	48% 38% 14%

2 Ensemble composition and analysis (i)

This entry contains 20 models. Model 3 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:7-A:42 (36)	0.26	3

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. No single-model clusters were found.

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

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 671 atoms, of which 319 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Defensin-like peptide 2/4.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	42	671	216	319	63	64	9	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	2	MED	MET	MODIFIED RESIDUE	UNP P82140

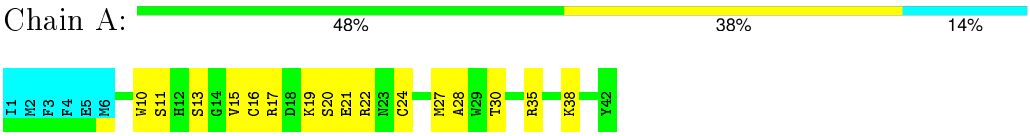
4 Residue-property plots (i)

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: Defensin-like peptide 2/4

Chain A:



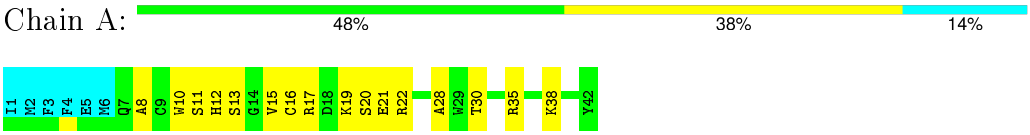
4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

- Molecule 1: Defensin-like peptide 2/4

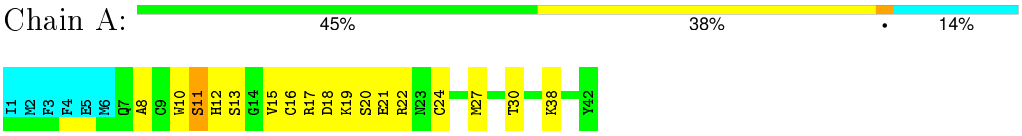
Chain A:



4.2.2 Score per residue for model 2

- Molecule 1: Defensin-like peptide 2/4

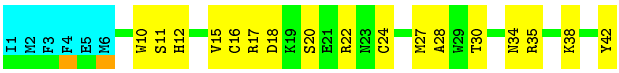
Chain A:



4.2.3 Score per residue for model 3 (medoid)

- Molecule 1: Defensin-like peptide 2/4

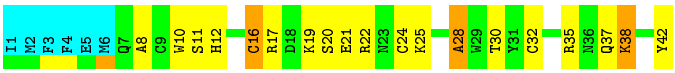
Chain A: 45% 40% 14%



4.2.4 Score per residue for model 4

- Molecule 1: Defensin-like peptide 2/4

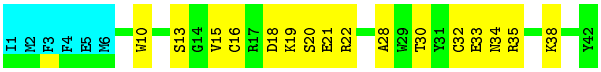
Chain A: 40% 38% 7% 14%



4.2.5 Score per residue for model 5

- Molecule 1: Defensin-like peptide 2/4

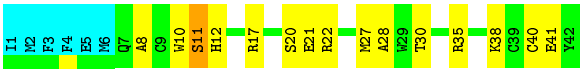
Chain A: 48% 38% 14%



4.2.6 Score per residue for model 6

- Molecule 1: Defensin-like peptide 2/4

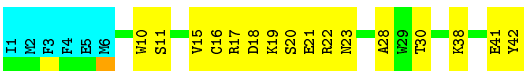
Chain A: 50% 33% • 14%



4.2.7 Score per residue for model 7

- Molecule 1: Defensin-like peptide 2/4

Chain A: 48% 38% 14%



4.2.8 Score per residue for model 8

- Molecule 1: Defensin-like peptide 2/4

Chain A: 40% 40% 5% 14%

I1 M2 F3 F4 E5 M6 Q7 A8 C9 W10 S11 H12 S13 G14 V15 C16 S20 E21 R22 M23 C24 M27 A28 W29 T30 Y31 C32 E33 N34 R35 K38 E41 Y42

4.2.9 Score per residue for model 9

- Molecule 1: Defensin-like peptide 2/4

Chain A: 45% 38% • 14%

I1 M2 F3 F4 E5 M6 Q7 A8 C9 W10 S11 H12 D18 K19 S20 E21 R22 M27 A28 W29 T30 Y31 C32 R35 N36 Q37 K38 E41 Y42

4.2.10 Score per residue for model 10

- Molecule 1: Defensin-like peptide 2/4

Chain A: 43% 38% 5% 14%

I1 M2 F3 F4 E5 M6 Q7 A8 C9 W10 S11 H12 V15 C16 R17 S20 E21 R22 M23 C24 M27 T30 Y31 R35 K38 Y42

4.2.11 Score per residue for model 11

- Molecule 1: Defensin-like peptide 2/4

Chain A: 48% 33% 5% 14%

I1 M2 F3 F4 E5 M6 Q7 A8 C9 W10 S11 H12 S13 G14 V15 C16 R17 D18 K19 S20 E21 R22 A28 W29 T30 N34 R35 N36 Q37 K38 Y42

4.2.12 Score per residue for model 12

- Molecule 1: Defensin-like peptide 2/4

Chain A: 55% 31% 14%

I1 M2 F3 F4 E5 M6 W10 S11 H12 S13 G14 V15 C16 R17 S20 E21 R22 M27 N34 R35 K38 E41 Y42

4.2.13 Score per residue for model 13

- Molecule 1: Defensin-like peptide 2/4

Chain A: 50% 33% • 14%

I1 M2 F3 F4 E5 M6 Q7 A8 C9 W10 S11 H12 S13 K19 S20 E21 R22 N23 C24 K25 A28 W29 T30 Y31 C32 K38 C39 C40 E41 Y42

4.2.14 Score per residue for model 14

- Molecule 1: Defensin-like peptide 2/4

Chain A: 50% 36% 14%

I1 M2 F3 F4 E5 M6 W10 S11 C16 R17 D18 K19 S20 E21 R22 N23 C24 K25 A28 W29 T30 Y31 C32 R35 K38 Y42

4.2.15 Score per residue for model 15

- Molecule 1: Defensin-like peptide 2/4

Chain A: 55% 31% 14%

I1 M2 F3 F4 E5 M6 W10 V15 C16 R17 D18 K19 S20 E21 R22 N23 C24 K25 P26 M27 K38 Y42

4.2.16 Score per residue for model 16

- Molecule 1: Defensin-like peptide 2/4

Chain A: 69% 17% 14%

I1 M2 F3 F4 E5 M6 W10 D18 K19 S20 E21 R22 R35 K38 Y42

4.2.17 Score per residue for model 17

- Molecule 1: Defensin-like peptide 2/4

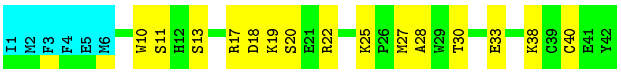
Chain A: 60% 26% 14%

I1 M2 F3 F4 E5 M6 W10 S11 S20 E21 R22 N23 C24 K25 A28 W29 T30 E33 N34 R35 C40 E41 Y42

4.2.18 Score per residue for model 18

- Molecule 1: Defensin-like peptide 2/4

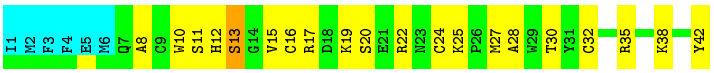
Chain A: 50% 36% 14%



4.2.19 Score per residue for model 19

- Molecule 1: Defensin-like peptide 2/4

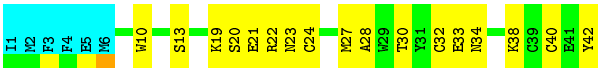
Chain A: 38% 45% • 14%



4.2.20 Score per residue for model 20

- Molecule 1: Defensin-like peptide 2/4

Chain A: 45% 40% 14%



5 Refinement protocol and experimental data overview (i)

The models were refined using the following method: *distance geometry, simulated annealing, molecular dynamics, torsion angle dynamics.*

Of the 500 calculated structures, 20 were deposited, based on the following criterion: *structures with the lowest energy.*

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

Software name	Classification	Version
NOAH	structure solution	
DYANA	structure solution	1.5
CNS	structure solution	1.1
CNS	refinement	1.1

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 (i)

6.1 Standard geometry (i)

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

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	297	264	263	2±1
All	All	5940	5280	5260	46

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 4.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:28:ALA:O	1:A:30:THR:HG22	0.78	1.79	14	15
1:A:27:MET:SD	1:A:30:THR:HG21	0.70	2.26	10	1
1:A:8:ALA:HB3	1:A:11:SER:HB2	0.68	1.66	1	8
1:A:12:HIS:O	1:A:13:SER:CB	0.53	2.56	19	1
1:A:27:MET:CG	1:A:30:THR:HG21	0.53	2.33	10	1
1:A:8:ALA:HB3	1:A:11:SER:CB	0.52	2.34	2	4
1:A:27:MET:HG3	1:A:30:THR:HG21	0.52	1.81	10	1
1:A:27:MET:O	1:A:30:THR:HG22	0.47	2.10	2	1
1:A:15:VAL:HG12	1:A:16:CYS:N	0.42	2.29	10	11
1:A:16:CYS:HA	1:A:38:LYS:O	0.41	2.16	4	1
1:A:8:ALA:HB1	1:A:10:TRP:CE2	0.41	2.50	9	1
1:A:7:GLN:O	1:A:31:TYR:CD1	0.40	2.74	10	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	35/42 (83%)	30±1 (85±3%)	5±1 (14±3%)	0±0 (1±1%)	24 71
All	All	700/840 (83%)	596 (85%)	97 (14%)	7 (1%)	24 71

All 2 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	13	SER	5
1	A	28	ALA	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	33/38 (87%)	21±2 (64±6%)	12±2 (36±6%)	1 9
All	All	660/760 (87%)	423 (64%)	237 (36%)	1 9

All 26 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	20	SER	20
1	A	10	TRP	20
1	A	22	ARG	20
1	A	38	LYS	19
1	A	35	ARG	14
1	A	21	GLU	13
1	A	19	LYS	12
1	A	11	SER	12

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Mol	Chain	Res	Type	Models (Total)
1	A	17	ARG	12
1	A	24	CYS	11
1	A	42	TYR	10
1	A	27	MET	9
1	A	32	CYS	8
1	A	18	ASP	8
1	A	12	HIS	8
1	A	25	LYS	7
1	A	13	SER	6
1	A	41	GLU	5
1	A	34	ASN	5
1	A	33	GLU	5
1	A	40	CYS	5
1	A	37	GLN	2
1	A	16	CYS	2
1	A	23	ASN	2
1	A	7	GLN	1
1	A	36	ASN	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)

1 non-standard protein/DNA/RNA residue is modelled in this entry.

In the following table, the Counts columns list the number of bonds for which Mogul statistics could be retrieved, the number of bonds that are observed in the model and the number of bonds that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length is the number of standard deviations the observed value is removed from the expected value. A bond length with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond lengths.

Mol	Type	Chain	Res	Link	Bond lengths		
					Counts	RMSZ	#Z>2
1	MED	A	2	1	5,7,8	0.39±0.01	0±0 (0±0%)

In the following table, the Counts columns list the number of angles for which Mogul statistics could be retrieved, the number of angles that are observed in the model and the number of angles that are defined in the chemical component dictionary. The Link column lists molecule types,

if any, to which the group is linked. The Z score for a bond angle is the number of standard deviations the observed value is removed from the expected value. A bond angle with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond angles.

Mol	Type	Chain	Res	Link	Bond angles		
					Counts	RMSZ	#Z>2
1	MED	A	2	1	4,7,9	0.92±0.01	0±0 (0±0%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	MED	A	2	1	-	0±0,4,6,8	0±0,0,0,0

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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)

No chemical shift data were provided