



wwPDB NMR Structure Validation Summary Report ⓘ

Feb 13, 2017 – 01:16 am GMT

PDB ID : 2MSX
Title : The solution structure of the MANEC-type domain from Hepatocyte Growth Factor Inhibitor 1 reveals an unexpected PAN/apple domain-type fold
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Deposited on : 2014-08-09

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

<http://wwpdb.org/validation/2016/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 : 20161228.v01 (using entries in the PDB archive December 28th 2016)
RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
ShiftChecker : trunk28760
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : recalc28949

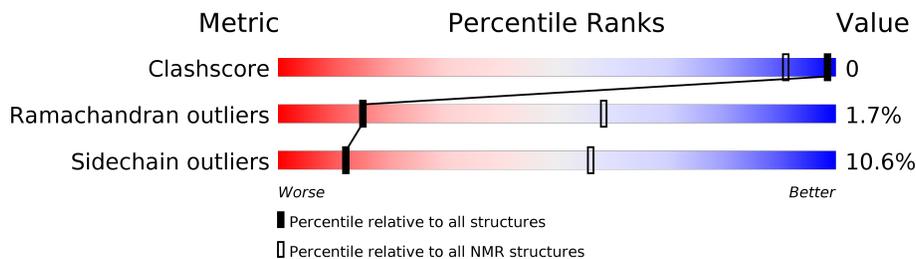
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 85%.

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	125131	11601
Ramachandran outliers	121729	10391
Sidechain outliers	121581	10367

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	114	 75% 11% • 12%

2 Ensemble composition and analysis i

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: *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:54-A:153 (100)	0.27	9

Ill-defined regions of proteins are excluded from the global statistics.

Ligands and non-protein polymers are included in the analysis.

NmrClust was unable to cluster the ensemble.

Error message: Inconsistent models

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 1741 atoms, of which 841 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Kunitz-type protease inhibitor 1.

Mol	Chain	Residues	Atoms					Trace	
			Total	C	H	N	O		S
1	A	114	1741	561	841	164	167	8	0

There are 9 discrepancies between the modelled and reference sequences:

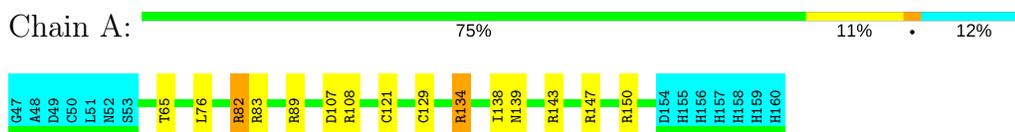
Chain	Residue	Modelled	Actual	Comment	Reference
A	66	GLN	ASN	CONFLICT	UNP O43278
A	153	VAL	-	EXPRESSION TAG	UNP O43278
A	154	ASP	-	EXPRESSION TAG	UNP O43278
A	155	HIS	-	EXPRESSION TAG	UNP O43278
A	156	HIS	-	EXPRESSION TAG	UNP O43278
A	157	HIS	-	EXPRESSION TAG	UNP O43278
A	158	HIS	-	EXPRESSION TAG	UNP O43278
A	159	HIS	-	EXPRESSION TAG	UNP O43278
A	160	HIS	-	EXPRESSION TAG	UNP O43278

4 Residue-property plots [i](#)

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.

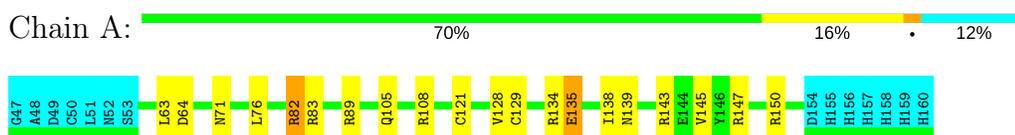
- Molecule 1: Kunitz-type protease inhibitor 1



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: Kunitz-type protease inhibitor 1



5 Refinement protocol and experimental data overview

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

Of the 80 calculated structures, 20 were deposited, based on the following criterion: *all calculated structures submitted*.

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

Software name	Classification	Version
CYANA	structure solution	
YASARA2	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)	2msx_cs.str
Number of chemical shift lists	2
Total number of shifts	2133
Number of shifts mapped to atoms	2133
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	85%

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](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the (average) root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#Z>5	RMSZ	#Z>5
1	A	1.38±0.02	8±1/803 (1.0±0.1%)	1.33±0.02	9±1/1093 (0.8±0.1%)
All	All	1.38	168/16060 (1.0%)	1.33	183/21860 (0.8%)

5 of 16 unique bond outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
1	A	150	ARG	CZ-NH2	-7.22	1.23	1.33	16	19
1	A	108	ARG	CZ-NH2	-6.97	1.24	1.33	16	20
1	A	83	ARG	CZ-NH2	-6.32	1.24	1.33	13	20
1	A	147	ARG	CZ-NH2	-6.20	1.25	1.33	16	20
1	A	134	ARG	CZ-NH2	-6.01	1.25	1.33	4	17

5 of 17 unique angle outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	134	ARG	NE-CZ-NH1	11.30	125.95	120.30	7	20
1	A	83	ARG	NE-CZ-NH1	10.91	125.76	120.30	11	20
1	A	150	ARG	NE-CZ-NH1	10.89	125.75	120.30	19	20
1	A	143	ARG	NE-CZ-NH1	10.89	125.75	120.30	8	20
1	A	147	ARG	NE-CZ-NH1	10.84	125.72	120.30	16	20

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	786	755	755	0±1
All	All	15720	15100	15100	7

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	
				Worst	Total
1:A:135:GLU:CD	1:A:135:GLU:H	0.47	2.13	9	1
1:A:63:LEU:HG	1:A:65:THR:H	0.46	1.69	4	3
1:A:71:ASN:HD22	1:A:128:VAL:HB	0.42	1.73	13	2
1:A:63:LEU:HD22	1:A:64:ASP:N	0.41	2.30	9	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	A	100/114 (88%)	93±2 (93±2%)	5±1 (5±1%)	2±1 (2±1%)	15	58
All	All	2000/2280 (88%)	1861 (93%)	105 (5%)	34 (2%)	15	58

5 of 9 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	107	ASP	11
1	A	65	THR	10
1	A	58	VAL	4
1	A	136	GLY	2
1	A	56	ALA	2

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	85/97 (88%)	76±2 (89±2%)	9±2 (11±2%)	12	56
All	All	1700/1940 (88%)	1519 (89%)	181 (11%)	12	56

5 of 25 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	76	LEU	20
1	A	138	ILE	19
1	A	121	CYS	18
1	A	139	ASN	18
1	A	134	ARG	16

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

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 85% for the well-defined parts and 79% for the entire structure.

7.1 Chemical shift list 1

File name: 2msx_cs.str

Chemical shift list name: *Assigned_chemical_shift_list_2*

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	1107
Number of shifts mapped to atoms	1107
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 i

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	99	-0.25 ± 0.15	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	95	0.00 ± 0.17	None needed (< 0.5 ppm)
$^{13}\text{C}'$	0	—	None (insufficient data)
^{15}N	99	0.32 ± 0.29	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 76%, i.e. 922 atoms were assigned a chemical shift out of a possible 1219. 17 out of 18 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	372/492 (76%)	186/196 (95%)	93/200 (46%)	93/96 (97%)
Sidechain	469/620 (76%)	288/362 (80%)	177/222 (80%)	4/36 (11%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	81/107 (76%)	41/57 (72%)	39/49 (80%)	1/1 (100%)
Overall	922/1219 (76%)	515/615 (84%)	309/471 (66%)	98/133 (74%)

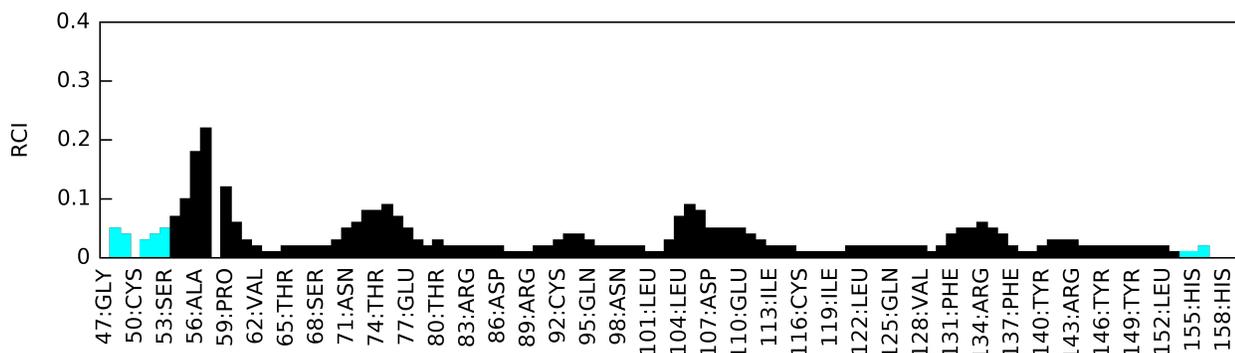
7.1.4 Statistically unusual chemical shifts [i](#)

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:



7.2 Chemical shift list 2

File name: 2msx_cs.str

Chemical shift list name: *assigned_chem_shift_list_1*

7.2.1 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	1026
Number of shifts mapped to atoms	1026
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

7.2.2 Chemical shift referencing [i](#)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	106	-0.16 ± 0.18	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	99	-0.03 ± 0.11	None needed (< 0.5 ppm)
$^{13}\text{C}'$	100	0.28 ± 0.11	None needed (< 0.5 ppm)
^{15}N	99	0.22 ± 0.28	None needed (< 0.5 ppm)

7.2.3 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 72%, i.e. 874 atoms were assigned a chemical shift out of a possible 1219. 9 out of 18 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	465/492 (95%)	177/196 (90%)	195/200 (98%)	93/96 (97%)
Sidechain	385/620 (62%)	227/362 (63%)	158/222 (71%)	0/36 (0%)
Aromatic	24/107 (22%)	23/57 (40%)	0/49 (0%)	1/1 (100%)
Overall	874/1219 (72%)	427/615 (69%)	353/471 (75%)	94/133 (71%)

7.2.4 Statistically unusual chemical shifts [i](#)

There are no statistically unusual chemical shifts.

7.2.5 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:

