Full wwPDB NMR Structure Validation Report (i)

Dec 10, 2022 – 08:26 PM EST

PDB ID	:	1K99
Title	:	Solution Structure of the first HMG box in human Upstream binding factor
Authors	:	Xu, Y.; Yang, W.; Wu, J.; Shi, Y.
Deposited on	:	2001-10-28

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 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:

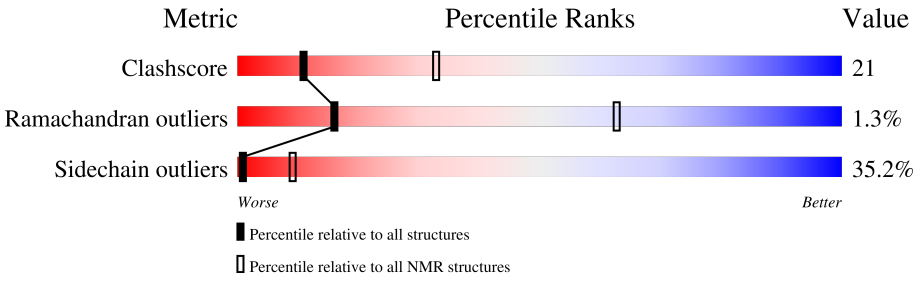
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	2.31.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

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	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	99	22% 29% • 36% 8%

2 Ensemble composition and analysis (i)

This entry contains 20 models. Model 17 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:14-A:68 (55)	0.37	17

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 5 clusters and 3 single-model clusters were found.

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

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 1638 atoms, of which 842 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Upstream binding factor 1.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	91	1638	518	842	142	132	4	0

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP P17480
A	92	LEU	-	expression tag	UNP P17480
A	93	GLU	-	expression tag	UNP P17480
A	94	HIS	-	expression tag	UNP P17480
A	95	HIS	-	expression tag	UNP P17480
A	96	HIS	-	expression tag	UNP P17480
A	97	HIS	-	expression tag	UNP P17480
A	98	HIS	-	expression tag	UNP P17480
A	99	HIS	-	expression tag	UNP P17480

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: Upstream binding factor 1

Chain A: 22% 29% • 36% 8%

M1 K2 K3 L4 K5 K6 H7 P8 D9 F10 P11 K12 K13 P14 L15 F19 F22 M23 E24 K25 R26 A27 K28 Y29 A30 K31 L32 H33 M36 S37 N38 L41 T42 K43 I44 L45 K48 Y49 K50 E51 L52 P53 E54 K55 K56 K57 M58 K59 Y60 I61 Q62 D63 F64 Q65 R66

E67 K68 Q69 E70 F71 E72 R73 N74 L75 A76 R77 F78 R79 E80 D81 H82 P83 D84 L85 I86 Q87 N88 A89 K90 K91 LEU GLU HIS HIS HIS HIS HIS HIS

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: Upstream binding factor 1

Chain A: 21% 27% 7% 36% 8%

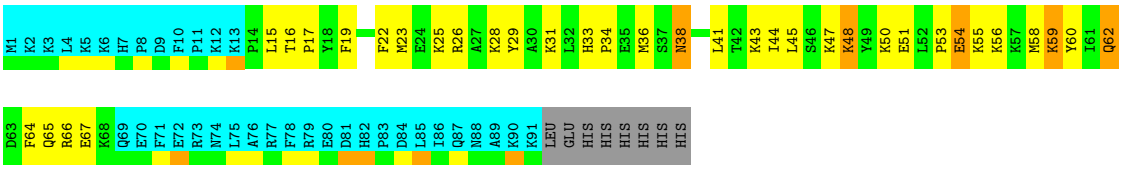
M1 K2 K3 L4 K5 K6 H7 P8 D9 F10 P11 K12 K13 P14 L15 F19 F22 M23 E24 K25 R26 A27 K28 Y29 A30 K31 L32 H33 M36 S37 N38 L41 T42 K43 I44 L45 S46 Y49 K50 E51 L52 P53 E54 K55 K56 K57 M58 K59 Y60 I61 Q62 D63 F64 Q65 R66

E67 K68 Q69 E70 F71 E72 R73 N74 L75 A76 R77 F78 R79 E80 D81 H82 P83 D84 L85 I86 Q87 N88 A89 K90 K91 LEU GLU HIS HIS HIS HIS HIS HIS

4.2.2 Score per residue for model 2

• Molecule 1: Upstream binding factor 1

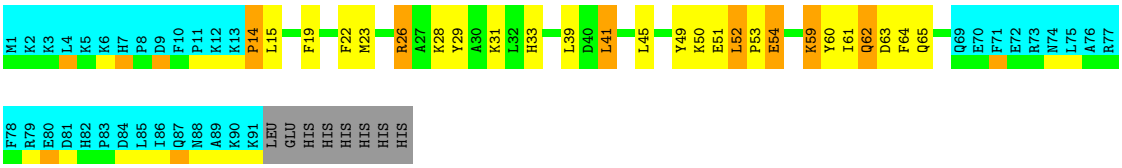
Chain A: 20% 30% 5% 36% 8%



4.2.3 Score per residue for model 3

- Molecule 1: Upstream binding factor 1

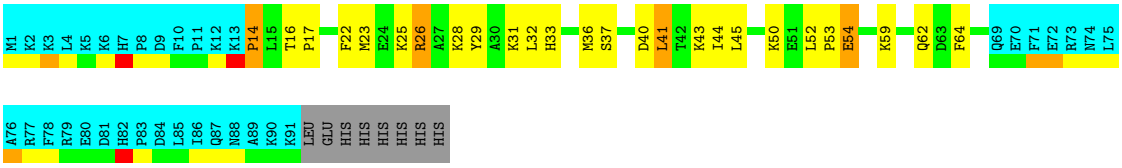
Chain A: 29% 19% 7% 36% 8%



4.2.4 Score per residue for model 4

- Molecule 1: Upstream binding factor 1

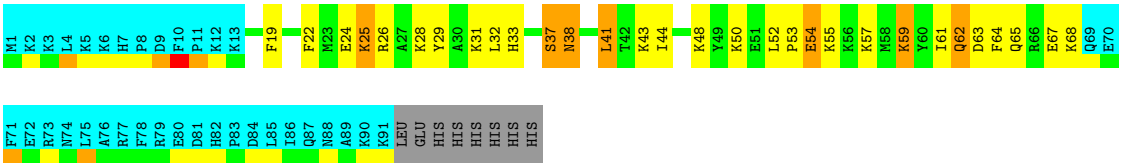
Chain A: 29% 22% • 36% 8%



4.2.5 Score per residue for model 5

- Molecule 1: Upstream binding factor 1

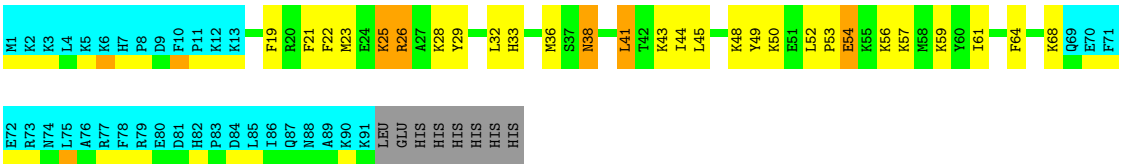
Chain A: 25% 23% 7% 36% 8%



4.2.6 Score per residue for model 6

- Molecule 1: Upstream binding factor 1

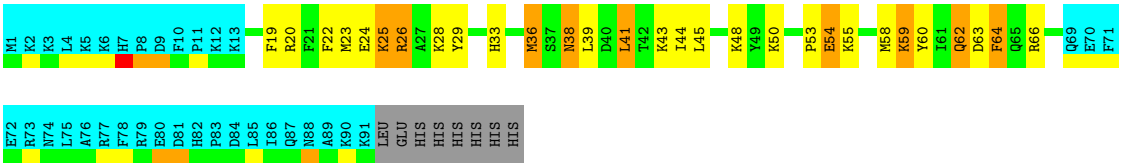
Chain A: 27% 23% 5% 36% 8%



4.2.7 Score per residue for model 7

- Molecule 1: Upstream binding factor 1

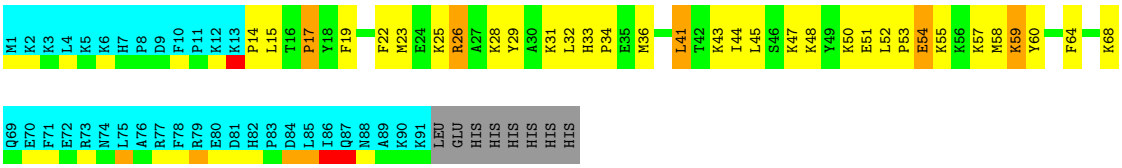
Chain A: 26% 20% 9% 36% 8%



4.2.8 Score per residue for model 8

- Molecule 1: Upstream binding factor 1

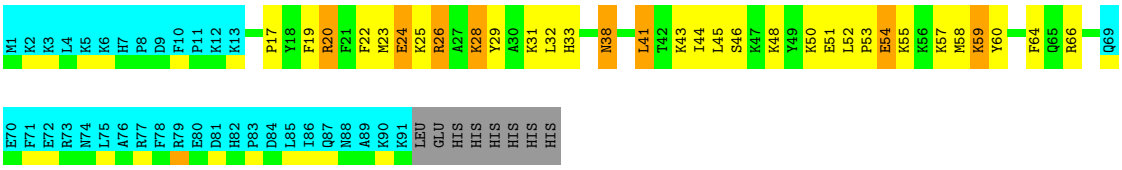
Chain A: 22% 28% 5% 36% 8%



4.2.9 Score per residue for model 9

- Molecule 1: Upstream binding factor 1

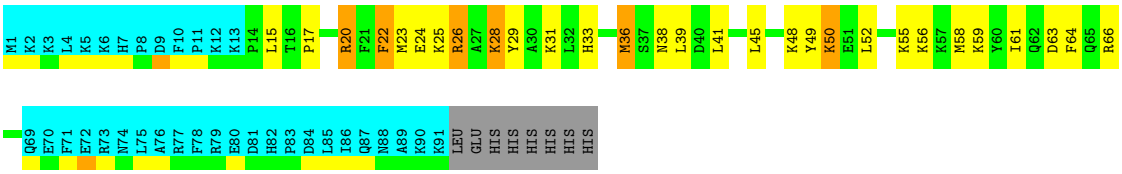
Chain A: 23% 24% 8% 36% 8%



4.2.10 Score per residue for model 10

- Molecule 1: Upstream binding factor 1

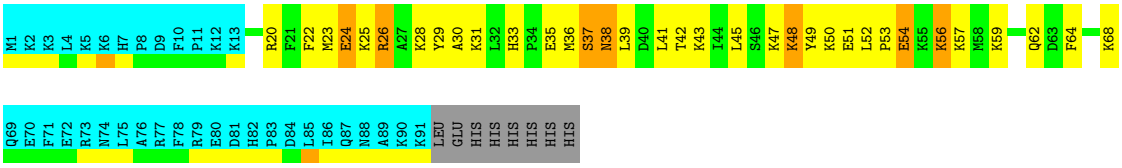
Chain A: 26% 23% 6% 36% 8%



4.2.11 Score per residue for model 11

- Molecule 1: Upstream binding factor 1

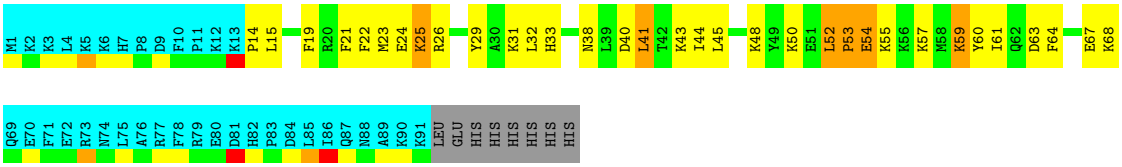
Chain A: 21% 27% 7% 36% 8%



4.2.12 Score per residue for model 12

- Molecule 1: Upstream binding factor 1

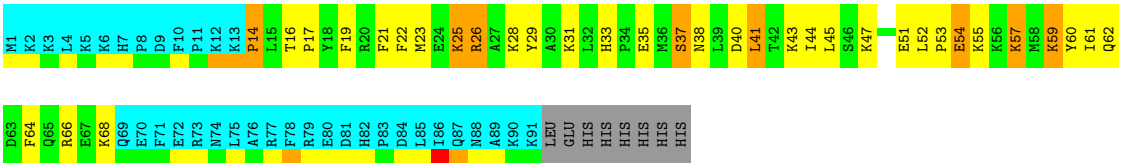
Chain A: 22% 27% 6% 36% 8%



4.2.13 Score per residue for model 13

- Molecule 1: Upstream binding factor 1

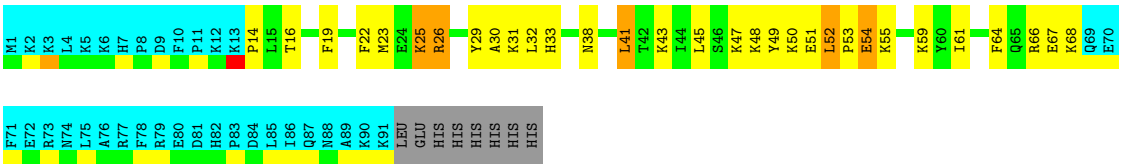
Chain A: 20% 27% 8% 36% 8%



4.2.14 Score per residue for model 14

- Molecule 1: Upstream binding factor 1

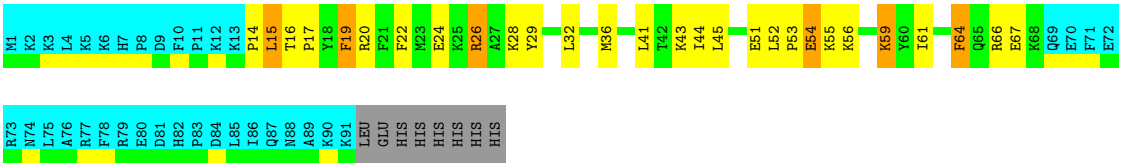
Chain A: 24% 26% 5% 36% 8%



4.2.15 Score per residue for model 15

- Molecule 1: Upstream binding factor 1

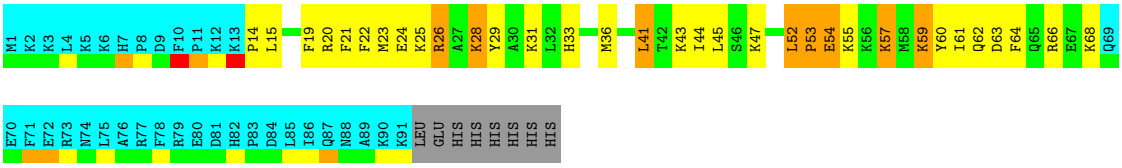
Chain A: 27% 22% 6% 36% 8%



4.2.16 Score per residue for model 16

- Molecule 1: Upstream binding factor 1

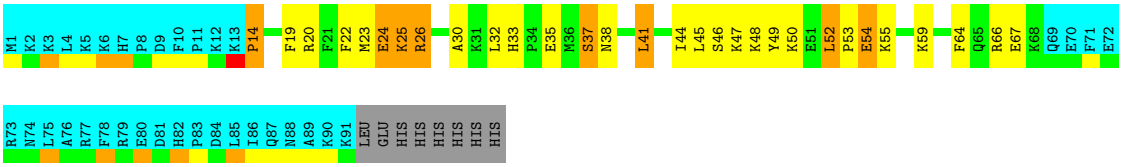
Chain A: 22% 25% 8% 36% 8%



4.2.17 Score per residue for model 17 (medoid)

- Molecule 1: Upstream binding factor 1

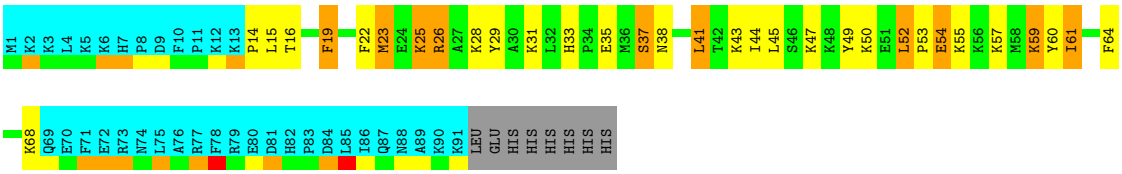
Chain A: 25% 22% 8% 36% 8%



4.2.18 Score per residue for model 18

- Molecule 1: Upstream binding factor 1

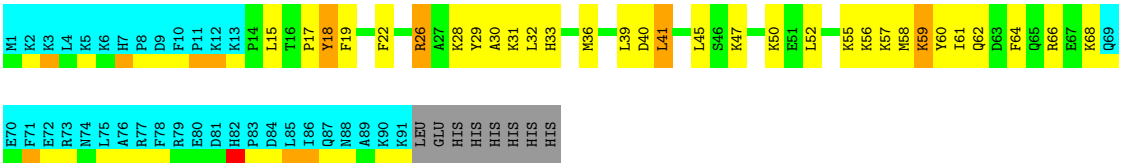
Chain A: 23% 22% 10% 36% 8%



4.2.19 Score per residue for model 19

- Molecule 1: Upstream binding factor 1

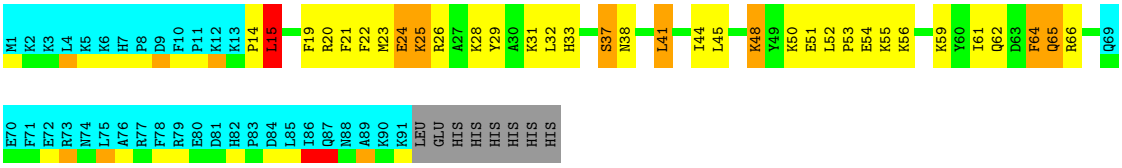
Chain A: 24% 27% • 36% 8%



4.2.20 Score per residue for model 20

- Molecule 1: Upstream binding factor 1

Chain A: 21% 26% 7% • 36% 8%



5 Refinement protocol and experimental data overview (i)

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

Of the 60 calculated structures, 20 were deposited, based on the following criterion: *structures with the least restraint violations, structures with the lowest energy.*

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

Software name	Classification	Version
CNS	refinement	1.0

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	482	512	511	20±4
All	All	9640	10240	10220	410

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 21.

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:ARG:NH1	1:A:41:LEU:HD12	0.81	1.90	3	6
1:A:29:TYR:CD1	1:A:32:LEU:HD23	0.78	2.14	19	1
1:A:41:LEU:HA	1:A:44:ILE:HD12	0.74	1.58	6	15
1:A:26:ARG:NH2	1:A:30:ALA:HB2	0.74	1.98	11	3
1:A:52:LEU:HD23	1:A:56:LYS:HB2	0.73	1.58	20	2
1:A:33:HIS:CD2	1:A:41:LEU:HD22	0.71	2.20	14	2
1:A:33:HIS:CG	1:A:41:LEU:HD22	0.71	2.20	8	5
1:A:26:ARG:CZ	1:A:41:LEU:HD13	0.71	2.16	7	4
1:A:29:TYR:CE2	1:A:45:LEU:HD21	0.70	2.21	2	13
1:A:26:ARG:CZ	1:A:41:LEU:HD12	0.70	2.16	4	6
1:A:49:TYR:HA	1:A:52:LEU:HD12	0.69	1.63	14	5
1:A:52:LEU:HD22	1:A:56:LYS:HB2	0.69	1.64	10	2
1:A:33:HIS:CG	1:A:41:LEU:HD23	0.68	2.23	1	7
1:A:22:PHE:CD2	1:A:45:LEU:HD12	0.67	2.24	10	4

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:22:PHE:HA	1:A:45:LEU:HD13	0.66	1.68	14	3
1:A:52:LEU:HD23	1:A:56:LYS:CB	0.66	2.20	20	1
1:A:38:ASN:OD1	1:A:41:LEU:HD11	0.65	1.92	5	2
1:A:29:TYR:HB3	1:A:41:LEU:HD13	0.65	1.68	19	5
1:A:52:LEU:HD11	1:A:57:LYS:HE3	0.65	1.67	9	1
1:A:48:LYS:O	1:A:52:LEU:HD12	0.64	1.91	11	2
1:A:29:TYR:HE2	1:A:45:LEU:HD21	0.62	1.54	11	12
1:A:25:LYS:HD3	1:A:45:LEU:HD22	0.62	1.72	17	4
1:A:61:ILE:HD13	1:A:61:ILE:N	0.61	2.10	6	2
1:A:52:LEU:HD11	1:A:57:LYS:CE	0.61	2.26	9	2
1:A:26:ARG:NE	1:A:26:ARG:HA	0.59	2.10	2	9
1:A:33:HIS:ND1	1:A:41:LEU:HD23	0.59	2.13	1	7
1:A:15:LEU:HD13	1:A:23:MET:SD	0.59	2.38	8	1
1:A:15:LEU:HD13	1:A:19:PHE:HB3	0.58	1.74	16	1
1:A:26:ARG:HH21	1:A:45:LEU:HD12	0.57	1.59	8	2
1:A:15:LEU:HD11	1:A:20:ARG:HB3	0.57	1.75	16	1
1:A:52:LEU:HD12	1:A:54:GLU:N	0.57	2.15	6	3
1:A:22:PHE:CD2	1:A:45:LEU:HD13	0.57	2.35	12	4
1:A:52:LEU:HD11	1:A:57:LYS:HG3	0.57	1.76	5	2
1:A:17:PRO:HG3	1:A:61:ILE:CG1	0.56	2.30	15	1
1:A:49:TYR:O	1:A:52:LEU:HD12	0.56	2.00	10	1
1:A:52:LEU:HD12	1:A:54:GLU:H	0.56	1.61	6	4
1:A:54:GLU:HA	1:A:57:LYS:HD2	0.55	1.79	13	2
1:A:33:HIS:CD2	1:A:41:LEU:CD2	0.55	2.89	14	2
1:A:52:LEU:HD22	1:A:56:LYS:CB	0.55	2.31	10	2
1:A:33:HIS:CB	1:A:41:LEU:HD22	0.54	2.32	13	3
1:A:29:TYR:CE1	1:A:32:LEU:HD23	0.54	2.38	19	1
1:A:33:HIS:CB	1:A:41:LEU:HD23	0.54	2.32	17	3
1:A:22:PHE:CE2	1:A:26:ARG:CZ	0.54	2.91	3	5
1:A:38:ASN:HA	1:A:41:LEU:HD21	0.53	1.79	18	12
1:A:56:LYS:O	1:A:59:LYS:CG	0.53	2.57	6	2
1:A:52:LEU:HD13	1:A:56:LYS:HB2	0.53	1.79	6	1
1:A:32:LEU:HD22	1:A:32:LEU:O	0.53	2.04	14	1
1:A:45:LEU:HD23	1:A:48:LYS:HD3	0.53	1.80	10	2
1:A:22:PHE:CZ	1:A:26:ARG:CZ	0.53	2.92	19	4
1:A:29:TYR:HD1	1:A:32:LEU:HD23	0.52	1.62	19	1
1:A:25:LYS:HD3	1:A:45:LEU:HD21	0.52	1.79	16	1
1:A:26:ARG:NE	1:A:41:LEU:HD13	0.52	2.18	6	5
1:A:41:LEU:HD12	1:A:42:THR:N	0.52	2.19	11	1
1:A:39:LEU:HD12	1:A:39:LEU:O	0.51	2.05	7	1
1:A:22:PHE:CE1	1:A:26:ARG:CG	0.51	2.94	13	14

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:44:ILE:HG22	1:A:48:LYS:HD2	0.51	1.82	6	3
1:A:22:PHE:CZ	1:A:26:ARG:HD3	0.51	2.41	6	12
1:A:29:TYR:CE1	1:A:45:LEU:HD21	0.51	2.40	8	1
1:A:22:PHE:O	1:A:26:ARG:HG2	0.50	2.06	15	9
1:A:49:TYR:HA	1:A:52:LEU:HD13	0.50	1.82	11	1
1:A:61:ILE:O	1:A:65:GLN:CG	0.50	2.60	20	1
1:A:52:LEU:HD11	1:A:57:LYS:CD	0.50	2.36	6	1
1:A:29:TYR:CE2	1:A:45:LEU:CD2	0.49	2.95	7	3
1:A:22:PHE:CD2	1:A:45:LEU:CD1	0.49	2.95	12	9
1:A:26:ARG:NH2	1:A:41:LEU:HD13	0.48	2.21	7	1
1:A:57:LYS:O	1:A:61:ILE:HG12	0.48	2.07	6	2
1:A:33:HIS:CE1	1:A:36:MET:CE	0.48	2.96	7	3
1:A:49:TYR:CE2	1:A:50:LYS:NZ	0.48	2.81	10	1
1:A:22:PHE:CZ	1:A:26:ARG:NH1	0.48	2.82	4	2
1:A:56:LYS:O	1:A:60:TYR:CD2	0.47	2.67	19	2
1:A:53:PRO:C	1:A:54:GLU:CG	0.47	2.82	6	17
1:A:61:ILE:N	1:A:61:ILE:HD12	0.47	2.24	5	7
1:A:32:LEU:C	1:A:32:LEU:HD13	0.47	2.30	14	1
1:A:15:LEU:HD22	1:A:19:PHE:CD1	0.47	2.45	1	1
1:A:59:LYS:HG3	1:A:60:TYR:N	0.47	2.24	18	2
1:A:15:LEU:HD13	1:A:19:PHE:CB	0.47	2.39	16	1
1:A:52:LEU:HD11	1:A:57:LYS:CG	0.47	2.39	6	2
1:A:15:LEU:O	1:A:64:PHE:CE1	0.47	2.68	20	2
1:A:21:PHE:CE1	1:A:25:LYS:CE	0.47	2.98	20	1
1:A:25:LYS:HB3	1:A:29:TYR:CE2	0.46	2.45	14	2
1:A:52:LEU:HD22	1:A:56:LYS:CG	0.46	2.40	19	1
1:A:22:PHE:CZ	1:A:26:ARG:NE	0.46	2.84	19	1
1:A:21:PHE:CD1	1:A:60:TYR:CE2	0.46	3.04	12	1
1:A:33:HIS:CG	1:A:33:HIS:O	0.46	2.69	19	1
1:A:22:PHE:CE2	1:A:26:ARG:NH2	0.46	2.84	8	1
1:A:59:LYS:HG2	1:A:60:TYR:CD1	0.46	2.46	12	2
1:A:26:ARG:NE	1:A:41:LEU:CD1	0.46	2.79	12	1
1:A:37:SER:O	1:A:38:ASN:CB	0.45	2.63	18	6
1:A:59:LYS:HA	1:A:62:GLN:HG2	0.45	1.88	16	2
1:A:20:ARG:O	1:A:24:GLU:HB2	0.45	2.10	20	1
1:A:22:PHE:CE1	1:A:26:ARG:HG3	0.45	2.46	11	5
1:A:15:LEU:C	1:A:64:PHE:CE1	0.45	2.90	20	2
1:A:25:LYS:O	1:A:28:LYS:N	0.45	2.48	16	2
1:A:17:PRO:HB3	1:A:60:TYR:HB3	0.45	1.88	2	4
1:A:33:HIS:CG	1:A:41:LEU:CD2	0.45	2.99	5	6
1:A:59:LYS:O	1:A:62:GLN:HG3	0.45	2.12	7	1

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:25:LYS:HB3	1:A:45:LEU:HD11	0.45	1.88	4	1
1:A:26:ARG:CZ	1:A:41:LEU:CD1	0.44	2.95	10	2
1:A:52:LEU:C	1:A:54:GLU:H	0.44	2.15	20	3
1:A:56:LYS:O	1:A:59:LYS:HG3	0.44	2.12	19	2
1:A:22:PHE:CE2	1:A:26:ARG:NH1	0.44	2.85	4	1
1:A:20:ARG:O	1:A:24:GLU:HB3	0.44	2.12	7	5
1:A:54:GLU:O	1:A:54:GLU:HG2	0.44	2.12	20	1
1:A:18:TYR:O	1:A:22:PHE:N	0.44	2.48	19	1
1:A:28:LYS:CE	1:A:32:LEU:HD13	0.44	2.42	9	1
1:A:22:PHE:CE1	1:A:26:ARG:CD	0.44	3.00	13	1
1:A:62:GLN:HA	1:A:65:GLN:HG2	0.44	1.89	5	3
1:A:29:TYR:O	1:A:33:HIS:CD2	0.44	2.71	18	2
1:A:30:ALA:HA	1:A:33:HIS:NE2	0.43	2.29	14	2
1:A:25:LYS:CD	1:A:45:LEU:HD22	0.43	2.42	17	1
1:A:22:PHE:CG	1:A:45:LEU:HD13	0.43	2.49	12	1
1:A:19:PHE:O	1:A:23:MET:N	0.43	2.49	18	1
1:A:33:HIS:CE1	1:A:41:LEU:N	0.43	2.86	6	1
1:A:52:LEU:HD12	1:A:54:GLU:CA	0.43	2.44	6	1
1:A:24:GLU:HG3	1:A:25:LYS:N	0.43	2.29	1	1
1:A:17:PRO:HA	1:A:20:ARG:CG	0.42	2.44	10	1
1:A:33:HIS:N	1:A:34:PRO:CD	0.42	2.83	2	2
1:A:52:LEU:HD22	1:A:56:LYS:HE2	0.42	1.90	15	1
1:A:59:LYS:O	1:A:62:GLN:CG	0.42	2.66	5	1
1:A:21:PHE:CE1	1:A:25:LYS:CD	0.42	3.02	6	1
1:A:59:LYS:CG	1:A:60:TYR:N	0.42	2.83	13	3
1:A:33:HIS:CE1	1:A:36:MET:HE3	0.42	2.50	10	1
1:A:33:HIS:ND1	1:A:36:MET:CE	0.42	2.83	10	1
1:A:38:ASN:O	1:A:41:LEU:CD1	0.42	2.68	17	1
1:A:22:PHE:CE2	1:A:26:ARG:HD3	0.42	2.50	18	1
1:A:22:PHE:CD1	1:A:22:PHE:C	0.42	2.93	12	2
1:A:21:PHE:CE1	1:A:25:LYS:HD3	0.42	2.50	6	1
1:A:33:HIS:O	1:A:33:HIS:CG	0.42	2.73	14	1
1:A:25:LYS:O	1:A:29:TYR:CD2	0.41	2.73	12	3
1:A:26:ARG:NH2	1:A:41:LEU:CD1	0.41	2.83	14	2
1:A:16:THR:OG1	1:A:17:PRO:HD2	0.41	2.15	15	1
1:A:29:TYR:CB	1:A:41:LEU:HD13	0.41	2.44	4	1
1:A:60:TYR:O	1:A:64:PHE:N	0.41	2.54	7	1
1:A:38:ASN:CG	1:A:41:LEU:HD11	0.41	2.36	5	1
1:A:49:TYR:O	1:A:52:LEU:CD2	0.41	2.69	6	1
1:A:20:ARG:O	1:A:24:GLU:HG2	0.41	2.16	11	1
1:A:61:ILE:N	1:A:61:ILE:CD1	0.41	2.84	16	1

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:16:THR:O	1:A:19:PHE:N	0.41	2.53	15	1
1:A:57:LYS:O	1:A:61:ILE:HD13	0.41	2.16	19	1
1:A:53:PRO:O	1:A:54:GLU:HG3	0.41	2.16	6	1
1:A:33:HIS:ND1	1:A:36:MET:HE3	0.41	2.31	11	1
1:A:16:THR:OG1	1:A:19:PHE:CG	0.41	2.73	13	1
1:A:20:ARG:O	1:A:24:GLU:CG	0.41	2.69	15	2
1:A:54:GLU:HA	1:A:57:LYS:CD	0.40	2.46	1	1
1:A:16:THR:HB	1:A:17:PRO:CD	0.40	2.46	4	1
1:A:57:LYS:O	1:A:61:ILE:CD1	0.40	2.70	12	1
1:A:57:LYS:O	1:A:60:TYR:N	0.40	2.53	16	1
1:A:26:ARG:NE	1:A:26:ARG:CA	0.40	2.84	17	1
1:A:26:ARG:CA	1:A:26:ARG:NE	0.40	2.84	1	1
1:A:17:PRO:HB3	1:A:60:TYR:CB	0.40	2.46	9	1
1:A:29:TYR:CZ	1:A:45:LEU:HD21	0.40	2.50	10	1
1:A:17:PRO:HB3	1:A:60:TYR:HB2	0.40	1.94	9	1
1:A:22:PHE:O	1:A:26:ARG:N	0.40	2.55	1	1
1:A:32:LEU:HD23	1:A:33:HIS:CD2	0.40	2.51	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	55/99 (56%)	49±2 (88±3%)	6±2 (10±3%)	1±1 (1±1%)	16	63
All	All	1100/1980 (56%)	973 (88%)	113 (10%)	14 (1%)	16	63

All 4 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	14	PRO	7
1	A	38	ASN	3
1	A	53	PRO	3
1	A	15	LEU	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	53/95 (56%)	34±2 (65±5%)	19±2 (35±5%)	1 9
All	All	1060/1900 (56%)	687 (65%)	373 (35%)	1 9

All 43 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	64	PHE	20
1	A	59	LYS	19
1	A	28	LYS	17
1	A	50	LYS	17
1	A	54	GLU	17
1	A	23	MET	16
1	A	26	ARG	16
1	A	31	LYS	16
1	A	41	LEU	16
1	A	55	LYS	16
1	A	19	PHE	15
1	A	43	LYS	15
1	A	25	LYS	14
1	A	66	ARG	12
1	A	68	LYS	10
1	A	32	LEU	9
1	A	36	MET	9
1	A	47	LYS	9
1	A	51	GLU	9
1	A	62	GLN	9
1	A	15	LEU	8
1	A	48	LYS	8
1	A	52	LEU	8
1	A	63	ASP	7
1	A	37	SER	7
1	A	58	MET	6
1	A	67	GLU	6
1	A	24	GLU	6
1	A	38	ASN	5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Models (Total)
1	A	39	LEU	4
1	A	40	ASP	4
1	A	35	GLU	4
1	A	46	SER	3
1	A	16	THR	3
1	A	57	LYS	3
1	A	20	ARG	2
1	A	21	PHE	2
1	A	17	PRO	1
1	A	22	PHE	1
1	A	56	LYS	1
1	A	61	ILE	1
1	A	18	TYR	1
1	A	65	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