wwPDB NMR Structure Validation Summary Report

Mar 16, 2022 – 12:33 PM EDT

PDB ID	:	5KRW
Title	:	Recognition and targeting mechanisms by chaperones in flagella assembly and operation
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Deposited on	:	2016-07-07

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
https://www.wwpdb.org/validation/2017/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:

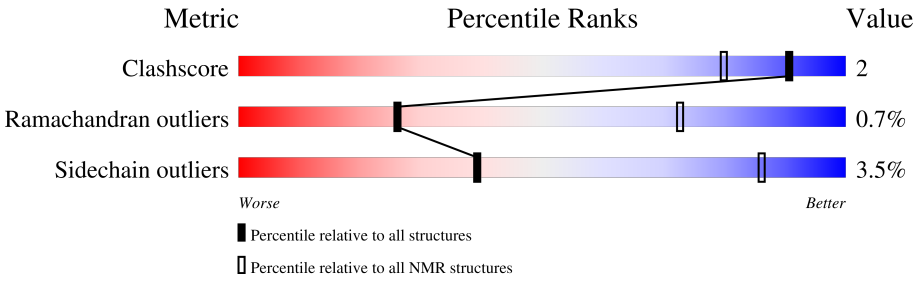
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	2.27
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.27

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 66%.

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	155	83% · 13%

2 Ensemble composition and analysis

This entry contains 20 models. Model 9 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	A:2-A:97, A:429-A:467 (135)	0.27	9

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 3 single-model clusters were found.

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

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 2452 atoms, of which 1234 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Flagellar protein FliT,Flagellar hook-associated protein 2 fusion.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	155	2452	763	1234	207	242	6	0

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	96	VAL	-	linker	UNP P0A1N2
A	97	LEU	-	linker	UNP P0A1N2
A	98	PHE	-	linker	UNP P0A1N2
A	99	GLN	-	linker	UNP P0A1N2
A	100	GLY	-	linker	UNP P0A1N2
A	101	PRO	-	linker	UNP P0A1N2
A	102	SER	-	linker	UNP P0A1N2
A	103	ALA	-	linker	UNP P0A1N2
A	104	GLY	-	linker	UNP P0A1N2
A	105	LEU	-	linker	UNP P0A1N2
A	106	VAL	-	linker	UNP P0A1N2
A	107	PRO	-	linker	UNP P0A1N2
A	108	ARG	-	linker	UNP P0A1N2
A	109	GLY	-	linker	UNP P0A1N2
A	110	SER	-	linker	UNP P0A1N2
A	111	GLY	-	linker	UNP P0A1N2
A	112	GLY	-	linker	UNP P0A1N2
A	113	ILE	-	linker	UNP P0A1N2
A	114	GLU	-	linker	UNP P0A1N2
A	115	GLY	-	linker	UNP P0A1N2

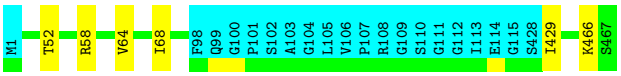
4 Residue-property plots (i)

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: Flagellar protein FliT,Flagellar hook-associated protein 2 fusion

Chain A:



4.2 Residue scores for the representative (medoid) model from the NMR ensemble

The representative model is number 9. Colouring as in section 4.1 above.

• Molecule 1: Flagellar protein FliT,Flagellar hook-associated protein 2 fusion

Chain A:

5 Refinement protocol and experimental data overview

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

Of the 100 calculated structures, 20 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
CNS	refinement	1.3
CYANA	structure calculation	3.97
TALOS	geometry optimization	

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	1431
Number of shifts mapped to atoms	1431
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	66%

6 Model quality

6.1 Standard geometry

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

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	1086	1104	1104	3±1
All	All	21720	22080	22080	68

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 2.

5 of 22 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:64:VAL:HG23	1:A:464:MET:SD	0.55	2.41	8	7
1:A:21:LEU:HB2	1:A:33:LEU:HD12	0.51	1.81	6	8
1:A:86:LEU:HD21	1:A:443:LEU:HB2	0.50	1.82	4	2
1:A:60:ILE:HA	1:A:63:MET:HE2	0.50	1.83	6	3
1:A:64:VAL:O	1:A:68:ILE:HG13	0.47	2.09	12	15

6.3 Torsion angles

6.3.1 Protein backbone

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	134/155 (86%)	128±1 (95±1%)	5±1 (4±1%)	1±0 (1±0%)	26 73
All	All	2680/3100 (86%)	2557 (95%)	103 (4%)	20 (1%)	26 73

All 3 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	52	THR	15
1	A	51	GLN	4
1	A	55	GLY	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	124/137 (91%)	120±1 (96±1%)	4±1 (4±1%)	39 86
All	All	2480/2740 (91%)	2392 (96%)	88 (4%)	39 86

5 of 16 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	429	ILE	20
1	A	466	LYS	20
1	A	58	ARG	14
1	A	27	ARG	6
1	A	69	LYS	5

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

The completeness of assignment taking into account all chemical shift lists is 66% for the well-defined parts and 63% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *assigned_chemical_shift_list_1*

7.1.1 Bookkeeping

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	1431
Number of shifts mapped to atoms	1431
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

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	137	-0.92 ± 0.10	Should be applied
$^{13}C_{\beta}$	122	0.30 ± 0.11	None needed (< 0.5 ppm)
$^{13}C'$	125	0.35 ± 0.15	None needed (< 0.5 ppm)
^{15}N	137	-0.25 ± 0.11	None needed (< 0.5 ppm)

7.1.3 Completeness of resonance assignments

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 66%, i.e. 1125 atoms were assigned a chemical shift out of a possible 1710. 26 out of 27 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	604/671 (90%)	231/268 (86%)	246/270 (91%)	127/133 (95%)
Sidechain	466/956 (49%)	256/556 (46%)	210/354 (59%)	0/46 (0%)

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	Total	^{1}H	^{13}C	^{15}N
Aromatic	55/83 (66%)	29/43 (67%)	24/38 (63%)	2/2 (100%)
Overall	1125/1710 (66%)	516/867 (60%)	480/662 (73%)	129/181 (71%)

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.

Random coil index (RCI) for chain A: