

Full wwPDB NMR Structure Validation Report (i)

Feb 23, 2022 – 12:49 PM EST

PDB ID	:	1Y03
Title	:	Solution structure of a recombinant type I sculpin antifreeze protein
Authors	:	Kwan, A.H.Y.; Fairley, K.; Anderberg, P.I.; Liew, C.W.; Harding, M.M.;
		Mackay, J.P.
Deposited on	:	2004-11-14

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

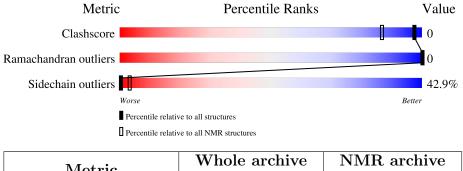
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	2.26
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.26

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 was not calculated.

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 $(\#\operatorname{Entries})$
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 ch	nain	
1	А	35	40%	6%	54%	-



2 Ensemble composition and analysis (i)

This entry contains 20 models. Model 2 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:13-A:28 (16)	0.18	2	

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. No single-model clusters were found.

Cluster number	Models
1	$\begin{array}{c}1,\ 2,\ 3,\ 5,\ 6,\ 7,\ 8,\ 9,\ 10,\ 11,\ 14,\ 15,\ 16,\ 17,\ 18,\ 19,\\20\end{array}$
2	4, 12, 13



3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 437 atoms, of which 222 are hydrogens and 0 are deuteriums.

• Molecule 1 is a protein called Antifreeze peptide SS-3.

Mol	Chain	Residues		A	Atom	S			Trace
1	٨	25	Total	С	Η	Ν	0	S	0
	A	35	437	128	222	42	44	1	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	1	GLY	-	cloning artifact	UNP P04367
А	2	SER	-	cloning artifact	UNP P04367

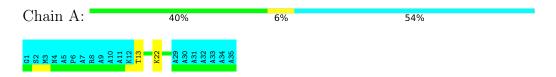


4 Residue-property plots (i)

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: Antifreeze peptide SS-3

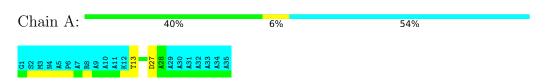


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

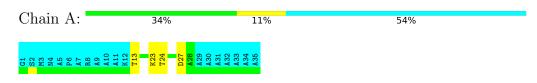
4.2.1 Score per residue for model 1

• Molecule 1: Antifreeze peptide SS-3



4.2.2 Score per residue for model 2 (medoid)

• Molecule 1: Antifreeze peptide SS-3





4.2.3 Score per residue for model 3

• Molecule 1: Antifreeze peptide SS-3

Chain A:	40%	6%	54%
G1 S2 M3 M4 M4 A1 A1 A11 A11 A11 A11 A11	D16 A29 A30 A31 A32 A33 A34 A35 A35		

4.2.4 Score per residue for model 4

• Molecule 1: Antifreeze peptide SS-3

Chain A:	31%	14%	54%
G1 S2 M3 M3 M4 M5 A5 A5 A10 A10 A11 T13 T13	D16 K22 K23 K23 A30 A31 A31	A32 A34 A35 A35	

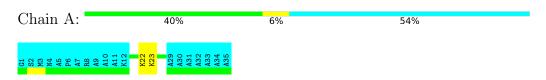
4.2.5 Score per residue for model 5

• Molecule 1: Antifreeze peptide SS-3

Chain A:	34%	6% 6%	54%
61 82 85 85 85 85 87 841 8110 81110 81110 81112 8112	K22 K23 T24 D27 D27 A28 A28 A33 A33 A32 A33	A 34 A 34 A 35	

4.2.6 Score per residue for model 6

• Molecule 1: Antifreeze peptide SS-3



4.2.7 Score per residue for model 7

G1 N4 N3 A5 A7 A9 A9 A9 A9

Molecule 1: Antifreeze peptide SS-3
Chain A: 37% 6% · 54%



4.2.8 Score per residue for model 8

• Molecule 1: Antifreeze peptide SS-3

Chain A:	40%	6%	54%
G1 S2 N4 M3 A1 A1 A11 A11 X12 A11 X12 X22 X22	A29 A30 A31 A32 A33 A34 A34 A35		

4.2.9 Score per residue for model 9

• Molecule 1: Antifreeze peptide SS-3

Chain A:	37%	9%	54%
G1 82 85 87 87 87 87 87 87 87 87 87 87 87 87 87	A9 A110 K12 T13 K22 K22 A34 A34 A33 A34 A34 A34 A34		

4.2.10 Score per residue for model 10

• Molecule 1: Antifreeze peptide SS-3

Chain A:	37%	9%	54%
61 82 82 83 83 84 84 84 8410 8410 8411 813 8113 8113	K22 K23 A29 A30 A32 A33 A35 A35		

4.2.11 Score per residue for model 11

• Molecule 1: Antifreeze peptide SS-3



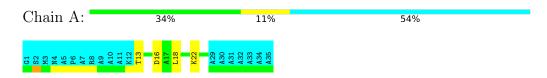
4.2.12 Score per residue for model 12

Molecule 1: Antifreeze peptide SS-3
Chain A: 40% 6% 54%



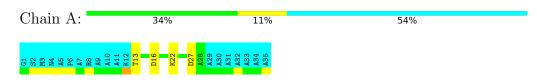
4.2.13 Score per residue for model 13

• Molecule 1: Antifreeze peptide SS-3



4.2.14 Score per residue for model 14

• Molecule 1: Antifreeze peptide SS-3



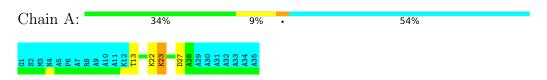
4.2.15 Score per residue for model 15

• Molecule 1: Antifreeze peptide SS-3

Chain A:	37%	9%	54%
61 82 82 85 85 84 84 84 84 84 84 84 84 84 84 84 84 84	T13 T13 K22 K23 A29 A31 A33 A33 A33 A34 A35	22	

4.2.16 Score per residue for model 16

• Molecule 1: Antifreeze peptide SS-3

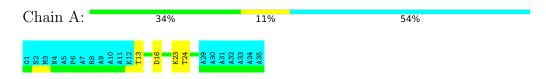


4.2.17 Score per residue for model 17



4.2.18 Score per residue for model 18

• Molecule 1: Antifreeze peptide SS-3



4.2.19 Score per residue for model 19

• Molecule 1: Antifreeze peptide SS-3

Chain A:	37%	9%	54%	
61 82 85 85 85 85 84 84 810 811 811	T13 K22 K23 K23 A30 A31 A33 A33 A33	A34 A35		

4.2.20 Score per residue for model 20

• Molecule 1: Antifreeze peptide SS-3

Chain A:	31%	14%	54%
G1 NN3 NA4 A76 A76 A76 A76 A76 A76 A76 A76 A76 A76	A11 A11 X12 A14 A15 A14 A15 X22 X22 X23 X23 X23 X23	A29 A31 A31 A32 A33 A34 A35 A35	



5 Refinement protocol and experimental data overview (i)

The models were refined using the following method: *simulated annealing, molecular dynamics, torsion angle dynamics.*

Of the 500 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
ARIA	structure solution	1.2
ARIA	refinement	1.2

No chemical shift data was provided.



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	А	101	104	104	0 ± 0
All	All	2020	2080	2080	2

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 0.

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

Atom-1	Atom 2	Clash(Å)	Distance(Å)	Models	
Atom-1	Atom-2 Clash(A)		$\operatorname{Distance}(\operatorname{\AA})$	Worst	Total
1:A:23:LYS:O	1:A:27:ASP:HB2	0.47	2.10	16	1
1:A:24:THR:HA	1:A:27:ASP:HB2	0.41	1.91	5	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	А	16/35~(46%)	$16\pm1 (99\pm3\%)$	$0\pm1~(1\pm3\%)$	0±0 (0±0%)	100 100
All	All	320/700~(46%)	316 (99%)	4 (1%)	0 (0%)	100 100

There are no Ramachandran outliers.

6.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent side chain 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 side chain conformation was analysed and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	А	7/13~(54%)	$4\pm1~(57\pm14\%)$	$3\pm1~(43\pm14\%)$	0 3
All	All	140/260~(54%)	80 (57%)	60 (43%)	0 3

All 7 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	А	13	THR	19
1	А	22	LYS	13
1	А	23	LYS	9
1	А	24	THR	7
1	А	16	ASP	7
1	А	27	ASP	4
1	А	18	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 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)

No chemical shift data were provided

