Full wwPDB NMR Structure Validation Report (i)

Jun 15, 2024 – 01:03 PM EDT

PDB ID	:	2JZM
Title	:	Chymotrypsin inhibitor C1 from Nicotiana alata
Authors	:	Schirra, H.J.; Anderson, M.A.; Craik, D.J.
Deposited on	:	2008-01-09

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 types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

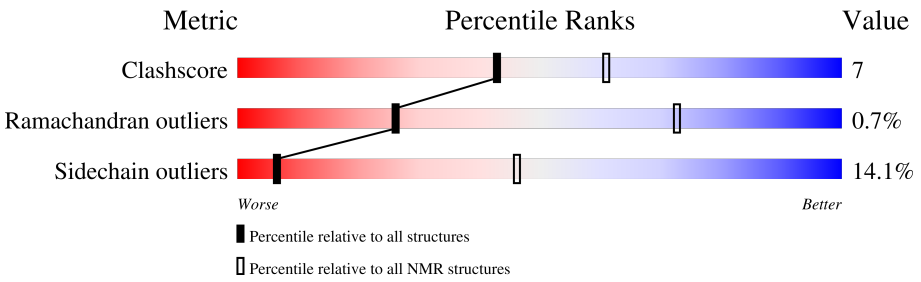
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

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 (#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	53	79% 13% 8%

2 Ensemble composition and analysis (i)

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: *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:3-A:51 (49)	1.32	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 1 single-model cluster was found.

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

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 758 atoms, of which 363 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Proteinase inhibitor.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	53	758	236	363	71	80	8	0

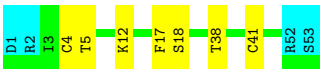
4 Residue-property plots (i)

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: Proteinase inhibitor

Chain A:



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

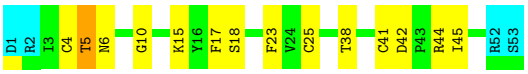
• Molecule 1: Proteinase inhibitor

Chain A:

4.2.2 Score per residue for model 2

• Molecule 1: Proteinase inhibitor

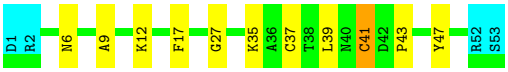
Chain A:



4.2.3 Score per residue for model 3

- Molecule 1: Proteinase inhibitor

Chain A:



4.2.4 Score per residue for model 4

- Molecule 1: Proteinase inhibitor

Chain A:

4.2.5 Score per residue for model 5

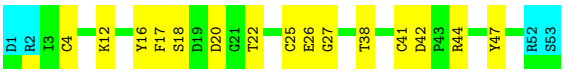
- Molecule 1: Proteinase inhibitor

Chain A:

4.2.6 Score per residue for model 6

- Molecule 1: Proteinase inhibitor

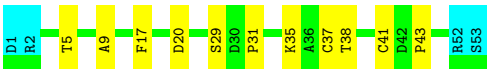
Chain A:



4.2.7 Score per residue for model 7 (medoid)

- Molecule 1: Proteinase inhibitor

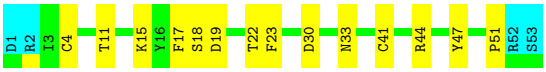
Chain A:



4.2.8 Score per residue for model 8

- Molecule 1: Proteinase inhibitor

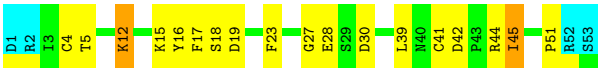
Chain A: 66% 26% 8%



4.2.9 Score per residue for model 9

- Molecule 1: Proteinase inhibitor

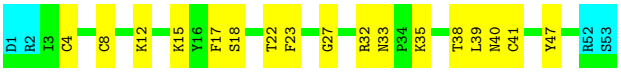
Chain A: 58% 30% • 8%



4.2.10 Score per residue for model 10

- Molecule 1: Proteinase inhibitor

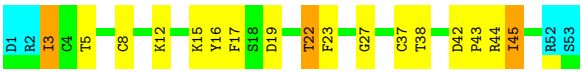
Chain A: 60% 32% 8%



4.2.11 Score per residue for model 11

- Molecule 1: Proteinase inhibitor

Chain A: 60% 26% 6% 8%



4.2.12 Score per residue for model 12

- Molecule 1: Proteinase inhibitor

Chain A: 64% 21% 8% 8%

4.2.13 Score per residue for model 13

- Molecule 1: Proteinase inhibitor

Chain A: 66% 26% 8%

D1 R2 I3 C4 T5 N6 G10 T11 K12 Y16 F17 S18 D19 G27 K35 T38 L39 N40 C41 R52 S53

4.2.14 Score per residue for model 14

- Molecule 1: Proteinase inhibitor

Chain A: 66% 25% • 8%

D1 R2 I3 C4 C8 K15 Y16 F17 S18 D19 D20 G21 T22 F23 V24 C25 E26 G27 E28 C41 R44 R52 S53

4.2.15 Score per residue for model 15

- Molecule 1: Proteinase inhibitor

Chain A: 68% 23% • 8%

D1 R2 I3 C4 T5 T11 S18 D19 D20 G21 T22 P31 R32 N33 T38 C41 R44 R52 S53

4.2.16 Score per residue for model 16

- Molecule 1: Proteinase inhibitor

Chain A: 60% 28% • 8%

D1 R2 I3 G10 T11 K12 Y16 F17 G21 T22 F23 E26 G27 E28 S29 D30 T38 D42 P43 R44 I45 A46 Y47 R52 S53

4.2.17 Score per residue for model 17

- Molecule 1: Proteinase inhibitor

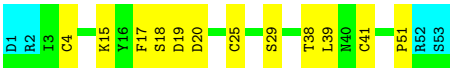
Chain A: 68% 25% 8%

D1 R2 I3 C4 T5 F17 S18 D19 T22 D30 N33 L39 N40 C41 Y47 G48 V49 C50 P51 R52 S53

4.2.18 Score per residue for model 18

- Molecule 1: Proteinase inhibitor

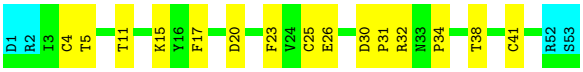
Chain A: 70% 23% 8%



4.2.19 Score per residue for model 19

- Molecule 1: Proteinase inhibitor

Chain A: 64% 28% 8%



4.2.20 Score per residue for model 20

- Molecule 1: Proteinase inhibitor

Chain A: 66% 26% 8%

5 Refinement protocol and experimental data overview (i)

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

Of the 50 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
CNSSOLVE	structure solution	1.2
CNSSOLVE	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.

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	Chirality	Planarity
1	A	0.0±0.0	0.1±0.4
All	All	0	3

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

All unique planar outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Group	Models (Total)
1	A	44	ARG	Sidechain	2
1	A	32	ARG	Sidechain	1

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	358	326	326	5±2
All	All	7160	6520	6520	97

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 7.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:12:LYS:HA	1:A:27:GLY:HA2	0.88	1.45	16	2
1:A:3:ILE:HB	1:A:43:PRO:HA	0.83	1.50	16	1
1:A:4:CYS:HA	1:A:41:CYS:HA	0.81	1.49	10	11
1:A:12:LYS:HA	1:A:27:GLY:HA3	0.72	1.58	11	2
1:A:4:CYS:HA	1:A:41:CYS:HB3	0.70	1.62	13	3
1:A:6:ASN:HD22	1:A:39:LEU:HD13	0.64	1.53	3	1
1:A:16:TYR:HB3	1:A:45:ILE:HG13	0.63	1.69	9	2
1:A:12:LYS:HA	1:A:27:GLY:O	0.61	1.95	13	3
1:A:44:ARG:HA	1:A:44:ARG:HE	0.60	1.55	14	1
1:A:35:LYS:HE3	1:A:35:LYS:HA	0.60	1.72	12	1
1:A:30:ASP:HB3	1:A:33:ASN:HB3	0.60	1.72	17	1
1:A:11:THR:HG23	1:A:31:PRO:HD3	0.59	1.74	15	1
1:A:42:ASP:HB3	1:A:45:ILE:HG22	0.58	1.73	11	2
1:A:18:SER:HB3	1:A:22:THR:HB	0.58	1.76	15	4
1:A:15:LYS:HG2	1:A:26:GLU:HG3	0.56	1.77	14	1
1:A:10:GLY:HA3	1:A:16:TYR:HE1	0.56	1.60	16	2
1:A:3:ILE:HG12	1:A:43:PRO:HA	0.55	1.77	11	1
1:A:11:THR:HG22	1:A:31:PRO:HA	0.55	1.76	5	1
1:A:44:ARG:HA	1:A:44:ARG:NE	0.54	2.17	14	1
1:A:12:LYS:HE3	1:A:30:ASP:HB2	0.53	1.79	9	1
1:A:15:LYS:HB3	1:A:23:PHE:HE1	0.53	1.64	14	4
1:A:18:SER:HB3	1:A:44:ARG:O	0.52	2.03	2	1
1:A:15:LYS:HE2	1:A:51:PRO:HB3	0.52	1.82	18	1
1:A:16:TYR:HE2	1:A:27:GLY:HA2	0.50	1.66	11	1
1:A:12:LYS:HA	1:A:26:GLU:O	0.49	2.07	4	1
1:A:10:GLY:O	1:A:29:SER:HB2	0.49	2.06	12	1
1:A:16:TYR:CE2	1:A:27:GLY:HA2	0.49	2.42	11	2
1:A:12:LYS:HG2	1:A:27:GLY:O	0.49	2.07	10	1
1:A:15:LYS:HA	1:A:26:GLU:HA	0.49	1.85	14	1
1:A:6:ASN:HA	1:A:42:ASP:HB3	0.48	1.84	2	1
1:A:3:ILE:CB	1:A:43:PRO:HA	0.47	2.34	16	1
1:A:15:LYS:HB3	1:A:23:PHE:HD1	0.46	1.69	11	1
1:A:10:GLY:HA3	1:A:16:TYR:CE1	0.46	2.43	16	3
1:A:17:PHE:CE2	1:A:21:GLY:HA2	0.46	2.45	16	2
1:A:42:ASP:OD1	1:A:44:ARG:HD3	0.46	2.09	9	1
1:A:7:CYS:HB2	1:A:45:ILE:HD11	0.46	1.87	4	1
1:A:4:CYS:HA	1:A:41:CYS:CA	0.46	2.37	5	3
1:A:15:LYS:HG2	1:A:26:GLU:HG2	0.45	1.88	19	1
1:A:8:CYS:HA	1:A:28:GLU:HB2	0.44	1.89	14	1
1:A:18:SER:OG	1:A:22:THR:HB	0.44	2.12	8	3
1:A:23:PHE:HZ	1:A:26:GLU:HG3	0.44	1.73	19	1
1:A:12:LYS:HG2	1:A:30:ASP:HA	0.44	1.88	16	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:23:PHE:CE1	1:A:26:GLU:HB2	0.44	2.48	16	1
1:A:30:ASP:HB3	1:A:33:ASN:ND2	0.43	2.27	8	1
1:A:5:THR:HB	1:A:45:ILE:HG23	0.43	1.90	2	1
1:A:42:ASP:OD1	1:A:44:ARG:HB3	0.43	2.13	6	1
1:A:9:ALA:HA	1:A:29:SER:OG	0.43	2.14	7	1
1:A:4:CYS:HA	1:A:41:CYS:CB	0.43	2.43	8	1
1:A:15:LYS:HB3	1:A:23:PHE:CE1	0.43	2.49	10	2
1:A:17:PHE:CE2	1:A:22:THR:HA	0.43	2.48	11	1
1:A:41:CYS:O	1:A:43:PRO:HD3	0.42	2.13	3	2
1:A:9:ALA:HB2	1:A:37:CYS:HB2	0.42	1.91	3	1
1:A:49:VAL:O	1:A:51:PRO:HD3	0.42	2.14	4	2
1:A:35:LYS:HB3	1:A:37:CYS:SG	0.41	2.55	7	1
1:A:8:CYS:HB3	1:A:40:ASN:OD1	0.41	2.15	10	1
1:A:15:LYS:HE2	1:A:51:PRO:HG3	0.41	1.90	8	1
1:A:32:ARG:O	1:A:34:PRO:HD3	0.41	2.15	19	1
1:A:16:TYR:CZ	1:A:27:GLY:HA2	0.41	2.51	6	1
1:A:42:ASP:O	1:A:45:ILE:HG22	0.40	2.17	16	1
1:A:23:PHE:HE1	1:A:26:GLU:HB2	0.40	1.76	16	1
1:A:8:CYS:HB3	1:A:37:CYS:HB3	0.40	1.71	11	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	49/53 (92%)	42±2 (85±4%)	7±2 (14±4%)	0±0 (1±1%)	26	73
All	All	980/1060 (92%)	832 (85%)	141 (14%)	7 (1%)	26	73

All 5 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	31	PRO	3
1	A	10	GLY	1
1	A	41	CYS	1

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Mol	Chain	Res	Type	Models (Total)
1	A	51	PRO	1
1	A	3	ILE	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	41/45 (91%)	35±2 (86±4%)	6±2 (14±4%)	6 46
All	All	820/900 (91%)	704 (86%)	116 (14%)	6 46

All 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	17	PHE	18
1	A	38	THR	14
1	A	5	THR	10
1	A	19	ASP	9
1	A	20	ASP	8
1	A	47	TYR	7
1	A	25	CYS	6
1	A	35	LYS	6
1	A	39	LEU	6
1	A	18	SER	4
1	A	12	LYS	4
1	A	11	THR	3
1	A	32	ARG	3
1	A	44	ARG	3
1	A	26	GLU	2
1	A	45	ILE	2
1	A	33	ASN	2
1	A	29	SER	2
1	A	15	LYS	1
1	A	31	PRO	1
1	A	28	GLU	1
1	A	22	THR	1
1	A	6	ASN	1

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Mol	Chain	Res	Type	Models (Total)
1	A	30	ASP	1
1	A	3	ILE	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