

wwPDB NMR Structure Validation Summary Report (i)

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PDB ID	:	1Y1C
Title	:	Solution structure of Anemonia elastase inhibitor analogue
Authors	:	Hemmi, H.; Kumazaki, T.; Yoshizawa-Kumagaye, K.; Nishiuchi, Y.; Yoshida,
		T.; Ohkubo, T.; Kobayashi, Y.
Deposited on	:	2004-11-18

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 (1)) were used in the production of this report:

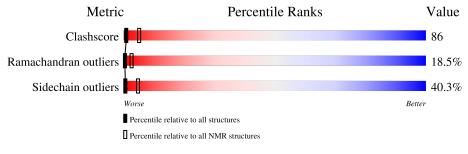
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	2.23.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.23.2

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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f NMR} ext{ archive} \ (\# ext{Entries})$					
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	А	48	10%	60%	21%	• 6%



2 Ensemble composition and analysis (i)

This entry contains 20 models. Model 19 is the overall representative, medoid model (most similar to other models). The authors have identified model 11 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	Well-defined core Residue range (total) Backbone RMSD (Å) Medoid model										
1	A:4-A:48 (45)	0.40	19								

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 1 single-model cluster was found.

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



3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 688 atoms, of which 338 are hydrogens and 0 are deuteriums.

• Molecule 1 is a protein called Elastase inhibitor.

Mol	Chain	Residues		Atoms											
1	٨	19	Total	С	Η	Ν	0	S	0						
	А	48	688	213	338	60	69	8	0						

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	4	ALA	CYS	engineered mutation	UNP P16895
А	6	CYS	LEU	engineered mutation	UNP P16895
А	31	CYS	GLY	engineered mutation	UNP P16895
А	34	ALA	CYS	engineered mutation	UNP P16895



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: Elastase inhibitor

Chain A:	10%		60%	21%	• 6%
K1 P2 P5 C6 C6 C8 C8 C8 C8	T9 M10 711 712 713 714 714	12 616 617 818 818 919 121 121 122 723 723 824 824 825	A 26 C27 C27 C27 C27 C27 L38 A 34 A 34 A 34 A 34 A 34 A 35 S33 S33 S33 S33 S33 S33 S33 S33 S33 S	L42 V43 H44 K45 C48	

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

The representative model is number 19. Colouring as in section 4.1 above.

• Molecule 1: Elastase inhibitor

Chain A	\ :			21	%			-								46	5%												2	239	%	_	1	•	6	%
K1 P2 D3 P5 C6	2 1-1 80 CB	T9	011 Q11	Y12	D13 P14	V15	C16	518 S18	D19	121 TOD	122 V93	G24	N25	A26	C27	M28	L29	130 191	100	S33	H	D37	140	E41	L42	V43	H44	R47	C48							



5 Refinement protocol and experimental data overview (i)

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

Of the 200 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				
X-PLOR	structure solution	3.851				
X-PLOR	refinement	3.851				

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	326	312	311	55 ± 5		
All	All	6520	6240	6220	1092		

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 86.

Atom-1	Atom-2	Clash(Å)	lash(Å) Distance(Å) Mean Mean Mean Mean Mean Mean Mean Mean		dels
Atom-1	Atom-2	Clash(A)	Distance(A)	Worst	Total
1:A:29:LEU:HD12	1:A:42:LEU:HD23	0.95	1.38	3	9
1:A:29:LEU:HD11	1:A:42:LEU:HD23	0.90	1.42	1	9
1:A:15:VAL:HB	1:A:42:LEU:HD11	0.85	1.46	14	20
1:A:4:ALA:HB3	1:A:30:LEU:HB3	0.84	1.46	16	7
1:A:23:TYR:CE2	1:A:29:LEU:HD21	0.81	2.09	17	19

5 of 216 unique clashes are listed below, sorted by their clash magnitude.

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	44/48~(92%)	$26\pm1~(58\pm3\%)$	$10\pm1~(23\pm2\%)$	$8\pm1~(19\pm3\%)$	0 2
All	All	880/960~(92%)	514 (58%)	203~(23%)	163 (19%)	0 2

5 of 14 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	А	12	TYR	20
1	А	18	SER	20
1	А	19	ASP	20
1	А	37	ASP	20
1	А	42	LEU	19

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	А	37/40~(92%)	22 ± 2 (60±6%)	$15\pm2~(40\pm6\%)$	0 5
All	All	740/800~(92%)	442 (60%)	298 (40%)	0 5

5 of 27 unique residues with a non-rotameric side chain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	А	16	CYS	20
1	А	29	LEU	20
1	А	40	ILE	20
1	А	42	LEU	20
1	А	44	HIS	20

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

