Full wwPDB NMR Structure Validation Report (i)

Apr 21, 2024 – 07:39 AM EDT

PDB ID	:	2LVN
BMRB ID	:	18581
Title	:	Structure of the gp78 CUE domain
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Deposited on	:	2012-07-09

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
https://www.wwpdb.org/validation/2017/NMRValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

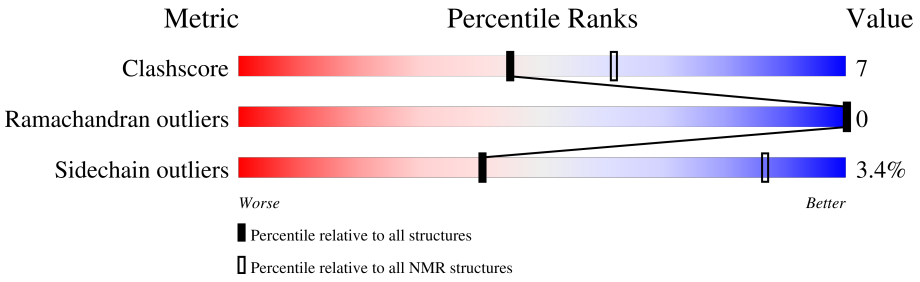
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

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 92%.

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	158937	12864
Ramachandran outliers	154571	11451
Sidechain outliers	154315	11428

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	C	52	65% 17% 17%

2 Ensemble composition and analysis (i)

This entry contains 20 models. Model 14 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	C:456-C:498 (43)	0.44	14

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 1 single-model cluster was found.

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

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 838 atoms, of which 419 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called E3 ubiquitin-protein ligase AMFR.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	C	52	838	264	419	72	81	2	0

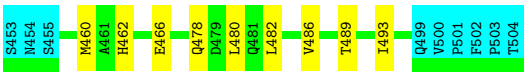
4 Residue-property plots (i)

4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA, DNA and oligosaccharide 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: E3 ubiquitin-protein ligase AMFR

Chain C: 65% 17% 17%



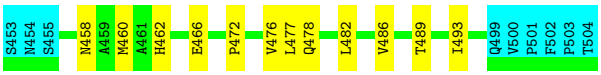
4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

• Molecule 1: E3 ubiquitin-protein ligase AMFR

Chain C: 60% 23% 17%



4.2.2 Score per residue for model 2

• Molecule 1: E3 ubiquitin-protein ligase AMFR

Chain C: 60% 23% 17%

4.2.3 Score per residue for model 3

- Molecule 1: E3 ubiquitin-protein ligase AMFR

Chain C: 58% 23% • 17%

S453 N454 S455 Q456 M460 A461 H462 E466 P472 V476 L477 Q478 D479 L480 Q481 L482 T483 R484 S485 V486 T489 I493 Q499 V500 P501 F502 P503 T504

4.2.4 Score per residue for model 4

- Molecule 1: E3 ubiquitin-protein ligase AMFR

Chain C: 58% 25% 17%

S453 N454 S455 Q456 M460 A461 H462 E466 P472 V476 L477 Q478 D479 L480 Q481 L482 T483 R484 S485 V486 T489 I493 Q499 V500 P501 F502 P503 T504

4.2.5 Score per residue for model 5

- Molecule 1: E3 ubiquitin-protein ligase AMFR

Chain C: 67% 15% 17%

S453 N454 S455 M460 A461 H462 E466 L480 V486 T489 N492 R497 I498 Q499 V500 P501 F502 P503 T504

4.2.6 Score per residue for model 6

- Molecule 1: E3 ubiquitin-protein ligase AMFR

Chain C: 65% 17% 17%

S453 N454 S455 H462 E466 Q478 D479 L480 Q481 L482 T483 R484 T489 I493 R497 I498 Q499 V500 P501 F502 P503 T504

4.2.7 Score per residue for model 7

- Molecule 1: E3 ubiquitin-protein ligase AMFR

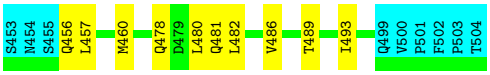
Chain C: 69% 13% 17%

S453 N454 S455 M460 Q478 L482 V486 T489 N492 I498 Q499 V500 P501 F502 P503 T504

4.2.8 Score per residue for model 8

- Molecule 1: E3 ubiquitin-protein ligase AMFR

Chain C: 63% 19% 17%



4.2.9 Score per residue for model 9

- Molecule 1: E3 ubiquitin-protein ligase AMFR

Chain C: 62% 21% 17%

4.2.10 Score per residue for model 10

- Molecule 1: E3 ubiquitin-protein ligase AMFR

Chain C: 62% 19% • 17%

4.2.11 Score per residue for model 11

- Molecule 1: E3 ubiquitin-protein ligase AMFR

Chain C: 65% 17% 17%

4.2.12 Score per residue for model 12

- Molecule 1: E3 ubiquitin-protein ligase AMFR

Chain C: 63% 19% 17%

4.2.13 Score per residue for model 13

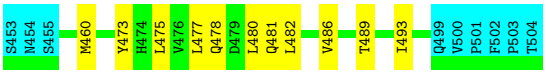
- Molecule 1: E3 ubiquitin-protein ligase AMFR

Chain C: 67% 15% 17%

4.2.14 Score per residue for model 14 (medoid)

- Molecule 1: E3 ubiquitin-protein ligase AMFR

Chain C: 62% 21% 17%



4.2.15 Score per residue for model 15

- Molecule 1: E3 ubiquitin-protein ligase AMFR

Chain C: 63% 19% 17%

4.2.16 Score per residue for model 16

- Molecule 1: E3 ubiquitin-protein ligase AMFR

Chain C: 73% 10% 17%

4.2.17 Score per residue for model 17

- Molecule 1: E3 ubiquitin-protein ligase AMFR

Chain C: 58% 25% 17%

4.2.18 Score per residue for model 18

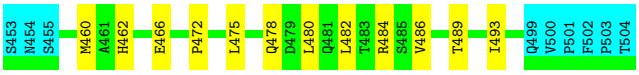
- Molecule 1: E3 ubiquitin-protein ligase AMFR

Chain C:

4.2.19 Score per residue for model 19

- Molecule 1: E3 ubiquitin-protein ligase AMFR

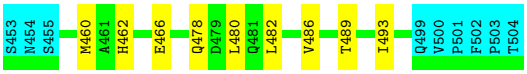
Chain C:



4.2.20 Score per residue for model 20

- Molecule 1: E3 ubiquitin-protein ligase AMFR

Chain C:



5 Refinement protocol and experimental data overview (i)

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

Of the 100 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
X-PLOR NIH	structure solution	
X-PLOR NIH	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)	working_cs.cif
Number of chemical shift lists	1
Total number of shifts	662
Number of shifts mapped to atoms	662
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	92%

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	C	350	354	352	5±1
All	All	7000	7080	7040	95

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 7.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:C:462:HIS:O	1:C:466:GLU:HG2	0.61	1.96	3	15
1:C:478:GLN:O	1:C:482:LEU:HG	0.58	1.98	14	9
1:C:489:THR:O	1:C:493:ILE:HG13	0.55	2.01	11	17
1:C:460:MET:HB3	1:C:486:VAL:CG1	0.52	2.33	14	14
1:C:457:LEU:HD23	1:C:460:MET:SD	0.50	2.47	10	2
1:C:475:LEU:HD23	1:C:478:GLN:NE2	0.49	2.23	14	1
1:C:480:LEU:O	1:C:484:ARG:HA	0.48	2.08	4	4
1:C:489:THR:HA	1:C:492:ASN:ND2	0.47	2.23	7	3
1:C:480:LEU:O	1:C:484:ARG:HG2	0.47	2.10	15	1
1:C:478:GLN:O	1:C:482:LEU:HD23	0.46	2.10	11	4
1:C:478:GLN:O	1:C:482:LEU:HD13	0.46	2.11	6	1
1:C:456:GLN:O	1:C:460:MET:HG3	0.45	2.11	3	6
1:C:474:HIS:O	1:C:478:GLN:HG3	0.45	2.10	9	1
1:C:472:PRO:O	1:C:476:VAL:HG23	0.45	2.11	1	6

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:C:460:MET:HE2	1:C:480:LEU:HD12	0.44	1.88	15	2
1:C:473:TYR:CE2	1:C:477:LEU:HD11	0.44	2.48	14	1
1:C:480:LEU:O	1:C:484:ARG:HD3	0.43	2.14	17	1
1:C:472:PRO:HG2	1:C:475:LEU:HD12	0.43	1.91	19	1
1:C:458:ASN:HA	1:C:477:LEU:CD2	0.42	2.43	1	1
1:C:489:THR:HA	1:C:492:ASN:HB2	0.42	1.91	15	1
1:C:457:LEU:HG	1:C:481:GLN:OE1	0.42	2.15	8	1
1:C:497:ARG:HA	1:C:497:ARG:NE	0.41	2.30	2	1
1:C:492:ASN:OD1	1:C:498:ILE:HD12	0.41	2.15	7	1
1:C:459:ALA:O	1:C:463:GLN:HG2	0.40	2.15	17	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	C	43/52 (83%)	43±0 (100±0%)	0±0 (0±0%)	0±0 (0±0%)	100	100
All	All	860/1040 (83%)	860 (100%)	0 (0%)	0 (0%)	100	100

There are no Ramachandran outliers.

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	C	40/49 (82%)	39±1 (97±3%)	1±1 (3±3%)	40	87
All	All	800/980 (82%)	773 (97%)	27 (3%)	40	87

All 9 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	C	480	LEU	8
1	C	497	ARG	5
1	C	486	VAL	3
1	C	481	GLN	3
1	C	477	LEU	3
1	C	456	GLN	2
1	C	465	GLN	1
1	C	484	ARG	1
1	C	463	GLN	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 monosaccharides 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 92% for the well-defined parts and 90% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

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	662
Number of shifts mapped to atoms	662
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

7.1.2 Chemical shift referencing (i)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	50	-0.42 ± 0.17	None needed (< 0.5 ppm)
$^{13}C_{\beta}$	48	0.33 ± 0.12	None needed (< 0.5 ppm)
$^{13}C'$	47	-0.30 ± 0.22	None needed (< 0.5 ppm)
^{15}N	45	0.41 ± 0.40	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 92%, i.e. 576 atoms were assigned a chemical shift out of a possible 625. 0 out of 9 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	211/212 (100%)	85/85 (100%)	85/86 (99%)	41/41 (100%)
Sidechain	339/378 (90%)	231/247 (94%)	101/117 (86%)	7/14 (50%)

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	Total	^{1}H	^{13}C	^{15}N
Aromatic	26/35 (74%)	13/17 (76%)	13/14 (93%)	0/4 (0%)
Overall	576/625 (92%)	329/349 (94%)	199/217 (92%)	48/59 (81%)

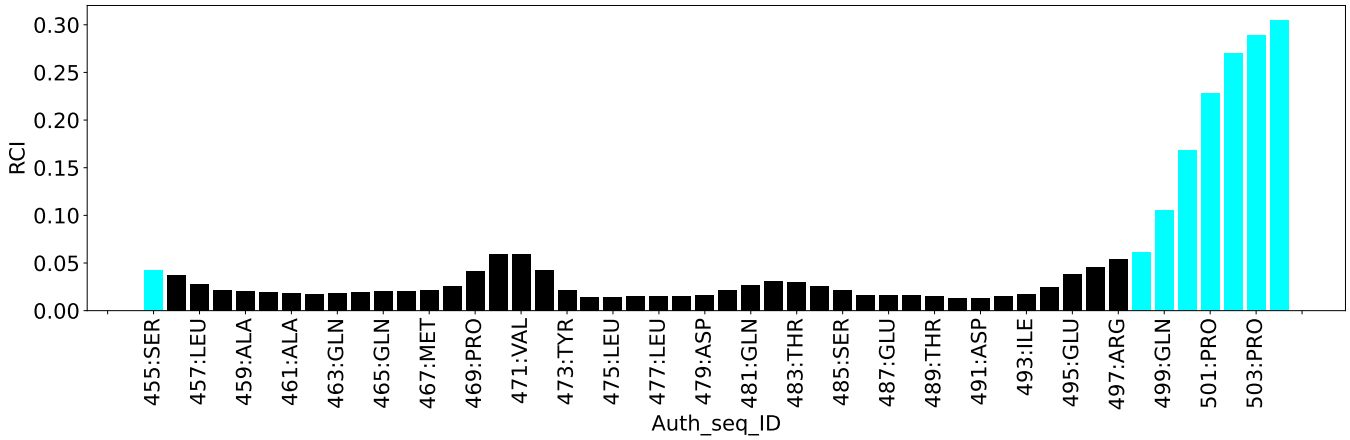
The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 90%, i.e. 662 atoms were assigned a chemical shift out of a possible 736. 0 out of 10 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	238/253 (94%)	96/101 (95%)	97/104 (93%)	45/48 (94%)
Sidechain	388/438 (89%)	264/286 (92%)	116/136 (85%)	8/16 (50%)
Aromatic	36/45 (80%)	18/22 (82%)	18/19 (95%)	0/4 (0%)
Overall	662/736 (90%)	378/409 (92%)	231/259 (89%)	53/68 (78%)

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.If well-defined core and ill-defined regions are not identified then it is shown as gray bars.

Random coil index (RCI) for chain C: