Full wwPDB NMR Structure Validation Report (i)

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PDB ID	:	2MPO
Title	:	Structural basis of Toxoplasma gondii MIC2-Associated Protein interaction with MIC2
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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:

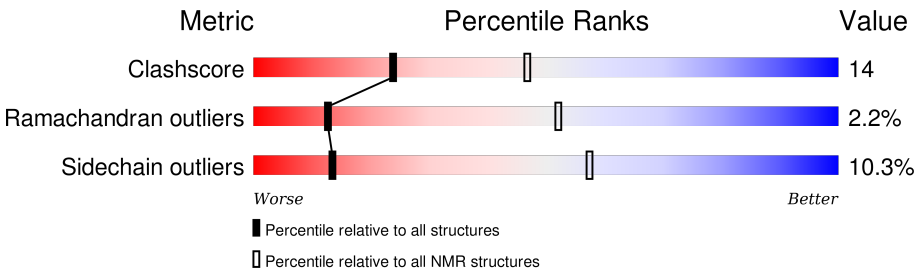
Cyrange	:	Kirchner and Güntert (2011)
NmrClust	:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Mogul	:	unknown
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	rb-20027457
Ideal 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 89%.

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	182	64% 31% 5%

2 Ensemble composition and analysis (i)

This entry contains 1 models. Identification of well-defined residues and clustering analysis are not possible.

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 2660 atoms, of which 1308 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called MIC2-associated protein.

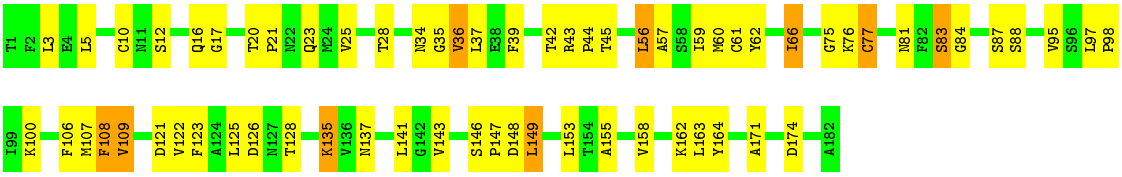
Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	182	2660	841	1308	222	279	10	0

4 Residue-property plots (i)

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: MIC2-associated protein

Chain A:



5 Refinement protocol and experimental data overview (i)

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

Of the 1 calculated structures, 1 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
ARIA	structure solution	
ARIA	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)	2mpo_cs.str
Number of chemical shift lists	1
Total number of shifts	2049
Number of shifts mapped to atoms	2049
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	89%

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	1352	1308	1305	38
All	All	1352	1308	1305	38

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 14.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)
1:A:59:ILE:HG22	1:A:77:CYS:SG	0.71	2.25
1:A:25:VAL:O	1:A:109:VAL:HB	0.65	1.90
1:A:75:GLY:O	1:A:98:PRO:HA	0.57	2.00
1:A:95:VAL:HB	1:A:97:LEU:CD2	0.57	2.30
1:A:28:THR:HG22	1:A:107:MET:SD	0.53	2.43
1:A:123:PHE:HA	1:A:135:LYS:O	0.53	2.03
1:A:34:ASN:O	1:A:66:ILE:HB	0.52	2.05
1:A:12:SER:C	1:A:163:LEU:HD21	0.52	2.24
1:A:84:GLY:H	1:A:87:SER:HB3	0.51	1.66
1:A:109:VAL:CG2	1:A:121:ASP:HB2	0.49	2.37
1:A:81:ASN:ND2	1:A:143:VAL:HG12	0.49	2.21
1:A:83:SER:HA	1:A:87:SER:OG	0.49	2.07
1:A:37:LEU:HG	1:A:106:PHE:CE2	0.49	2.43
1:A:36:VAL:HA	1:A:61:CYS:O	0.48	2.09
1:A:83:SER:OG	1:A:88:SER:HA	0.47	2.09

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Atom-1	Atom-2	Clash(Å)	Distance(Å)
1:A:97:LEU:HG	1:A:122:VAL:HG21	0.47	1.86
1:A:84:GLY:N	1:A:87:SER:HB3	0.47	2.24
1:A:37:LEU:O	1:A:60:MET:HA	0.47	2.10
1:A:126:ASP:OD1	1:A:128:THR:HG22	0.46	2.10
1:A:16:GLN:H	1:A:171:ALA:HB3	0.46	1.71
1:A:37:LEU:HD22	1:A:37:LEU:H	0.45	1.71
1:A:76:LYS:HA	1:A:97:LEU:O	0.45	2.12
1:A:39:PHE:HB2	1:A:108:PHE:CD2	0.45	2.46
1:A:42:THR:O	1:A:149:LEU:HD22	0.45	2.12
1:A:57:ALA:HB2	1:A:143:VAL:HG11	0.44	1.89
1:A:155:ALA:HB3	1:A:158:VAL:CG2	0.43	2.43
1:A:43:ARG:CG	1:A:44:PRO:HD2	0.43	2.43
1:A:10:CYS:HB2	1:A:12:SER:O	0.42	2.14
1:A:35:GLY:O	1:A:155:ALA:HB1	0.42	2.14
1:A:37:LEU:HG	1:A:106:PHE:CD2	0.42	2.50
1:A:146:SER:H	1:A:149:LEU:HG	0.41	1.76
1:A:17:GLY:N	1:A:147:PRO:HA	0.41	2.31
1:A:20:THR:HB	1:A:21:PRO:HD2	0.41	1.91
1:A:109:VAL:HG22	1:A:121:ASP:HB2	0.41	1.91
1:A:56:LEU:HD21	1:A:84:GLY:HA3	0.41	1.93
1:A:39:PHE:HB2	1:A:108:PHE:CE2	0.41	2.51
1:A:44:PRO:HD3	1:A:148:ASP:O	0.40	2.16
1:A:162:LYS:HB3	1:A:164:TYR:CE2	0.40	2.51

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	180/182 (99%)	154 (86%)	22 (12%)	4 (2%)	13 52
All	All	180/182 (99%)	154 (86%)	22 (12%)	4 (2%)	13 52

All 4 Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type
1	A	23	GLN
1	A	5	LEU
1	A	83	SER
1	A	36	VAL

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	155/155 (100%)	139 (90%)	16 (10%)	13	57
All	All	155/155 (100%)	139 (90%)	16 (10%)	13	57

All 16 residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type
1	A	56	LEU
1	A	135	LYS
1	A	153	LEU
1	A	62	TYR
1	A	137	ASN
1	A	45	THR
1	A	149	LEU
1	A	174	ASP
1	A	100	LYS
1	A	125	LEU
1	A	3	LEU
1	A	108	PHE
1	A	141	LEU
1	A	77	CYS
1	A	66	ILE
1	A	109	VAL

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 89% for the well-defined parts and 89% for the entire structure.

7.1 Chemical shift list 1

File name: 2mpo_cs.str

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	2049
Number of shifts mapped to atoms	2049
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	7

7.1.2 Chemical shift referencing (i)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	180	-0.14 ± 0.05	None needed (< 0.5 ppm)
$^{13}C_{\beta}$	164	-0.26 ± 0.12	None needed (< 0.5 ppm)
$^{13}C'$	180	0.30 ± 0.11	None needed (< 0.5 ppm)
^{15}N	169	0.31 ± 0.26	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 89%, i.e. 1812 atoms were assigned a chemical shift out of a possible 2037. 33 out of 33 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	876/896 (98%)	347/357 (97%)	360/364 (99%)	169/175 (97%)
Sidechain	826/997 (83%)	500/579 (86%)	317/386 (82%)	9/32 (28%)

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	Total	^{1}H	^{13}C	^{15}N
Aromatic	110/144 (76%)	62/76 (82%)	46/60 (77%)	2/8 (25%)
Overall	1812/2037 (89%)	909/1012 (90%)	723/810 (89%)	180/215 (84%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 89%, i.e. 1812 atoms were assigned a chemical shift out of a possible 2037. 33 out of 33 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	876/896 (98%)	347/357 (97%)	360/364 (99%)	169/175 (97%)
Sidechain	826/997 (83%)	500/579 (86%)	317/386 (82%)	9/32 (28%)
Aromatic	110/144 (76%)	62/76 (82%)	46/60 (77%)	2/8 (25%)
Overall	1812/2037 (89%)	909/1012 (90%)	723/810 (89%)	180/215 (84%)

7.1.4 Statistically unusual chemical shifts (i)

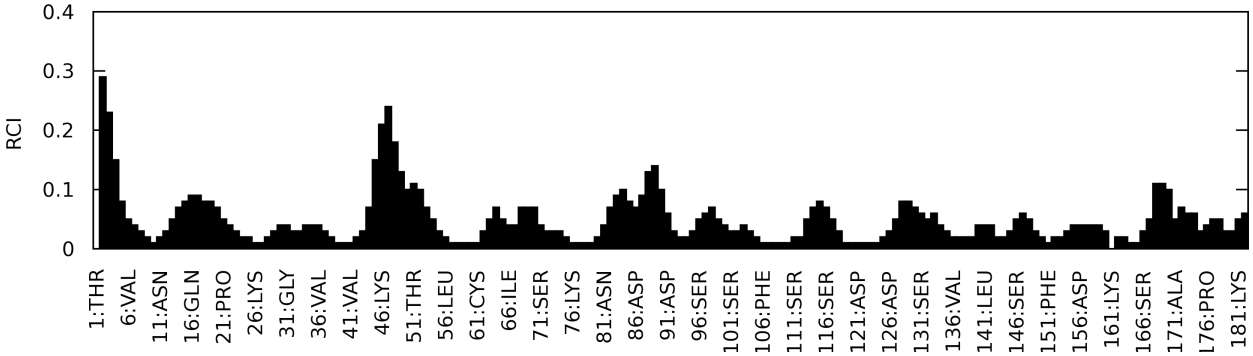
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

Mol	Chain	Res	Type	Atom	Shift, *ppm*	Expected range, *ppm*	Z-score
1	A	125	LEU	CG	43.70	32.55 – 21.05	14.7
1	A	37	LEU	CG	42.20	32.55 – 21.05	13.4
1	A	37	LEU	HG	-1.00	3.16 – -0.14	-7.6
1	A	125	LEU	HG	-0.76	3.16 – -0.14	-6.9
1	A	76	LYS	HZ2	3.03	10.62 – 4.22	-6.9
1	A	76	LYS	HZ3	3.03	10.62 – 4.22	-6.9
1	A	76	LYS	HZ1	3.03	10.62 – 4.22	-6.9

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:


RCI
0.4
0.3
0.2
0.1
0
1:THR
6:VAL
11:ASN
16:GLN
21:PRO
26:LYS
31:GLY
36:VAL
41:VAL
46:LYS
51:THR
56:LEU
61:CYS
66:ILE
71:SER
76:LYS
81:ASN
86:ASP
91:ASP
96:SER
101:SER
106:PHE
111:SER
116:SER
121:ASP
126:ASP
131:SER
136:VAL
141:LEU
146:SER
151:PHE
156:ASP
161:LYS
166:SER
171:ALA
176:PRO
181:LYS