



Full wwPDB NMR Structure Validation Report ⓘ

May 29, 2020 – 07:23 am BST

PDB ID : 5JZR
Title : Solid-state MAS NMR structure of Acinetobacter phage 205 (AP205) coat protein in assembled capsid particles
Authors : Jaudzems, K.; Andreas, L.B.; Stanek, J.; Lalli, D.; Bertarello, A.; Le Marchand, T.; Cala-De Paepe, D.; Kotlovica, S.; Akopjana, I.; Knott, B.; Wegner, S.; Engelke, F.; Lesage, A.; Emsley, L.; Tars, K.; Herrmann, T.; Pintacuda, G.
Deposited on : 2016-05-17

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 ⓘ symbol.

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

Cyrange : Kirchner and Güntert (2011)
NmrClust : Kelley et al. (1996)
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 : 2.11
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLID-STATE NMR



The overall completeness of chemical shifts assignment is 34%.

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

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 $\leq 5\%$

Mol	Chain	Length	Quality of chain	
1	A	131		
1	B	131		

2 Ensemble composition and analysis

This entry contains 20 models. Model 7 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *closest to the average*.

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:4-A:8, A:15-A:35, A:44-A:59, A:72-A:128, B:204-B:208, B:215-B:235, B:244-B:259, B:272-B:328 (198)	0.93	7

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 4 clusters and 2 single-model clusters were found.

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

3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 3936 atoms, of which 1974 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Coat protein.

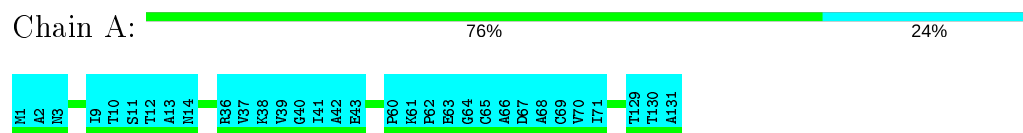
Mol	Chain	Residues	Atoms						Trace
1	A	131	Total	C	H	N	O	S	0
			1968	610	987	173	193	5	
1	B	131	Total	C	H	N	O	S	0
			1968	610	987	173	193	5	

4 Residue-property plots

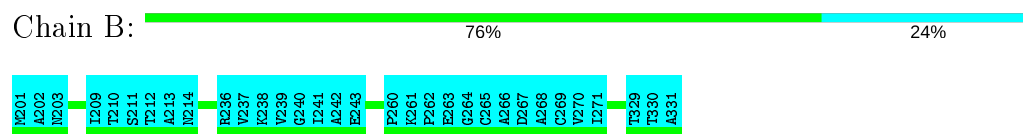
4.1 Average score per residue in the NMR ensemble

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: Coat protein



- Molecule 1: Coat protein

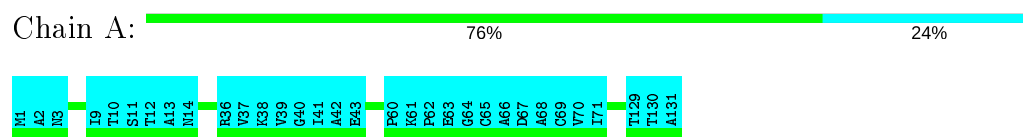


4.2 Scores per residue for each member of the ensemble

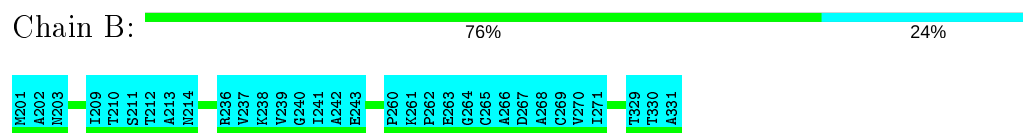
Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

- Molecule 1: Coat protein

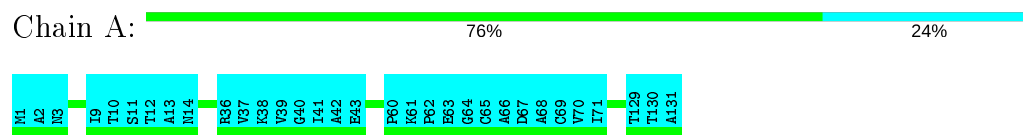


- Molecule 1: Coat protein

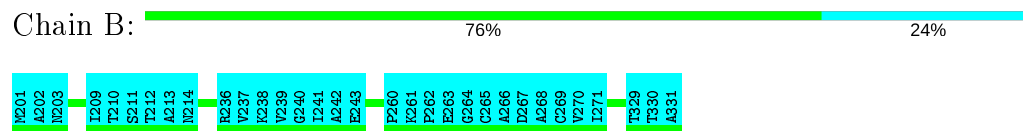


4.2.2 Score per residue for model 2

- Molecule 1: Coat protein

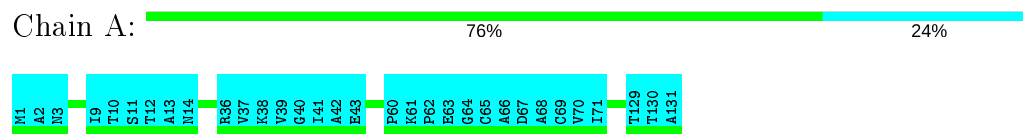


- Molecule 1: Coat protein

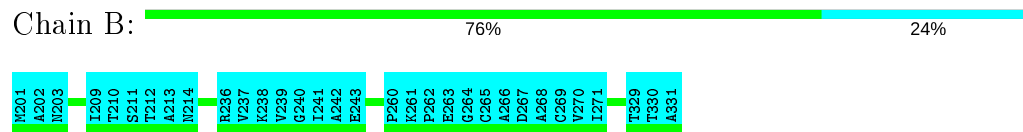


4.2.3 Score per residue for model 3

- Molecule 1: Coat protein

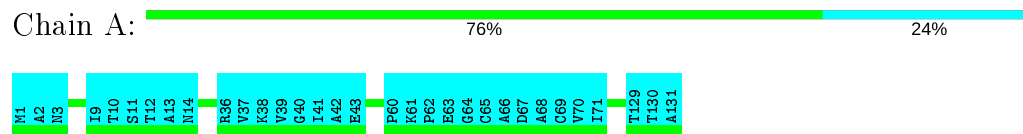


- Molecule 1: Coat protein

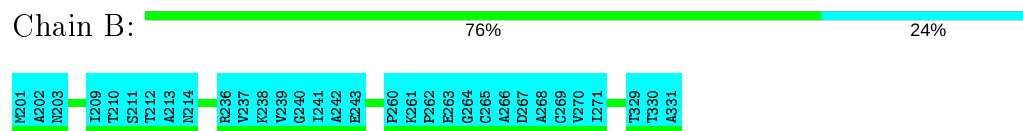


4.2.4 Score per residue for model 4

- Molecule 1: Coat protein

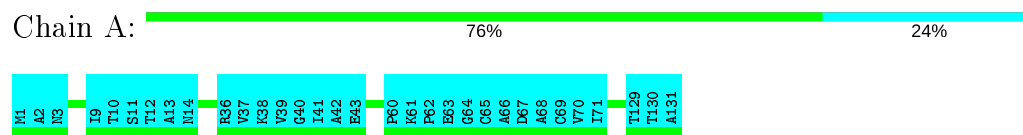


- Molecule 1: Coat protein

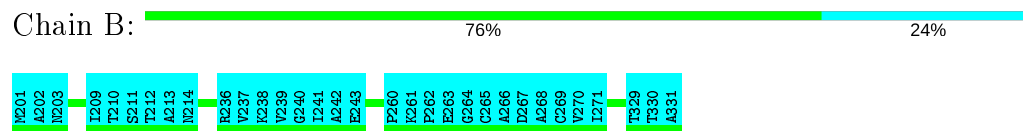


4.2.5 Score per residue for model 5

- Molecule 1: Coat protein

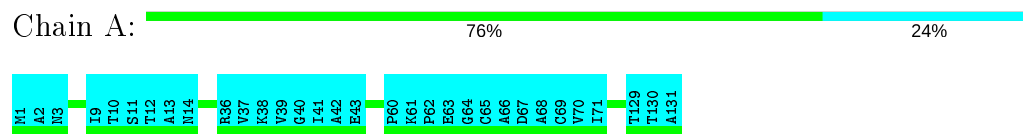


- Molecule 1: Coat protein

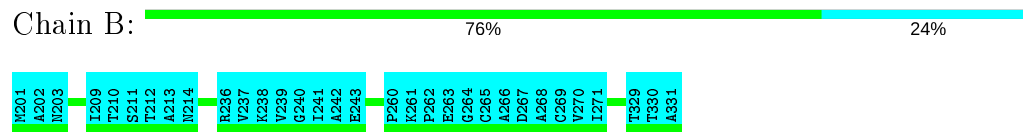


4.2.6 Score per residue for model 6

- Molecule 1: Coat protein

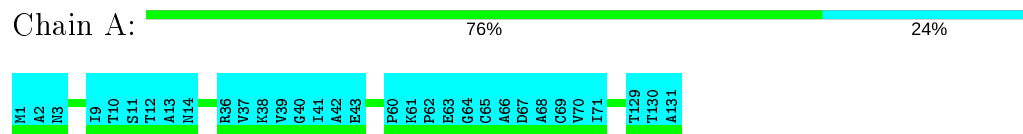


- Molecule 1: Coat protein

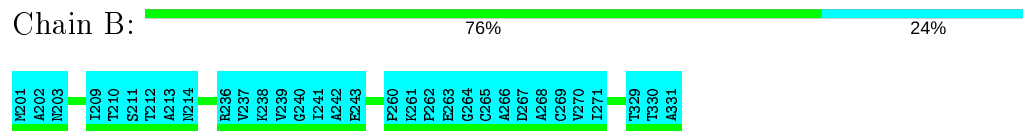


4.2.7 Score per residue for model 7 (medoid)

- Molecule 1: Coat protein

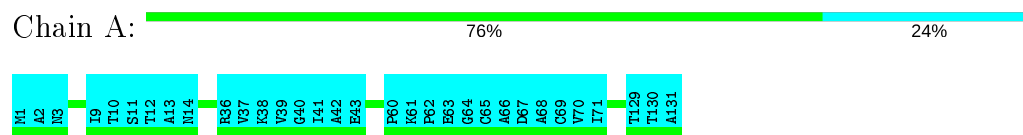


- Molecule 1: Coat protein

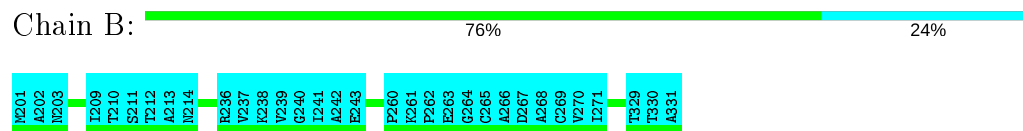


4.2.8 Score per residue for model 8

- Molecule 1: Coat protein

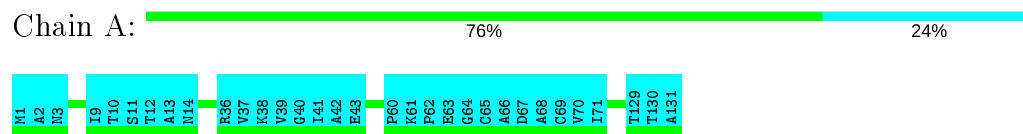


- Molecule 1: Coat protein

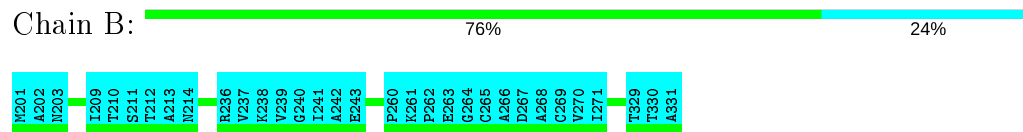


4.2.9 Score per residue for model 9

- Molecule 1: Coat protein

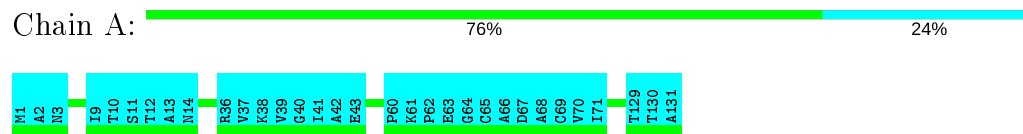


- Molecule 1: Coat protein

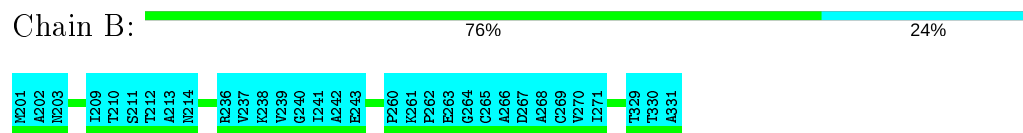


4.2.10 Score per residue for model 10

- Molecule 1: Coat protein

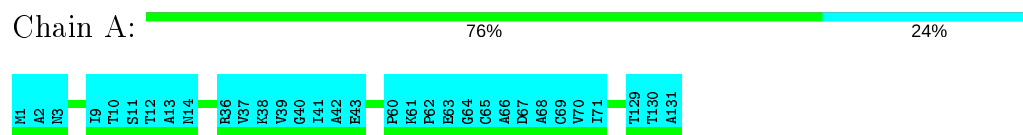


- Molecule 1: Coat protein

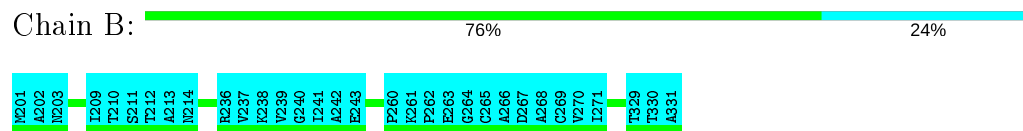


4.2.11 Score per residue for model 11

- Molecule 1: Coat protein

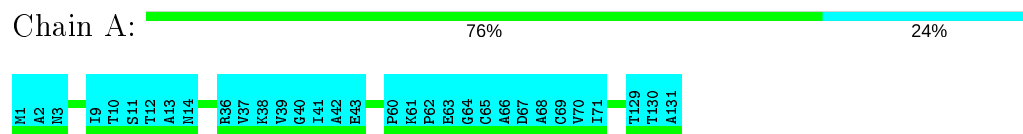


- Molecule 1: Coat protein

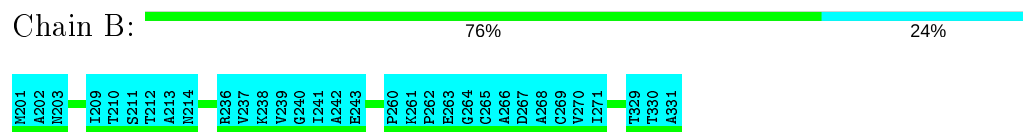


4.2.12 Score per residue for model 12

- Molecule 1: Coat protein

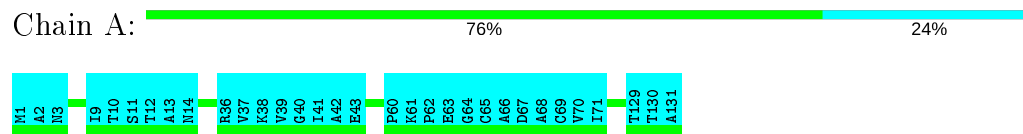


- Molecule 1: Coat protein

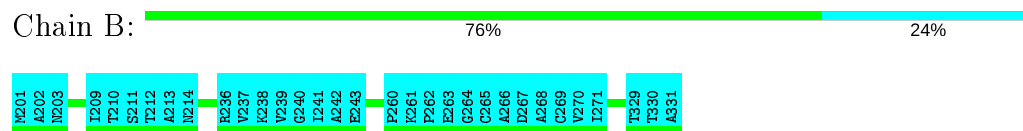


4.2.13 Score per residue for model 13

- Molecule 1: Coat protein

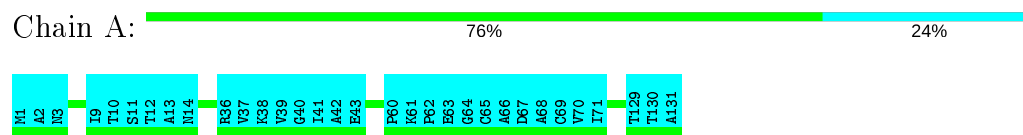


- Molecule 1: Coat protein

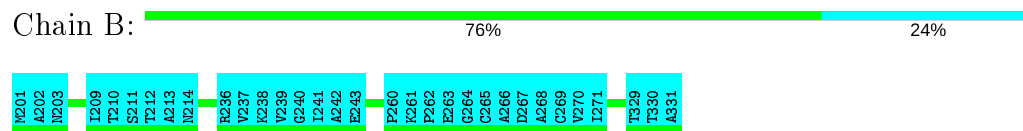


4.2.14 Score per residue for model 14

- Molecule 1: Coat protein

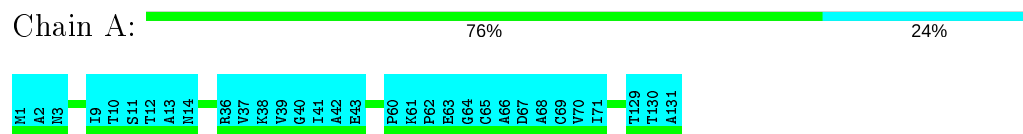


- Molecule 1: Coat protein

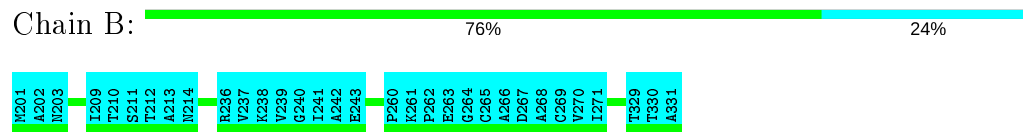


4.2.15 Score per residue for model 15

- Molecule 1: Coat protein

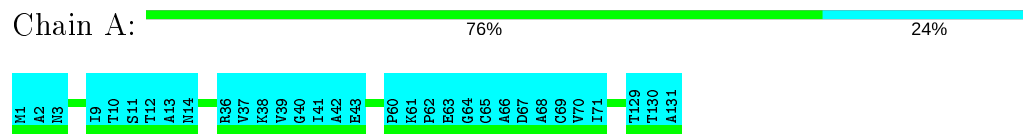


- Molecule 1: Coat protein

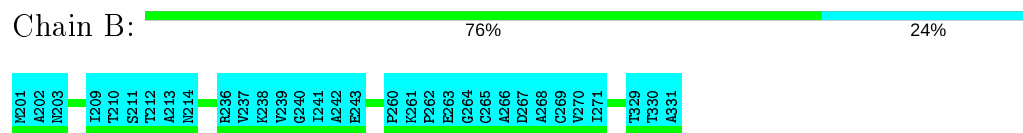


4.2.16 Score per residue for model 16

- Molecule 1: Coat protein

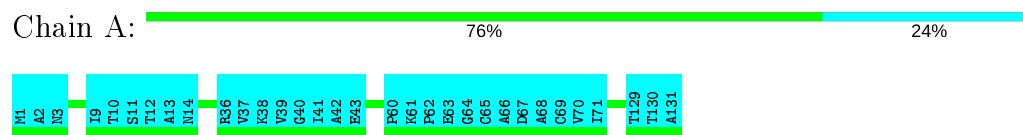


- Molecule 1: Coat protein

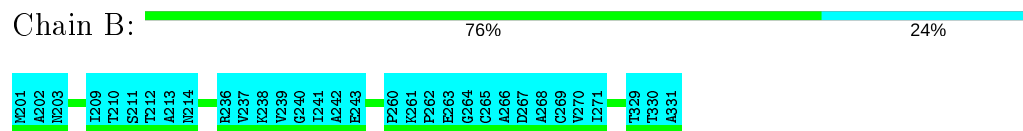


4.2.17 Score per residue for model 17

- Molecule 1: Coat protein

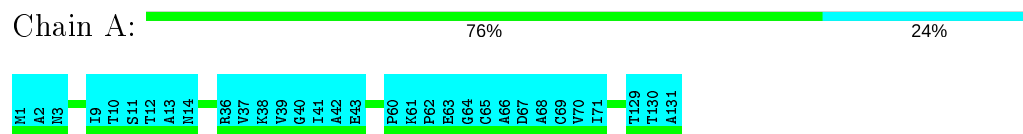


- Molecule 1: Coat protein

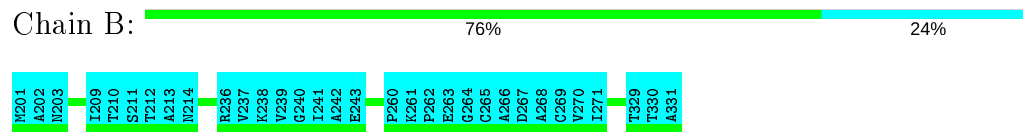


4.2.18 Score per residue for model 18

- Molecule 1: Coat protein

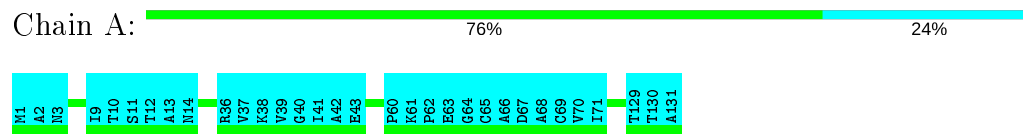


- Molecule 1: Coat protein

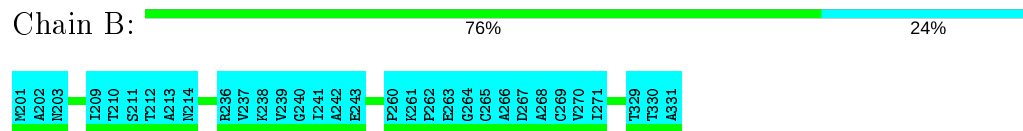


4.2.19 Score per residue for model 19

- Molecule 1: Coat protein

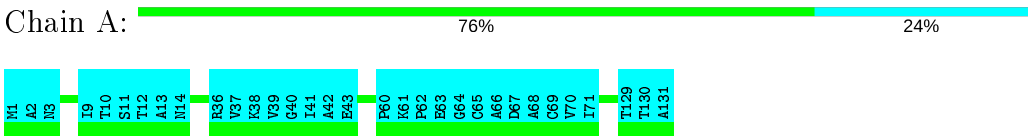


- Molecule 1: Coat protein

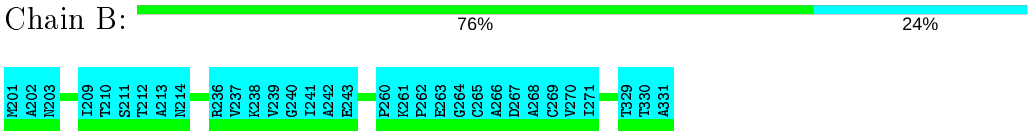


4.2.20 Score per residue for model 20

● Molecule 1: Coat protein



● Molecule 1: Coat protein



5 Refinement protocol and experimental data overview

The models were refined using the following method: *torsion angle 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
UNIO	structure calculation	2.6
CYANA	structure calculation	3.97

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)	input_cs.cif
Number of chemical shift lists	1
Total number of shifts	1018
Number of shifts mapped to atoms	1018
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	34%

Note: This is a solid-state NMR structure, where hydrogen atoms are typically not assigned a chemical shift value, which may lead to lower completeness of assignment measure.

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
All	All	30360	30320	0	-

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 -.

There are no clashes.

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	0	-	-	-	-
1	B	0	-	-	-	-
All	All	0	-	-	-	-

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	A	0	-	-	-
1	B	0	-	-	-
All	All	0	-	-	-

There are no protein residues with a non-rotameric sidechain to report.

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 34% for the well-defined parts and 29% for the entire structure.

7.1 Chemical shift list 1

File name: input_cs.cif

Chemical shift list name: AP205_BMRB.str

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	1018
Number of shifts mapped to atoms	1018
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 \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	110	-0.03 ± 0.23	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	97	0.28 ± 0.19	None needed (< 0.5 ppm)
$^{13}\text{C}'$	101	0.08 ± 0.14	None needed (< 0.5 ppm)
^{15}N	100	-0.49 ± 0.37	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 34%, i.e. 807 atoms were assigned a chemical shift out of a possible 2368. 7 out of 32 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	450/966 (47%)	180/384 (47%)	184/396 (46%)	86/186 (46%)
Sidechain	353/1254 (28%)	206/736 (28%)	147/456 (32%)	0/62 (0%)

Continued on next page...

Continued from previous page...

	Total	¹H	¹³C	¹⁵N
Aromatic	4/148 (3%)	3/78 (4%)	0/64 (0%)	1/6 (17%)
Overall	807/2368 (34%)	389/1198 (32%)	331/916 (36%)	87/254 (34%)

Note: This is a solid-state NMR structure, where hydrogen atoms are typically not assigned a chemical shift value, which may lead to lower completeness of assignment measure.

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 29%, i.e. 895 atoms were assigned a chemical shift out of a possible 3048. 7 out of 38 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Backbone	513/1278 (40%)	204/508 (40%)	211/524 (40%)	98/246 (40%)
Sidechain	378/1622 (23%)	219/948 (23%)	159/598 (27%)	0/76 (0%)
Aromatic	4/148 (3%)	3/78 (4%)	0/64 (0%)	1/6 (17%)
Overall	895/3048 (29%)	426/1534 (28%)	370/1186 (31%)	99/328 (30%)

Note: This is a solid-state NMR structure, where hydrogen atoms are typically not assigned a chemical shift value, which may lead to lower completeness of assignment measure.

7.1.4 Statistically unusual chemical shifts ⓘ

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	103	ASN	HB2	0.79	4.36 – 1.26	-6.5
1	A	83	ILE	HD11	-1.19	2.13 – -0.77	-6.4
1	A	83	ILE	HD12	-1.19	2.13 – -0.77	-6.4
1	A	83	ILE	HD13	-1.19	2.13 – -0.77	-6.4
1	A	104	VAL	HG13	-0.80	2.13 – -0.47	-6.3
1	A	104	VAL	HG12	-0.80	2.13 – -0.47	-6.3
1	A	104	VAL	HG11	-0.80	2.13 – -0.47	-6.3

7.1.5 Random Coil Index (RCI) plots ⓘ

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:

