wwPDB NMR Structure Validation Summary Report (i)

Apr 26, 2016 – 11:27 PM BST

PDB ID	:	2KHD
Title	:	Solution NMR structure of VC_A0919 from Vibrio cholerae. Northeast Structural Genomics Consortium Target VcR52
Authors	:	Ramelot, T.A.; Cort, J.R.; Wang, H.; Ciccosanti, C.; Jiang, M.; Liu, J.; Rost, B.; Swapna, G.V.T.; Acton, T.B.; Xiao, R.; Everett, J.K.; Montelione, G.T.; Kennedy, M.A.; Northeast Structural Genomics Consortium (NESG)
Deposited on	:	2009-04-02

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:

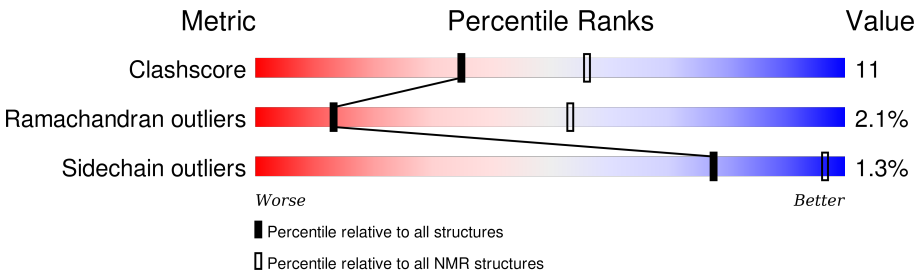
Cyrange	:	Kirchner and Güntert (2011)
NmrClust	:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Mogul	:	unknown
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	rb-20027457
Ideal 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 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	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	108	59% • 37%

2 Ensemble composition and analysis (i)

This entry contains 20 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:30-A:97 (68)	0.41	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. No single-model clusters were found.

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

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 1657 atoms, of which 811 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Uncharacterized protein VC_A0919.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	108	1657	529	811	148	164	5	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	101	LEU	-	EXPRESSION TAG	UNP Q9KL30
A	102	GLU	-	EXPRESSION TAG	UNP Q9KL30
A	103	HIS	-	EXPRESSION TAG	UNP Q9KL30
A	104	HIS	-	EXPRESSION TAG	UNP Q9KL30
A	105	HIS	-	EXPRESSION TAG	UNP Q9KL30
A	106	HIS	-	EXPRESSION TAG	UNP Q9KL30
A	107	HIS	-	EXPRESSION TAG	UNP Q9KL30
A	108	HIS	-	EXPRESSION TAG	UNP Q9KL30

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: Uncharacterized protein VC_A0919

Chain A: 59% • 37%

M1 S2 N3 Q4 T5 C6 V7 E8 N9 E10 V11 C12 E13 A14 C15 G16 C17 A18 G19 E20 I21 G22 F23 I24 I25 R26 E27 G28 D29 S39 A60 T74 E87 L98 A99 R100 L101 E102 H103 H104 H105 H106 H107 H108

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: Uncharacterized protein VC_A0919

Chain A: 49% 13% • 37%

M1 S2 N3 Q4 T5 C6 V7 E8 N9 E10 V11 C12 E13 A14 C15 G16 C17 A18 G19 E20 I21 G22 F23 I24 I25 R26 E27 G28 D29 L36 S39 H43 Y51 I52 S53 I54 A55 K56 A67 P68 E75 L76 H77 E87 H88 L89 T95 R96 A97 L98 A99 R100

L101 E102 H103 H104 H105 H106 H107 H108

5 Refinement protocol and experimental data overview (i)

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

Of the 125 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	2.20
X-PLOR NIH	refinement	2.20

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 16238
Number of chemical shift lists	1
Total number of shifts	1231
Number of shifts mapped to atoms	1231
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%

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	535	531	531	11±5
All	All	10700	10620	10620	224

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 11.

5 of 139 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:43:HIS:CE1	1:A:47:LYS:HZ3	0.71	2.03	20	2
1:A:72:ASN:O	1:A:74:THR:HG23	0.67	1.89	5	2
1:A:70:ALA:O	1:A:72:ASN:N	0.66	2.29	15	3
1:A:43:HIS:CE1	1:A:47:LYS:NZ	0.64	2.66	6	3
1:A:74:THR:OG1	1:A:74:THR:O	0.63	2.14	14	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	68/108 (63%)	64±2 (94±3%)	2±1 (4±2%)	1±1 (2±2%)	13 53
All	All	1360/2160 (63%)	1283 (94%)	48 (4%)	29 (2%)	13 53

5 of 9 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	39	SER	11
1	A	60	ALA	5
1	A	71	ASP	3
1	A	30	ASP	2
1	A	40	ASP	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	55/88 (62%)	54±1 (99±1%)	1±1 (1±1%)	78 96
All	All	1100/1760 (62%)	1086 (99%)	14 (1%)	78 96

5 of 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	A	87	GLU	3
1	A	74	THR	3
1	A	48	LEU	2
1	A	75	GLU	1
1	A	93	LEU	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 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 92% for the well-defined parts and 84% for the entire structure.

7.1 Chemical shift list 1

File name: BMRB entry 16238

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	1231
Number of shifts mapped to atoms	1231
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	1

7.1.2 Chemical shift referencing (i)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	102	-0.13 ± 0.20	None needed (< 0.5 ppm)
$^{13}C_{\beta}$	96	0.06 ± 0.07	None needed (< 0.5 ppm)
$^{13}C'$	95	0.07 ± 0.09	None needed (< 0.5 ppm)
^{15}N	97	0.02 ± 0.15	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. 763 atoms were assigned a chemical shift out of a possible 826. 13 out of 14 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	333/338 (99%)	134/135 (99%)	133/136 (98%)	66/67 (99%)
Sidechain	375/414 (91%)	226/239 (95%)	145/160 (91%)	4/15 (27%)

Continued on next page...

Continued from previous page...

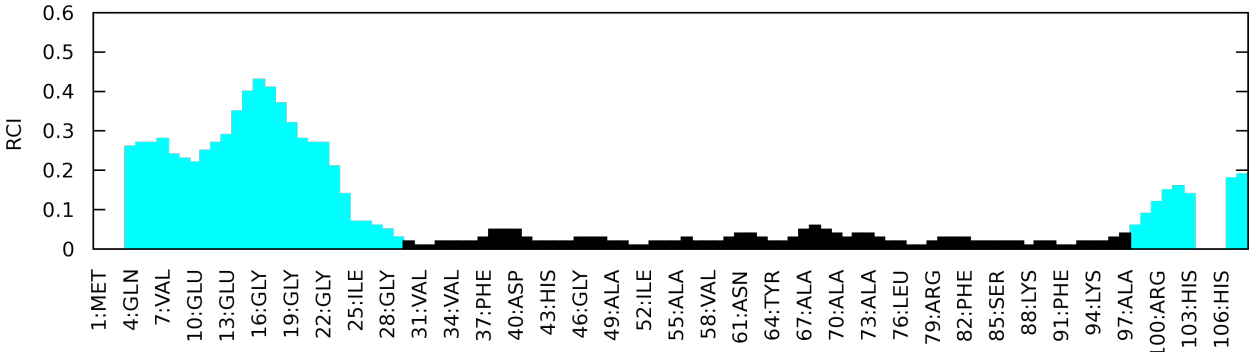
	Total	^{1}H	^{13}C	^{15}N
Aromatic	55/74 (74%)	29/40 (72%)	26/32 (81%)	0/2 (0%)
Overall	763/826 (92%)	389/414 (94%)	304/328 (93%)	70/84 (83%)

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	79	ARG	CG	34.40	33.23 – 21.23	6.0

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: