Full wwPDB NMR Structure Validation Report (i)

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PDB ID	:	2N57
BMRB ID	:	25695
Title	:	NMR structure of Acyl carrier protein from Brucella melitensis
Authors	:	Barnwal, R.; Varani, G.; Seattle Structural Genomics Center for Infectious Disease (SSGCID)
Deposited on	:	2015-07-08

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:

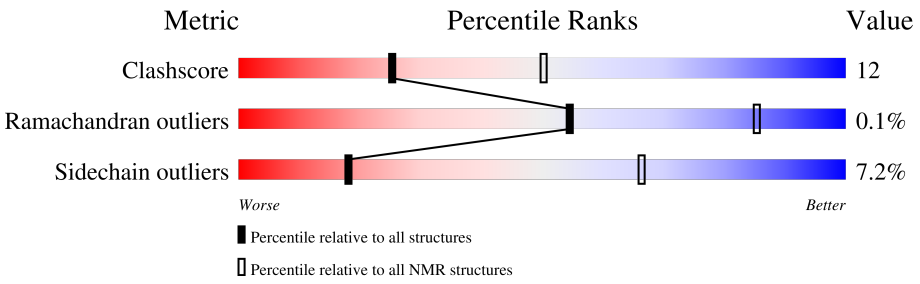
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson 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 87%.

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	A	78	77% 19% • •

2 Ensemble composition and analysis (i)

This entry contains 10 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:3-A:78 (76)	0.36	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 2 clusters and 2 single-model clusters were found.

Cluster number	Models
1	1, 2, 5, 6, 7, 9
2	3, 4
Single-model clusters	8; 10

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 1145 atoms, of which 564 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Acyl carrier protein.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	78	1145	364	564	88	127	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: Acyl carrier protein

Chain A:

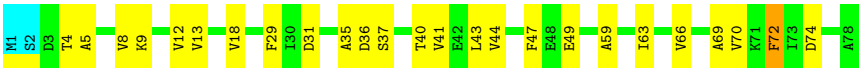
4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1 (medoid)

• Molecule 1: Acyl carrier protein

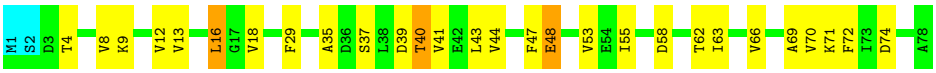
Chain A:



4.2.2 Score per residue for model 2

• Molecule 1: Acyl carrier protein

Chain A:



4.2.3 Score per residue for model 3

- Molecule 1: Acyl carrier protein

Chain A: 68% 27%

M1 S2 D3 T4 V8 K9 V12 V13 E14 H15 L16 G17 V18 F29 A35 D36 S37 T40 V41 E42 L43 V44 E48 V53 E54 I55 I63 V66 F72 I73 D74 K75 A78

4.2.4 Score per residue for model 4

- Molecule 1: Acyl carrier protein

Chain A: 71% 26%

M1 S2 D3 T4 V8 K9 V12 V13 E14 H15 V18 F29 I30 D31 A35 D36 S37 T40 V41 V44 E48 V53 E54 I55 V66 V70 K71 F72 I73 D74 A78

4.2.5 Score per residue for model 5

- Molecule 1: Acyl carrier protein

Chain A: 67% 27%

M1 S2 D3 T4 R7 V8 K9 K10 I11 V12 V13 V18 V23 F29 I30 A35 D39 T40 V44 F47 E48 V53 L64 T65 V66 G67 D68 A69 V70 K71 F72 I73 D74 A78

4.2.6 Score per residue for model 6

- Molecule 1: Acyl carrier protein

Chain A: 74% 21%

M1 S2 V8 V12 V13 L16 G17 V18 D21 F29 I30 D31 A35 D36 S37 T40 V41 E42 L43 V44 F47 A59 V66 F72 A78

4.2.7 Score per residue for model 7

- Molecule 1: Acyl carrier protein

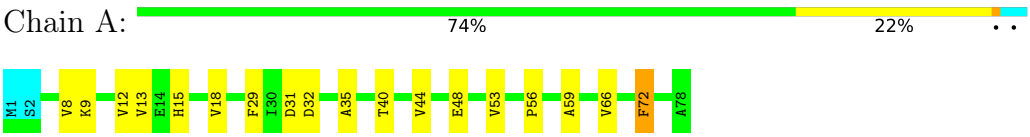
Chain A: 72% 24%

M1 S2 V8 K9 V12 V13 L16 G17 V18 S28 F29 A35 D39 T40 V44 E48 E49 E50 I63 L64 T65 V66 A69 V70 K71 F72 A78

4.2.8 Score per residue for model 8

- Molecule 1: Acyl carrier protein

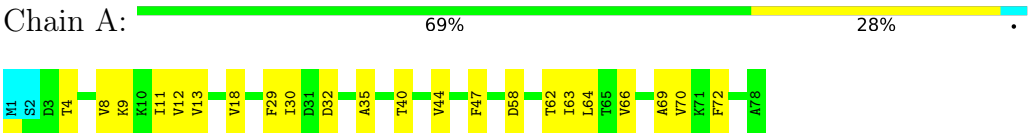
Chain A:



4.2.9 Score per residue for model 9

- Molecule 1: Acyl carrier protein

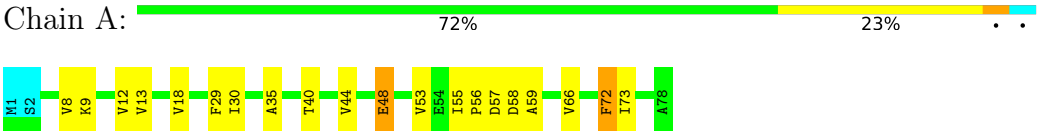
Chain A:



4.2.10 Score per residue for model 10

- Molecule 1: Acyl carrier protein

Chain A:



5 Refinement protocol and experimental data overview (i)

The models were refined using the following method: *torsion angle dynamics*.

Of the 200 calculated structures, 10 were deposited, based on the following criterion: *target function*.

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

Software name	Classification	Version
CYANA	geometry optimization	
CYANA	refinement	
CYANA	structure solution	

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	858
Number of shifts mapped to atoms	858
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	87%

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	567	550	550	13±3
All	All	5670	5500	5500	129

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 12.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:8:VAL:HG21	1:A:70:VAL:HG22	0.79	1.53	5	3
1:A:16:LEU:HD12	1:A:18:VAL:HG13	0.75	1.58	7	3
1:A:43:LEU:HD12	1:A:47:PHE:CZ	0.65	2.27	1	1
1:A:59:ALA:HB1	1:A:72:PHE:CE2	0.64	2.28	8	3
1:A:43:LEU:HD22	1:A:47:PHE:CZ	0.64	2.27	6	2
1:A:13:VAL:HG13	1:A:18:VAL:O	0.63	1.94	7	10
1:A:40:THR:O	1:A:44:VAL:HG23	0.61	1.96	8	9
1:A:44:VAL:HG12	1:A:48:GLU:OE2	0.60	1.96	7	1
1:A:48:GLU:OE2	1:A:53:VAL:HG23	0.60	1.96	8	1
1:A:9:LYS:O	1:A:13:VAL:HG23	0.60	1.97	7	9
1:A:8:VAL:O	1:A:12:VAL:HG23	0.59	1.97	6	10
1:A:58:ASP:O	1:A:62:THR:HG23	0.59	1.97	2	2
1:A:29:PHE:CZ	1:A:66:VAL:HG22	0.59	2.32	8	10
1:A:8:VAL:CG2	1:A:70:VAL:HG22	0.59	2.25	5	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:37:SER:O	1:A:41:VAL:HG23	0.59	1.97	2	5
1:A:48:GLU:HG3	1:A:53:VAL:HG23	0.57	1.77	5	4
1:A:11:ILE:HD12	1:A:47:PHE:CE1	0.56	2.35	9	2
1:A:8:VAL:HG11	1:A:70:VAL:HG22	0.56	1.77	9	1
1:A:9:LYS:CB	1:A:23:VAL:HG11	0.56	2.31	5	1
1:A:30:ILE:HD11	1:A:40:THR:OG1	0.55	2.02	10	3
1:A:4:THR:HG21	1:A:74:ASP:HB2	0.54	1.77	4	5
1:A:9:LYS:HB3	1:A:23:VAL:HG11	0.54	1.79	5	1
1:A:16:LEU:HD12	1:A:18:VAL:CG1	0.53	2.30	7	3
1:A:59:ALA:HB1	1:A:72:PHE:CZ	0.53	2.39	10	1
1:A:4:THR:O	1:A:8:VAL:HG23	0.52	2.05	9	1
1:A:66:VAL:O	1:A:70:VAL:HG23	0.51	2.04	2	3
1:A:29:PHE:O	1:A:35:ALA:HB3	0.51	2.06	9	10
1:A:16:LEU:HD21	1:A:43:LEU:HD21	0.51	1.83	3	1
1:A:56:PRO:HG2	1:A:59:ALA:HB2	0.48	1.85	8	1
1:A:48:GLU:OE2	1:A:55:ILE:HD11	0.47	2.09	2	1
1:A:8:VAL:HG21	1:A:70:VAL:HA	0.47	1.87	1	1
1:A:55:ILE:HG21	1:A:72:PHE:CE1	0.46	2.45	4	2
1:A:63:ILE:CG2	1:A:69:ALA:HB2	0.46	2.41	7	3
1:A:8:VAL:CB	1:A:70:VAL:HG22	0.46	2.40	7	4
1:A:28:SER:OG	1:A:65:THR:HG22	0.45	2.11	7	1
1:A:48:GLU:CG	1:A:53:VAL:HG23	0.45	2.42	4	1
1:A:48:GLU:HG2	1:A:53:VAL:HG23	0.45	1.89	4	1
1:A:8:VAL:HG11	1:A:70:VAL:CG2	0.43	2.43	9	2
1:A:55:ILE:HD12	1:A:56:PRO:O	0.43	2.14	10	1
1:A:8:VAL:CG1	1:A:70:VAL:HG22	0.42	2.43	9	1
1:A:44:VAL:CG2	1:A:63:ILE:HG21	0.42	2.43	3	1
1:A:8:VAL:HG22	1:A:73:ILE:HD13	0.41	1.92	10	1
1:A:63:ILE:HG21	1:A:69:ALA:HB2	0.40	1.92	2	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	75/78 (96%)	71±1 (94±1%)	4±1 (5±1%)	0±0 (0±0%)	54 85

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	750/780 (96%)	708 (94%)	41 (5%)	1 (0%)	54 85

All 1 unique Ramachandran outliers are listed below.

Mol	Chain	Res	Type	Models (Total)
1	A	23	VAL	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	61/63 (97%)	57±1 (93±2%)	4±1 (7±2%)	18 66
All	All	610/630 (97%)	566 (93%)	44 (7%)	18 66

All 19 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	72	PHE	10
1	A	31	ASP	4
1	A	48	GLU	4
1	A	16	LEU	3
1	A	39	ASP	3
1	A	40	THR	3
1	A	15	HIS	3
1	A	64	LEU	2
1	A	32	ASP	2
1	A	36	ASP	1
1	A	49	GLU	1
1	A	71	LYS	1
1	A	75	LYS	1
1	A	7	ARG	1
1	A	68	ASP	1
1	A	21	ASP	1
1	A	50	GLU	1
1	A	57	ASP	1
1	A	58	ASP	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 87% for the well-defined parts and 87% 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	858
Number of shifts mapped to atoms	858
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
$^{13}C_{\alpha}$	78	-0.34 ± 0.16	None needed (< 0.5 ppm)
$^{13}C_{\beta}$	73	0.16 ± 0.14	None needed (< 0.5 ppm)
$^{13}C'$	75	-0.31 ± 0.11	None needed (< 0.5 ppm)
^{15}N	77	0.85 ± 0.38	Should be applied

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 87%, i.e. 842 atoms were assigned a chemical shift out of a possible 963. 0 out of 15 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	378/383 (99%)	154/156 (99%)	149/152 (98%)	75/75 (100%)
Sidechain	443/533 (83%)	292/348 (84%)	151/177 (85%)	0/8 (0%)

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	Total	^{1}H	^{13}C	^{15}N
Aromatic	21/47 (45%)	17/24 (71%)	4/22 (18%)	0/1 (0%)
Overall	842/963 (87%)	463/528 (88%)	304/351 (87%)	75/84 (89%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 87%, i.e. 858 atoms were assigned a chemical shift out of a possible 986. 0 out of 15 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	387/393 (98%)	157/160 (98%)	153/156 (98%)	77/77 (100%)
Sidechain	450/546 (82%)	296/357 (83%)	154/181 (85%)	0/8 (0%)
Aromatic	21/47 (45%)	17/24 (71%)	4/22 (18%)	0/1 (0%)
Overall	858/986 (87%)	470/541 (87%)	311/359 (87%)	77/86 (90%)

7.1.4 Statistically unusual chemical shifts (i)

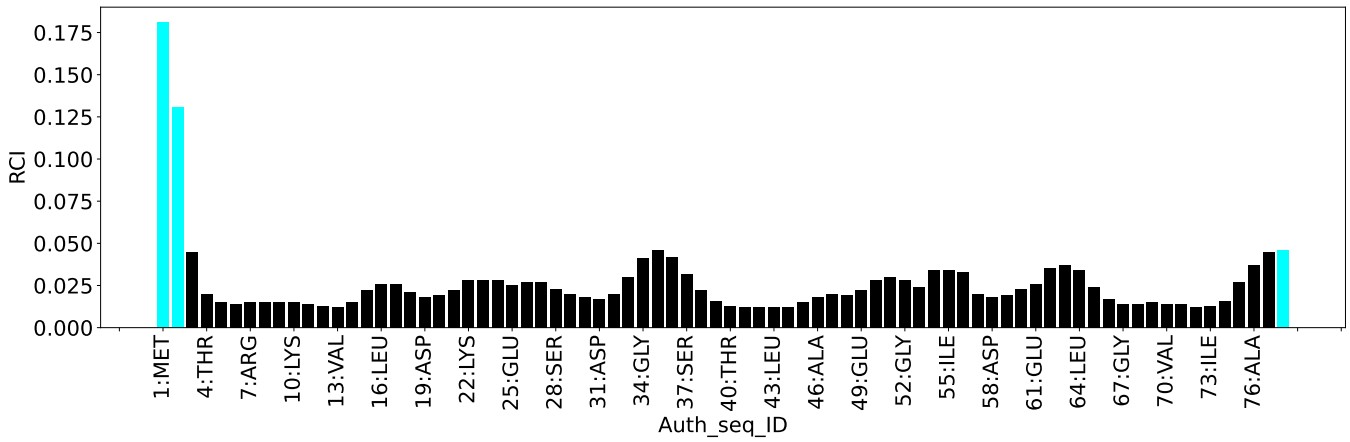
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, *ppm*	Expected range, *ppm*	Z-score
1	A	50	GLU	HG3	0.70	1.20 – 3.30	-7.3

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 A:


RCI
0.175
0.150
0.125
0.100
0.075
0.050
0.025
0.000
1:MET
4:THR
7:ARG
10:LYS
13:VAL
16:LEU
19:ASP
22:LYS
25:GLU
28:SER
31:ASP
34:GLY
37:SER
40:THR
43:LEU
46:ALA
49:GLU
52:GLY
55:ILE
58:ASP
61:GLU
64:LEU
67:GLY
70:VAL
73:ILE
76:ALA
Auth_seq_ID