Full wwPDB NMR Structure Validation Report (i)

Jun 16, 2024 – 04:37 AM EDT

PDB ID	:	1TXB
Title	:	SOLUTION NMR STRUCTURE OF TOXIN B, A LONG NEUROTOXIN FROM THE VENOM OF THE KING COBRA, 10 STRUCTURES
Authors	:	Peng, S.-S.; Kumar, T.K.S.; Jayaraman, G.; Chang, C.-C.; Yu, C.
Deposited on	:	1996-07-20

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:

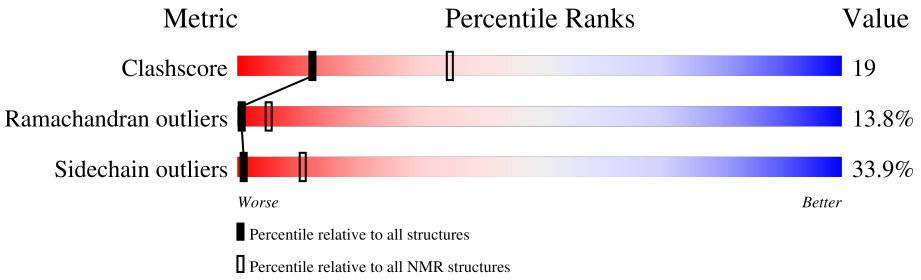
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson 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	73	36% 52% 5% • 5%

2 Ensemble composition and analysis (i)

This entry contains 10 models. Model 10 is the overall representative, medoid model (most similar to other models).

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:1-A:69 (69)	2.73	10

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 and 2 single-model clusters were found.

Cluster number	Models
1	1, 4, 6, 10
2	2, 3, 8, 9
Single-model clusters	5; 7

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 1087 atoms, of which 530 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called TOXIN B.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	73	1087	342	530	98	107	10	0

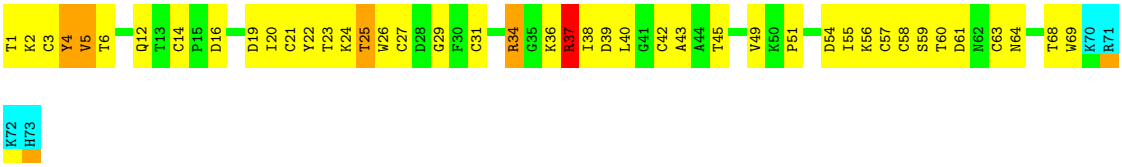
4 Residue-property plots (i)

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: TOXIN B

Chain A: 36% 52% 5% • 5%



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

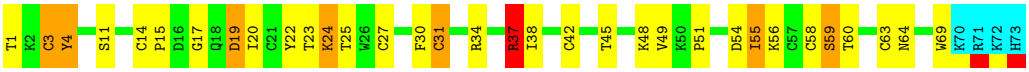
• Molecule 1: TOXIN B

Chain A: 37% 36% 19% • 5%

4.2.2 Score per residue for model 2

• Molecule 1: TOXIN B

Chain A: 49% 34% 10% • 5%



4.2.3 Score per residue for model 3

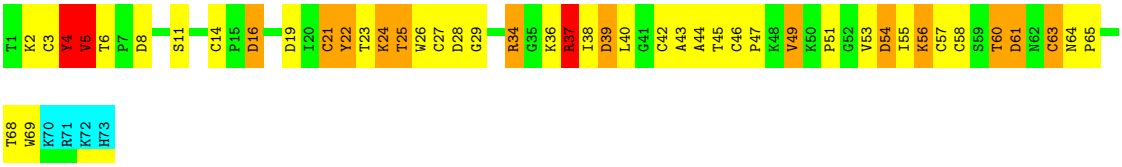
- Molecule 1: TOXIN B

Chain A: 49% 29% 11% 5% 5%

4.2.4 Score per residue for model 4

- Molecule 1: TOXIN B

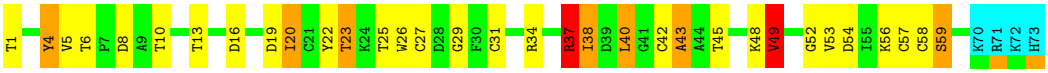
Chain A: 32% 41% 18% • 5%



4.2.5 Score per residue for model 5

- Molecule 1: TOXIN B

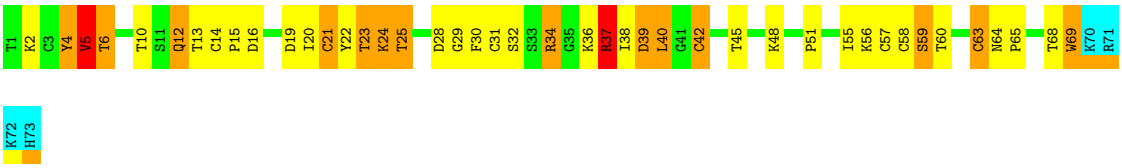
Chain A: 49% 33% 10% • 5%



4.2.6 Score per residue for model 6

- Molecule 1: TOXIN B

Chain A: 36% 37% 19% • 5%



4.2.7 Score per residue for model 7

- Molecule 1: TOXIN B

Chain A: 53% 29% 11% • 5%

T1 K2 C3 Y4 V5 T6 T10 S11 Q12 T13 C14 P15 D16 G17 Q18 D19 I20 C21 Y22 T23 K24 T25 R34 R37 I38 D39 L40 V49 K50 P51 D54 C57 C58 S59 C63 T68 W69 K70 R71 K72 H73

4.2.8 Score per residue for model 8

- Molecule 1: TOXIN B

Chain A: 37% 40% 18% 5%

T1 K2 C3 Y4 V5 T6 P7 D8 A9 T10 S11 Q12 T13 C14 Q18 D19 I20 C21 Y22 T23 K24 T25 W26 C27 S32 S33 R34 G35 K36 R37 I38 D39 L40 G41 C42 A43 A44 T45 C46 P47 K48 V49 K50 P51 G52 I55 C58 S59 T60 D61 N62 C63 N64 P65 T68

W69 K70 R71 K72 H73

4.2.9 Score per residue for model 9

- Molecule 1: TOXIN B

Chain A: 49% 34% 10% • 5%

T1 K2 C3 Y4 S11 C14 P15 D16 G17 Q18 D19 I20 C21 Y22 T23 K24 T25 W26 C27 F30 C31 R34 R37 I38 C42 T45 K48 V49 K50 P51 D54 I55 K56 C57 C58 S59 T60 C63 N64 W69 K70 R71 K72 H73

4.2.10 Score per residue for model 10 (medoid)

- Molecule 1: TOXIN B

Chain A: 32% 41% 18% • 5%

T1 K2 C3 Y4 V5 T6 P7 D8 S11 C14 P15 D16 D19 I20 C21 Y22 T23 K24 T25 W26 C27 D28 G29 R34 G35 K36 R37 I38 D39 L40 G41 C42 A43 A44 T45 C46 P47 K48 V49 K50 P51 G52 V53 D54 I55 K56 C57 C58 S59 T60 D61 N62 C63 N64 P65

T68 W69 K70 R71 K72 H73

5 Refinement protocol and experimental data overview (i)

Of the ? calculated structures, 10 were deposited, based on the following criterion: *?*.

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

Software name	Classification	Version
X-PLOR	refinement	

No chemical shift data was provided.

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	0.72±0.03	0±0/531 (0.0± 0.0%)	1.30±0.07	1±1/725 (0.2± 0.2%)
All	All	0.72	0/5310 (0.0%)	1.30	13/7250 (0.2%)

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	1.9±0.7
All	All	0	19

There are no bond-length outliers.

All 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(^{o})	Ideal(^{o})	Models	
								Worst	Total
1	A	37	ARG	NE-CZ-NH2	-7.38	116.61	120.30	3	2
1	A	54	ASP	CB-CG-OD1	6.98	124.58	118.30	4	2
1	A	4	TYR	CB-CG-CD1	-6.55	117.07	121.00	7	1
1	A	39	ASP	CB-CG-OD1	5.46	123.22	118.30	7	1
1	A	54	ASP	CB-CG-OD2	-5.44	113.41	118.30	4	2
1	A	34	ARG	CD-NE-CZ	-5.33	116.14	123.60	3	1
1	A	14	CYS	CA-CB-SG	-5.21	104.63	114.00	7	1
1	A	4	TYR	CB-CG-CD2	-5.17	117.90	121.00	4	2
1	A	37	ARG	CD-NE-CZ	-5.16	116.38	123.60	5	1

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	37	ARG	Sidechain	10
1	A	34	ARG	Sidechain	7
1	A	4	TYR	Sidechain	1
1	A	22	TYR	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	517	484	484	19±6
All	All	5170	4840	4840	190

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 19.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:26:TRP:CG	1:A:53:VAL:HG12	0.81	2.09	5	1
1:A:23:THR:HG23	1:A:40:LEU:HD12	0.80	1.54	5	1
1:A:5:VAL:CG1	1:A:40:LEU:HD13	0.78	2.09	4	2
1:A:22:TYR:CE2	1:A:40:LEU:HD13	0.77	2.13	7	1
1:A:20:ILE:HG23	1:A:58:CYS:O	0.76	1.81	6	1
1:A:23:THR:HG22	1:A:38:ILE:HG12	0.75	1.57	5	1
1:A:22:TYR:CD2	1:A:40:LEU:HD13	0.74	2.16	7	1
1:A:46:CYS:SG	1:A:55:ILE:HG22	0.73	2.24	4	2
1:A:5:VAL:HG13	1:A:40:LEU:HD11	0.73	1.58	5	1
1:A:5:VAL:HG11	1:A:38:ILE:HG13	0.71	1.62	3	1
1:A:5:VAL:CG1	1:A:40:LEU:HD11	0.70	2.15	5	1
1:A:5:VAL:HG11	1:A:40:LEU:HD13	0.69	1.63	4	2
1:A:4:TYR:CZ	1:A:40:LEU:HD13	0.69	2.22	1	1
1:A:2:LYS:HE2	1:A:42:CYS:SG	0.68	2.28	6	1
1:A:24:LYS:HB2	1:A:55:ILE:HG23	0.67	1.65	4	3
1:A:25:THR:CG2	1:A:38:ILE:HG22	0.66	2.20	3	1
1:A:48:LYS:O	1:A:49:VAL:HG13	0.66	1.90	5	1
1:A:4:TYR:CG	1:A:40:LEU:HD22	0.66	2.25	6	1
1:A:5:VAL:HG13	1:A:40:LEU:HG	0.66	1.68	8	1
1:A:3:CYS:N	1:A:21:CYS:SG	0.65	2.70	4	3

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:27:CYS:SG	1:A:31:CYS:N	0.65	2.69	2	2
1:A:25:THR:OG1	1:A:38:ILE:HD13	0.65	1.91	1	1
1:A:25:THR:HG22	1:A:54:ASP:O	0.64	1.92	2	2
1:A:5:VAL:HG11	1:A:38:ILE:CG1	0.64	2.22	3	1
1:A:24:LYS:HB3	1:A:55:ILE:HG23	0.63	1.68	1	1
1:A:2:LYS:CE	1:A:42:CYS:SG	0.62	2.88	6	1
1:A:25:THR:HG22	1:A:38:ILE:HG23	0.58	1.76	7	1
1:A:23:THR:CG2	1:A:40:LEU:HD12	0.57	2.29	5	1
1:A:26:TRP:CD2	1:A:53:VAL:HG12	0.57	2.33	5	1
1:A:25:THR:HG21	1:A:38:ILE:HG22	0.57	1.76	3	1
1:A:23:THR:HG23	1:A:56:LYS:HG2	0.57	1.75	4	2
1:A:23:THR:OG1	1:A:40:LEU:HD11	0.56	2.00	4	2
1:A:20:ILE:HG22	1:A:59:SER:HB3	0.56	1.77	1	3
1:A:26:TRP:CH2	1:A:27:CYS:SG	0.56	2.98	1	1
1:A:5:VAL:HG22	1:A:40:LEU:HD23	0.56	1.77	6	1
1:A:59:SER:O	1:A:63:CYS:SG	0.56	2.63	6	1
1:A:4:TYR:N	1:A:40:LEU:HD23	0.56	2.16	5	1
1:A:23:THR:HG22	1:A:40:LEU:HA	0.56	1.75	1	1
1:A:5:VAL:HG13	1:A:23:THR:HG21	0.56	1.78	1	1
1:A:40:LEU:HD22	1:A:40:LEU:O	0.56	2.01	5	1
1:A:5:VAL:HG12	1:A:40:LEU:HD22	0.55	1.77	3	1
1:A:25:THR:OG1	1:A:38:ILE:HA	0.55	2.02	8	5
1:A:38:ILE:HG22	1:A:40:LEU:CD1	0.55	2.32	4	2
1:A:23:THR:HG22	1:A:39:ASP:O	0.55	2.02	6	1
1:A:5:VAL:CG2	1:A:23:THR:HG21	0.55	2.32	7	1
1:A:5:VAL:CG2	1:A:40:LEU:HD23	0.54	2.31	6	1
1:A:5:VAL:CG2	1:A:23:THR:CG2	0.54	2.85	7	1
1:A:23:THR:HG23	1:A:40:LEU:CD1	0.53	2.30	5	1
1:A:4:TYR:CD2	1:A:14:CYS:SG	0.53	3.02	3	1
1:A:46:CYS:SG	1:A:57:CYS:N	0.53	2.82	4	2
1:A:23:THR:HG23	1:A:40:LEU:HB3	0.52	1.82	3	2
1:A:40:LEU:O	1:A:40:LEU:HD12	0.52	2.05	6	1
1:A:1:THR:OG1	1:A:13:THR:HG22	0.52	2.05	5	1
1:A:40:LEU:HD13	1:A:40:LEU:N	0.52	2.20	5	1
1:A:2:LYS:NZ	1:A:60:THR:O	0.52	2.35	8	1
1:A:23:THR:HG23	1:A:56:LYS:CG	0.51	2.35	4	2
1:A:4:TYR:H	1:A:40:LEU:HD23	0.51	1.66	5	1
1:A:2:LYS:NZ	1:A:41:GLY:O	0.51	2.41	1	1
1:A:59:SER:O	1:A:60:THR:HG22	0.50	2.05	2	2
1:A:23:THR:HG22	1:A:25:THR:HG22	0.50	1.83	3	1
1:A:31:CYS:O	1:A:37:ARG:NH2	0.50	2.44	2	2

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:4:TYR:CD1	1:A:40:LEU:HD22	0.50	2.41	6	1
1:A:21:CYS:SG	1:A:61:ASP:O	0.50	2.69	8	1
1:A:20:ILE:H	1:A:43:ALA:HB2	0.50	1.66	1	2
1:A:4:TYR:CE2	1:A:14:CYS:SG	0.50	3.05	3	1
1:A:23:THR:HB	1:A:38:ILE:HG21	0.49	1.82	6	1
1:A:5:VAL:HG13	1:A:40:LEU:CG	0.49	2.35	8	1
1:A:3:CYS:SG	1:A:63:CYS:HB3	0.49	2.48	3	1
1:A:22:TYR:CG	1:A:43:ALA:HB2	0.49	2.42	4	2
1:A:1:THR:HG21	1:A:12:GLN:OE1	0.49	2.07	1	1
1:A:21:CYS:HB2	1:A:63:CYS:SG	0.49	2.48	1	1
1:A:5:VAL:HG13	1:A:40:LEU:HD13	0.48	1.84	4	2
1:A:2:LYS:HG2	1:A:21:CYS:SG	0.48	2.49	6	1
1:A:2:LYS:HG2	1:A:42:CYS:SG	0.47	2.49	1	1
1:A:23:THR:OG1	1:A:40:LEU:HD22	0.47	2.08	8	1
1:A:38:ILE:HD11	1:A:54:ASP:OD2	0.47	2.09	1	1
1:A:4:TYR:CG	1:A:5:VAL:N	0.47	2.80	4	2
1:A:4:TYR:HB2	1:A:42:CYS:SG	0.47	2.49	5	1
1:A:38:ILE:HG23	1:A:40:LEU:HD12	0.47	1.87	5	1
1:A:60:THR:HG22	1:A:61:ASP:N	0.46	2.26	4	2
1:A:22:TYR:O	1:A:22:TYR:CG	0.46	2.69	3	2
1:A:28:ASP:O	1:A:37:ARG:NH1	0.46	2.49	6	1
1:A:36:LYS:C	1:A:38:ILE:HD13	0.46	2.31	3	1
1:A:14:CYS:SG	1:A:19:ASP:OD2	0.46	2.74	4	2
1:A:49:VAL:HG12	1:A:49:VAL:O	0.45	2.11	7	1
1:A:53:VAL:O	1:A:53:VAL:HG23	0.45	2.11	5	1
1:A:54:ASP:OD2	1:A:56:LYS:NZ	0.45	2.40	4	2
1:A:51:PRO:HG2	1:A:55:ILE:CD1	0.45	2.42	1	1
1:A:31:CYS:SG	1:A:32:SER:N	0.45	2.89	6	1
1:A:51:PRO:CG	1:A:55:ILE:CD1	0.45	2.94	8	1
1:A:4:TYR:O	1:A:5:VAL:HG13	0.45	2.11	1	1
1:A:21:CYS:O	1:A:57:CYS:HA	0.45	2.12	1	1
1:A:60:THR:CG2	1:A:63:CYS:SG	0.45	3.04	2	2
1:A:3:CYS:SG	1:A:20:ILE:O	0.44	2.75	8	1
1:A:25:THR:HA	1:A:37:ARG:O	0.44	2.11	2	2
1:A:5:VAL:N	1:A:40:LEU:HD21	0.44	2.27	5	2
1:A:5:VAL:HG11	1:A:38:ILE:CG2	0.43	2.42	1	1
1:A:22:TYR:CB	1:A:57:CYS:SG	0.43	3.06	7	1
1:A:22:TYR:O	1:A:40:LEU:CB	0.43	2.66	5	1
1:A:2:LYS:NZ	1:A:16:ASP:O	0.43	2.51	3	1
1:A:23:THR:O	1:A:55:ILE:HA	0.43	2.14	2	2
1:A:21:CYS:CB	1:A:63:CYS:SG	0.43	3.06	1	1

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:23:THR:HG22	1:A:25:THR:CG2	0.43	2.43	3	1
1:A:2:LYS:HB3	1:A:42:CYS:SG	0.43	2.54	4	2
1:A:25:THR:OG1	1:A:37:ARG:O	0.43	2.32	1	1
1:A:20:ILE:HD13	1:A:57:CYS:SG	0.42	2.53	1	1
1:A:19:ASP:O	1:A:20:ILE:HD13	0.42	2.14	2	2
1:A:3:CYS:O	1:A:12:GLN:HA	0.42	2.14	3	1
1:A:25:THR:O	1:A:53:VAL:HG12	0.42	2.14	4	2
1:A:44:ALA:O	1:A:45:THR:HG23	0.42	2.15	3	1
1:A:58:CYS:SG	1:A:58:CYS:O	0.42	2.77	5	1
1:A:23:THR:CG2	1:A:38:ILE:HG22	0.42	2.45	8	1
1:A:37:ARG:N	1:A:38:ILE:HD13	0.42	2.29	3	1
1:A:60:THR:HG21	1:A:63:CYS:SG	0.42	2.55	2	2
1:A:22:TYR:O	1:A:40:LEU:HA	0.42	2.14	8	1
1:A:29:GLY:O	1:A:34:ARG:NH1	0.42	2.52	3	1
1:A:4:TYR:CE2	1:A:40:LEU:HD13	0.42	2.48	1	1
1:A:2:LYS:O	1:A:12:GLN:CB	0.42	2.68	6	1
1:A:5:VAL:HG12	1:A:6:THR:OG1	0.42	2.15	7	1
1:A:39:ASP:C	1:A:40:LEU:HD12	0.42	2.35	4	2
1:A:20:ILE:N	1:A:43:ALA:HB2	0.42	2.30	5	1
1:A:25:THR:HG21	1:A:37:ARG:C	0.41	2.34	4	2
1:A:3:CYS:HA	1:A:21:CYS:CB	0.41	2.45	7	1
1:A:25:THR:HB	1:A:37:ARG:O	0.41	2.14	4	2
1:A:25:THR:CB	1:A:37:ARG:O	0.41	2.68	6	2
1:A:7:PRO:CD	1:A:10:THR:O	0.41	2.67	3	1
1:A:38:ILE:HG22	1:A:40:LEU:HD11	0.41	1.93	4	2
1:A:3:CYS:SG	1:A:63:CYS:HB2	0.41	2.56	2	2
1:A:24:LYS:CG	1:A:55:ILE:HD11	0.41	2.45	2	2
1:A:5:VAL:CG1	1:A:23:THR:HG21	0.41	2.45	6	1
1:A:26:TRP:CZ2	1:A:27:CYS:SG	0.41	3.14	1	1
1:A:23:THR:C	1:A:40:LEU:HD12	0.41	2.37	7	1
1:A:46:CYS:N	1:A:47:PRO:CD	0.41	2.84	4	2
1:A:63:CYS:O	1:A:64:ASN:HB2	0.41	2.16	4	2
1:A:3:CYS:O	1:A:4:TYR:CB	0.40	2.68	2	2
1:A:59:SER:O	1:A:60:THR:CG2	0.40	2.69	2	2
1:A:25:THR:CG2	1:A:38:ILE:HA	0.40	2.46	6	1
1:A:20:ILE:HD12	1:A:21:CYS:N	0.40	2.31	1	1
1:A:2:LYS:CE	1:A:16:ASP:O	0.40	2.69	3	1
1:A:1:THR:O	1:A:2:LYS:HG3	0.40	2.16	8	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	68/73 (93%)	36±3 (53±4%)	23±4 (33±5%)	9±2 (14±3%)	1 5
All	All	680/730 (93%)	360 (53%)	226 (33%)	94 (14%)	1 5

All 29 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	51	PRO	8
1	A	49	VAL	7
1	A	4	TYR	7
1	A	63	CYS	6
1	A	29	GLY	5
1	A	60	THR	5
1	A	14	CYS	5
1	A	65	PRO	5
1	A	5	VAL	4
1	A	15	PRO	4
1	A	37	ARG	4
1	A	45	THR	3
1	A	64	ASN	3
1	A	16	ASP	3
1	A	44	ALA	3
1	A	43	ALA	2
1	A	11	SER	2
1	A	17	GLY	2
1	A	59	SER	2
1	A	47	PRO	2
1	A	52	GLY	2
1	A	6	THR	2
1	A	18	GLN	2
1	A	26	TRP	1
1	A	7	PRO	1
1	A	34	ARG	1
1	A	69	TRP	1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Models (Total)
1	A	8	ASP	1
1	A	68	THR	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	61/65 (94%)	40±4 (66±7%)	21±4 (34±7%)	1 11
All	All	610/650 (94%)	403 (66%)	207 (34%)	1 11

All 52 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	37	ARG	10
1	A	24	LYS	8
1	A	22	TYR	7
1	A	25	THR	7
1	A	56	LYS	7
1	A	58	CYS	7
1	A	16	ASP	6
1	A	34	ARG	6
1	A	36	LYS	6
1	A	39	ASP	6
1	A	42	CYS	6
1	A	69	TRP	6
1	A	4	TYR	5
1	A	21	CYS	5
1	A	40	LEU	5
1	A	45	THR	5
1	A	38	ILE	5
1	A	6	THR	5
1	A	5	VAL	4
1	A	12	GLN	4
1	A	59	SER	4
1	A	61	ASP	4
1	A	1	THR	4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Models (Total)
1	A	3	CYS	4
1	A	19	ASP	4
1	A	48	LYS	4
1	A	20	ILE	4
1	A	8	ASP	4
1	A	27	CYS	4
1	A	49	VAL	4
1	A	68	THR	4
1	A	10	THR	4
1	A	33	SER	3
1	A	55	ILE	3
1	A	57	CYS	3
1	A	30	PHE	3
1	A	31	CYS	3
1	A	26	TRP	3
1	A	13	THR	2
1	A	18	GLN	2
1	A	32	SER	2
1	A	11	SER	2
1	A	28	ASP	2
1	A	23	THR	2
1	A	54	ASP	2
1	A	66	PHE	1
1	A	14	CYS	1
1	A	60	THR	1
1	A	50	LYS	1
1	A	46	CYS	1
1	A	63	CYS	1
1	A	64	ASN	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