Full wwPDB NMR Structure Validation Report (i)

Feb 22, 2022 – 04:13 PM EST

PDB ID	:	1WHJ
Title	:	Solution structure of the 1st CAP-Gly domain in mouse 1700024K14Rik hypothetical protein
Authors	:	Saito, K.; Tochio, N.; Koshiba, S.; Inoue, M.; Kigawa, T.; Yokoyama, S.; RIKEN Structural Genomics/Proteomics Initiative (RSGI)
Deposited on	:	2004-05-28

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:

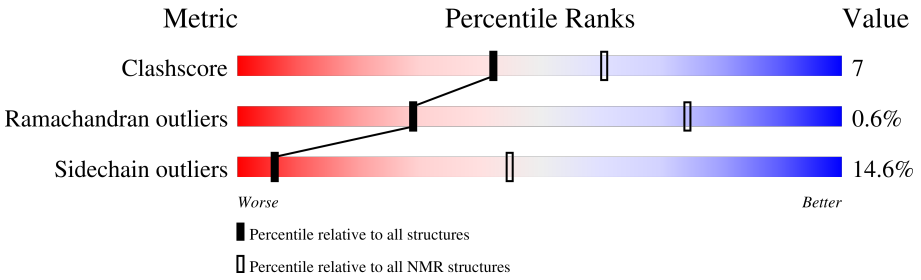
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	2.26
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
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 (#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	102	60% 15% 25%

2 Ensemble composition and analysis (i)

This entry contains 20 models. Model 5 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:19-A:94 (76)	0.30	5

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 3 clusters. No single-model clusters were found.

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

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 1485 atoms, of which 743 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called RIKEN cDNA 1700024K14.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	102	1485	461	743	131	147	3	0

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	cloning artifact	UNP Q8CI96
A	2	SER	-	cloning artifact	UNP Q8CI96
A	3	SER	-	cloning artifact	UNP Q8CI96
A	4	GLY	-	cloning artifact	UNP Q8CI96
A	5	SER	-	cloning artifact	UNP Q8CI96
A	6	SER	-	cloning artifact	UNP Q8CI96
A	7	GLY	-	cloning artifact	UNP Q8CI96
A	97	SER	-	cloning artifact	UNP Q8CI96
A	98	GLY	-	cloning artifact	UNP Q8CI96
A	99	PRO	-	cloning artifact	UNP Q8CI96
A	100	SER	-	cloning artifact	UNP Q8CI96
A	101	SER	-	cloning artifact	UNP Q8CI96
A	102	GLY	-	cloning artifact	UNP Q8CI96

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: RIKEN cDNA 1700024K14

Chain A: 60% 15% 25%

G1 S2 S3 G4 S5 S6 G7 L8 P9 N10 S11 D12 H13 T14 T15 S16 R17 A18 T21 L25 K26 V31 T40 F49 I57 K77 C78 A79 A86 P87 L88 S89 K90 I91 S92 K93 L94 K95 D96 S97 G98 P99 S100 S101 G102

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: RIKEN cDNA 1700024K14

Chain A: 57% 18% 25%

G1 S2 S3 G4 S5 S6 G7 L8 P9 N10 S11 D12 H13 T14 T15 S16 R17 A18 T21 S22 L25 V31 R42 S51 A55 G56 I57 E63 Y75 F76 K77 C78 A79 P80 K81 Y82 A86 P87 L88 S89 K90 I91 K95 D96 S97 G98 P99 S100 S101 G102

4.2.2 Score per residue for model 2

• Molecule 1: RIKEN cDNA 1700024K14

Chain A: 56% 19% 25%

G1 S2 S3 G4 S5 S6 G7 L8 P9 N10 S11 D12 H13 T14 T15 S16 R17 A18 L25 K26 D29 R30 V31 V32 K37 T40 I57 R72 K77 C78 A79 P80 K81 Y82 A86 S89 K90 I91 S92 K93 L94 K95 D96 S97 G98 P99 S100 S101 G102

4.2.3 Score per residue for model 3

- Molecule 1: RIKEN cDNA 1700024K14

Chain A: 56% 18% • 25%

4.2.4 Score per residue for model 4

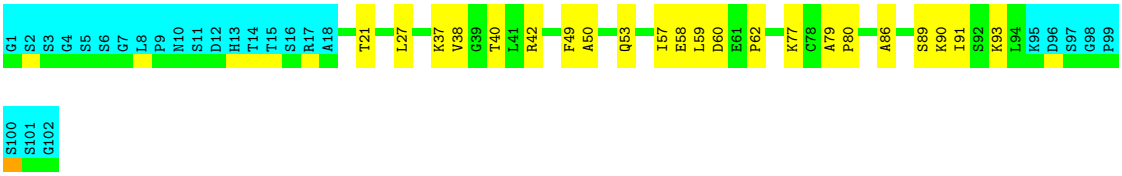
- Molecule 1: RIKEN cDNA 1700024K14

Chain A: 57% 17% • 25%

4.2.5 Score per residue for model 5 (medoid)

- Molecule 1: RIKEN cDNA 1700024K14

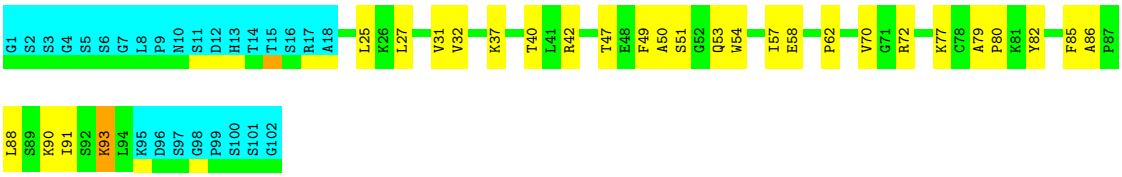
Chain A: 53% 22% 25%



4.2.6 Score per residue for model 6

- Molecule 1: RIKEN cDNA 1700024K14

Chain A: 47% 26% • 25%



4.2.7 Score per residue for model 7

- Molecule 1: RIKEN cDNA 1700024K14

Chain A: 53% 20% • 25%

G1 S2 S3 G4 S5 S6 G7 L8 P9 N10 S11 D12 H13 T14 T15 S16 R17 A18 T21 L25 K26 V31 V32 K37 V38 G39 T40 L41 F49 A50 Q53 I57 E58 K65 A79 Y82 A86 P87 K90 I91 L94 K95 D96 S97 G98 P99 S100

S101 G102

4.2.8 Score per residue for model 8

- Molecule 1: RIKEN cDNA 1700024K14

Chain A: 52% 20% • 25%

G1 S2 S3 G4 S5 S6 G7 L8 P9 N10 S11 D12 H13 T14 T15 S16 R17 A18 T21 S22 L25 K26 R30 V31 V32 V38 G39 T40 F43 C44 S51 G52 Q53 I57 P62 E63 A79 Y82 A86 P87 L88 S89 K90 I91 K95 D96 S97 G98

P99 S100 S101 G102

4.2.9 Score per residue for model 9

- Molecule 1: RIKEN cDNA 1700024K14

Chain A: 50% 25% 25%

G1 S2 S3 G4 S5 S6 G7 L8 P9 N10 S11 D12 H13 T14 T15 S16 R17 A18 M19 L20 T21 L25 R30 T40 L41 R42 T46 T47 F48 F49 A50 Q53 W54 A55 G56 I57 K65 Y75 F76 K77 G78 A79 P80 K81 Y82 A86 P87 L88 S89 K90 I91 S92

K93 L94 K95 D96 S97 G98 P99 S100 S101 G102

4.2.10 Score per residue for model 10

- Molecule 1: RIKEN cDNA 1700024K14

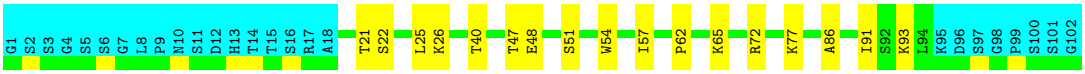
Chain A: 56% 18% • 25%

G1 S2 S3 G4 S5 S6 G7 L8 P9 N10 S11 D12 H13 T14 T15 S16 R17 A18 M19 S22 L25 V31 T40 T46 T47 S51 G52 Q53 W54 I57 E58 K65 A86 P87 L88 S89 K90 I91 S92 K93 L94 K95 D96 S97 G98 P99 S100 S101 G102

4.2.11 Score per residue for model 11

- Molecule 1: RIKEN cDNA 1700024K14

Chain A: 58% 17% 25%



4.2.12 Score per residue for model 12

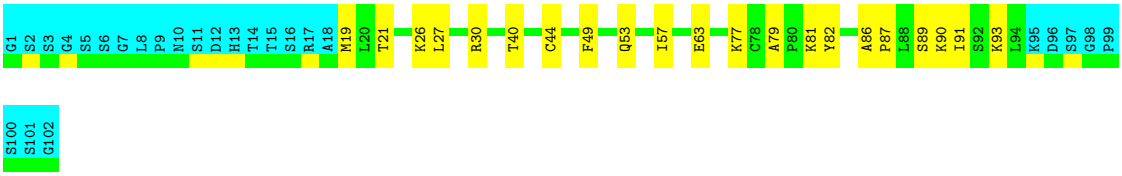
- Molecule 1: RIKEN cDNA 1700024K14

Chain A:

4.2.13 Score per residue for model 13

- Molecule 1: RIKEN cDNA 1700024K14

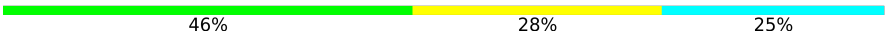
Chain A:



4.2.14 Score per residue for model 14

- Molecule 1: RIKEN cDNA 1700024K14

Chain A:



4.2.15 Score per residue for model 15

- Molecule 1: RIKEN cDNA 1700024K14

Chain A:

4.2.16 Score per residue for model 16

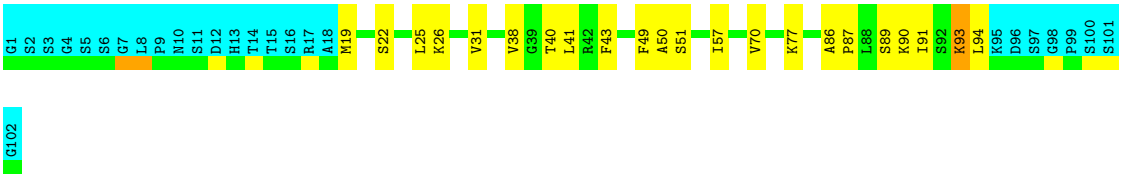
- Molecule 1: RIKEN cDNA 1700024K14

Chain A:

4.2.17 Score per residue for model 17

- Molecule 1: RIKEN cDNA 1700024K14

Chain A:



4.2.18 Score per residue for model 18

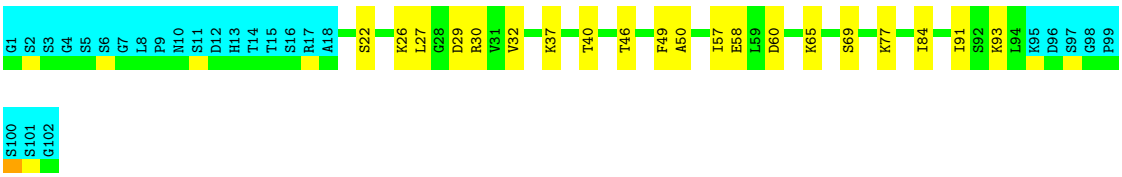
- Molecule 1: RIKEN cDNA 1700024K14

Chain A:

4.2.19 Score per residue for model 19

- Molecule 1: RIKEN cDNA 1700024K14

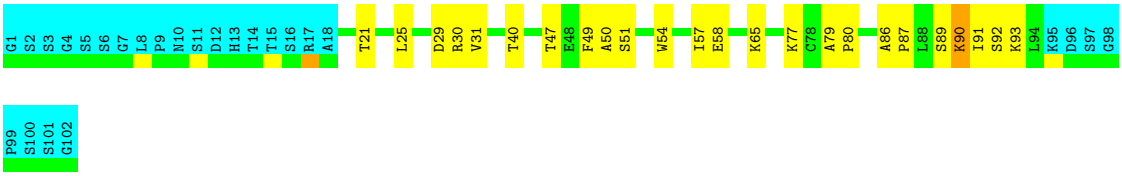
Chain A:



4.2.20 Score per residue for model 20

- Molecule 1: RIKEN cDNA 1700024K14

Chain A: 51% 23% • 25%



5 Refinement protocol and experimental data overview (i)

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

Of the 100 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
CNS	structure solution	1.1
CNS	refinement	1.1

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	A	572	590	590	8±3
All	All	11440	11800	11800	168

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:57:ILE:HD11	1:A:91:ILE:HD13	0.77	1.56	11	9
1:A:86:ALA:HB3	1:A:91:ILE:HD11	0.74	1.59	18	11
1:A:46:THR:HG23	1:A:53:GLN:NE2	0.73	1.99	10	2
1:A:57:ILE:CD1	1:A:91:ILE:HD12	0.65	2.22	8	5
1:A:57:ILE:HD11	1:A:91:ILE:HD12	0.63	1.70	14	7
1:A:37:LYS:NZ	1:A:84:ILE:HD13	0.63	2.09	19	1
1:A:30:ARG:NH1	1:A:38:VAL:HG12	0.63	2.08	8	1
1:A:48:GLU:HB2	1:A:73:VAL:HG21	0.61	1.72	15	2
1:A:27:LEU:HD21	1:A:44:CYS:SG	0.61	2.36	13	1
1:A:25:LEU:HD22	1:A:31:VAL:HG12	0.60	1.73	18	11
1:A:32:VAL:HG23	1:A:37:LYS:O	0.59	1.96	2	4
1:A:79:ALA:HB1	1:A:80:PRO:HD2	0.59	1.73	14	9
1:A:40:THR:C	1:A:57:ILE:HG23	0.58	2.18	8	1
1:A:57:ILE:HD11	1:A:91:ILE:HG21	0.58	1.76	10	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:79:ALA:HB3	1:A:82:TYR:CD2	0.57	2.35	1	8
1:A:27:LEU:HD22	1:A:42:ARG:O	0.56	2.00	6	4
1:A:86:ALA:O	1:A:91:ILE:HD11	0.56	2.00	3	7
1:A:47:THR:HG23	1:A:54:TRP:HB2	0.52	1.80	15	5
1:A:38:VAL:O	1:A:59:LEU:HD23	0.51	2.06	5	3
1:A:59:LEU:HD13	1:A:63:GLU:CB	0.51	2.36	14	1
1:A:55:ALA:HB2	1:A:88:LEU:HD13	0.51	1.82	9	3
1:A:88:LEU:HA	1:A:91:ILE:HD12	0.50	1.82	6	3
1:A:48:GLU:CB	1:A:73:VAL:HG21	0.50	2.36	14	2
1:A:25:LEU:HD21	1:A:93:LYS:N	0.48	2.22	4	3
1:A:49:PHE:CD1	1:A:50:ALA:N	0.47	2.82	20	7
1:A:20:LEU:HD23	1:A:25:LEU:HB2	0.47	1.86	9	1
1:A:32:VAL:O	1:A:32:VAL:HG13	0.47	2.10	7	5
1:A:25:LEU:HD21	1:A:93:LYS:HG3	0.46	1.86	15	1
1:A:19:MET:O	1:A:23:LEU:HD12	0.46	2.11	3	1
1:A:26:LYS:O	1:A:41:LEU:HD23	0.45	2.11	12	3
1:A:87:PRO:O	1:A:90:LYS:N	0.45	2.49	10	11
1:A:75:TYR:CD1	1:A:75:TYR:N	0.45	2.85	1	2
1:A:57:ILE:HD11	1:A:91:ILE:CD1	0.45	2.41	18	5
1:A:59:LEU:HD13	1:A:63:GLU:HB2	0.45	1.89	14	1
1:A:41:LEU:HD11	1:A:43:PHE:O	0.45	2.12	17	1
1:A:25:LEU:HD11	1:A:93:LYS:HB2	0.44	1.88	11	1
1:A:49:PHE:CZ	1:A:70:VAL:HG21	0.44	2.47	17	1
1:A:25:LEU:HD21	1:A:93:LYS:HB2	0.44	1.90	11	1
1:A:38:VAL:HG13	1:A:94:LEU:HD13	0.44	1.88	4	2
1:A:43:PHE:CD1	1:A:44:CYS:N	0.44	2.85	14	3
1:A:46:THR:HG23	1:A:53:GLN:HE21	0.44	1.66	10	1
1:A:70:VAL:CG2	1:A:85:PHE:CE2	0.43	3.01	3	1
1:A:62:PRO:N	1:A:82:TYR:CE1	0.43	2.86	6	1
1:A:49:PHE:CE1	1:A:70:VAL:HG21	0.43	2.48	4	1
1:A:47:THR:HG22	1:A:75:TYR:CE2	0.42	2.50	9	1
1:A:49:PHE:CD2	1:A:50:ALA:N	0.42	2.87	5	1
1:A:70:VAL:CG2	1:A:85:PHE:CE1	0.42	3.02	6	1
1:A:32:VAL:O	1:A:91:ILE:HG23	0.41	2.15	2	1
1:A:25:LEU:HD21	1:A:93:LYS:CA	0.41	2.44	6	1
1:A:57:ILE:CD1	1:A:91:ILE:HD13	0.41	2.42	7	1
1:A:47:THR:HG21	1:A:49:PHE:CE2	0.41	2.51	12	1
1:A:25:LEU:HD21	1:A:93:LYS:CG	0.41	2.44	15	1
1:A:49:PHE:CD2	1:A:70:VAL:HG11	0.41	2.51	18	1
1:A:49:PHE:CG	1:A:70:VAL:HG11	0.41	2.50	17	1
1:A:38:VAL:HG13	1:A:94:LEU:HD11	0.41	1.91	7	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:49:PHE:CE2	1:A:70:VAL:HG21	0.41	2.51	17	1
1:A:32:VAL:HG13	1:A:32:VAL:O	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	76/102 (75%)	68±1 (89±2%)	8±1 (10±2%)	0±0 (1±1%)	29	74
All	All	1520/2040 (75%)	1359 (89%)	152 (10%)	9 (1%)	29	74

All 6 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	62	PRO	4
1	A	63	GLU	1
1	A	49	PHE	1
1	A	50	ALA	1
1	A	27	LEU	1
1	A	51	SER	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	60/80 (75%)	51±1 (85±2%)	9±1 (15±2%)	6	45
All	All	1200/1600 (75%)	1025 (85%)	175 (15%)	6	45

All 26 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	40	THR	17
1	A	77	LYS	13
1	A	89	SER	13
1	A	93	LYS	11
1	A	21	THR	10
1	A	22	SER	9
1	A	26	LYS	9
1	A	58	GLU	9
1	A	51	SER	8
1	A	30	ARG	8
1	A	72	ARG	7
1	A	90	LYS	7
1	A	65	LYS	7
1	A	19	MET	6
1	A	60	ASP	6
1	A	53	GLN	6
1	A	48	GLU	5
1	A	92	SER	5
1	A	63	GLU	4
1	A	46	THR	4
1	A	29	ASP	3
1	A	69	SER	3
1	A	42	ARG	2
1	A	37	LYS	1
1	A	81	LYS	1
1	A	36	GLN	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