Full wwPDB NMR Structure Validation Report (i)

Apr 26, 2016 – 04:07 PM BST

PDB ID	:	1OT0
Title	:	Structure of Antimicrobial Peptide, HP (2-20) and its Analogues Derived from Helicobacter pylori, as Determined by 1H NMR Spectroscopy
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Deposited on	:	2003-03-21

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:

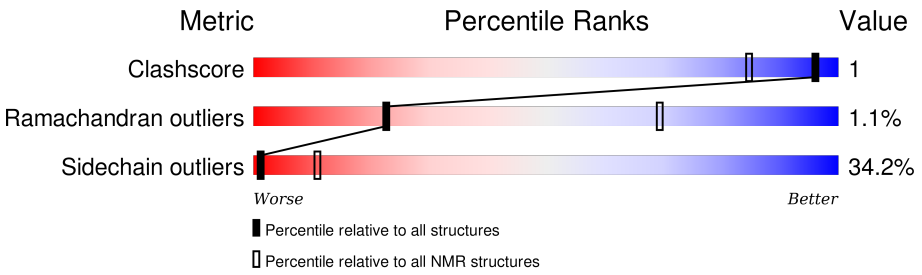
Cyrange	:	Kirchner and Güntert (2011)
NmrClust	:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Mogul	:	unknown
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	rb-20027457
Ideal 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 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	20	75% 25%

2 Ensemble composition and analysis (i)

This entry contains 20 models.

Cyrange was unable to find well-defined residues.

Error message: Only domains with < 8 residues could be identified.

NmrClust was unable to cluster the ensemble.

Error message: Wrapper check: not enough residues in core to run NmrClust

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 365 atoms, of which 195 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					Trace
			Total	C	H	N	O	
1	A	20	365	114	195	32	24	1

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	18	TRP	ASP	CONFLICT	UNP P56029

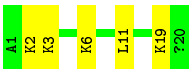
4 Residue-property plots (i)

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: 50S ribosomal protein L1

Chain A:



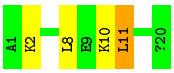
4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

- Molecule 1: 50S ribosomal protein L1

Chain A:



4.2.2 Score per residue for model 2

- Molecule 1: 50S ribosomal protein L1

Chain A:

4.2.3 Score per residue for model 3

- Molecule 1: 50S ribosomal protein L1

Chain A: 40% 55% 5%

4.2.4 Score per residue for model 4

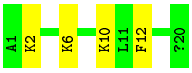
- Molecule 1: 50S ribosomal protein L1

Chain A: 50% 50%

4.2.5 Score per residue for model 5

- Molecule 1: 50S ribosomal protein L1

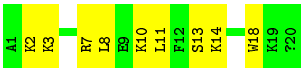
Chain A: 80% 20%



4.2.6 Score per residue for model 6

- Molecule 1: 50S ribosomal protein L1

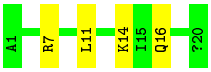
Chain A: 55% 45%



4.2.7 Score per residue for model 7

- Molecule 1: 50S ribosomal protein L1

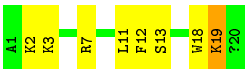
Chain A: 80% 20%



4.2.8 Score per residue for model 8

- Molecule 1: 50S ribosomal protein L1

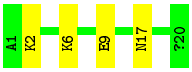
Chain A:



4.2.9 Score per residue for model 9

- Molecule 1: 50S ribosomal protein L1

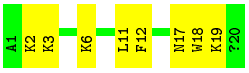
Chain A:



4.2.10 Score per residue for model 10

- Molecule 1: 50S ribosomal protein L1

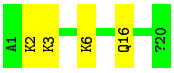
Chain A:



4.2.11 Score per residue for model 11

- Molecule 1: 50S ribosomal protein L1

Chain A:



4.2.12 Score per residue for model 12

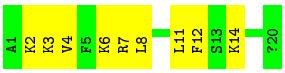
- Molecule 1: 50S ribosomal protein L1

Chain A:

4.2.13 Score per residue for model 13

- Molecule 1: 50S ribosomal protein L1

Chain A: 55% 45%



4.2.14 Score per residue for model 14

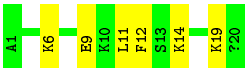
- Molecule 1: 50S ribosomal protein L1

Chain A: 55% 45%

4.2.15 Score per residue for model 15

- Molecule 1: 50S ribosomal protein L1

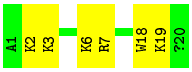
Chain A: 70% 30%



4.2.16 Score per residue for model 16

- Molecule 1: 50S ribosomal protein L1

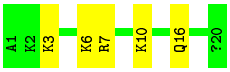
Chain A: 70% 30%



4.2.17 Score per residue for model 17

- Molecule 1: 50S ribosomal protein L1

Chain A: 75% 25%



4.2.18 Score per residue for model 18

- Molecule 1: 50S ribosomal protein L1

Chain A:

4.2.19 Score per residue for model 19

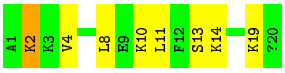
- Molecule 1: 50S ribosomal protein L1

Chain A:

4.2.20 Score per residue for model 20

- Molecule 1: 50S ribosomal protein L1

Chain A:



5 Refinement protocol and experimental data overview (i)

The models were refined using the following method: *DISTANCE GEOMETRY-DYNAMICAL SIMULATED ANNEALING*.

Of the 80 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
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: NH2

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	170	195	193	0±1
All	All	3400	3900	3860	9

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 1.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:11:LEU:HD23	1:A:11:LEU:O	0.61	1.95	13	1
1:A:11:LEU:O	1:A:11:LEU:HD13	0.58	1.99	1	1
1:A:11:LEU:HD12	1:A:12:PHE:N	0.53	2.19	8	1
1:A:4:VAL:HG23	1:A:7:ARG:HD2	0.45	1.87	13	1
1:A:4:VAL:HG13	1:A:7:ARG:HD3	0.45	1.89	2	1
1:A:4:VAL:HG23	1:A:7:ARG:CD	0.44	2.42	13	1
1:A:2:LYS:CG	1:A:4:VAL:HG23	0.43	2.43	20	1
1:A:6:LYS:O	1:A:9:GLU:CG	0.41	2.68	15	2

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	18/20 (90%)	16±1 (89±4%)	2±1 (10±4%)	0±1 (1±3%)	23	69
All	All	360/400 (90%)	321 (89%)	35 (10%)	4 (1%)	23	69

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	3	LYS	3
1	A	19	LYS	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	18/18 (100%)	12±2 (66±13%)	6±2 (34±13%)	1	11
All	All	360/360 (100%)	237 (66%)	123 (34%)	1	11

All 15 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	2	LYS	15
1	A	6	LYS	11
1	A	11	LEU	11
1	A	19	LYS	10
1	A	10	LYS	9
1	A	14	LYS	9
1	A	3	LYS	8
1	A	7	ARG	8

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Mol	Chain	Res	Type	Models (Total)
1	A	16	GLN	8
1	A	12	PHE	8
1	A	8	LEU	8
1	A	18	TRP	7
1	A	13	SER	6
1	A	17	ASN	3
1	A	9	GLU	2

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)

No chemical shift data were provided