Full wwPDB NMR Structure Validation Report (i)

Nov 2, 2021 – 03:10 AM EDT

PDB ID	:	1X4H
Title	:	Solution structure of RRM domain in RNA-binding protein 28
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Deposited on	:	2005-05-14

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:

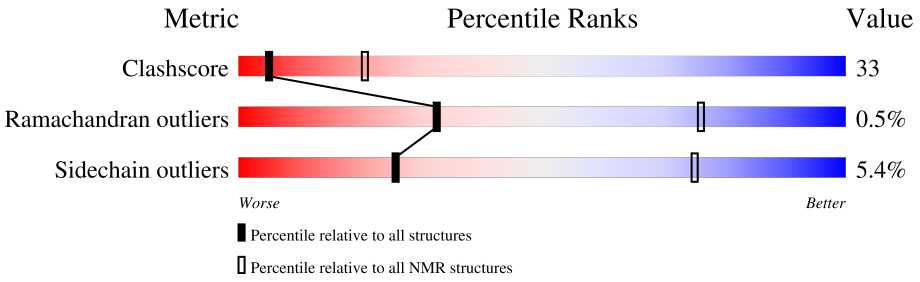
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	2.23.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (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	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	111	39% 23% • 38%

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 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:15-A:48, A:58-A:78, A:86-A:99 (69)	0.15	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 2 clusters and 2 single-model clusters were found.

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

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 1604 atoms, of which 791 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called RNA-binding protein 28.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	111	1604	500	791	140	170	3	0

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	cloning artifact	UNP Q8CGC6
A	2	SER	-	cloning artifact	UNP Q8CGC6
A	3	SER	-	cloning artifact	UNP Q8CGC6
A	4	GLY	-	cloning artifact	UNP Q8CGC6
A	5	SER	-	cloning artifact	UNP Q8CGC6
A	6	SER	-	cloning artifact	UNP Q8CGC6
A	7	GLY	-	cloning artifact	UNP Q8CGC6
A	79	LEU	PRO	engineered mutation	UNP Q8CGC6
A	106	SER	-	cloning artifact	UNP Q8CGC6
A	107	GLY	-	cloning artifact	UNP Q8CGC6
A	108	PRO	-	cloning artifact	UNP Q8CGC6
A	109	SER	-	cloning artifact	UNP Q8CGC6
A	110	SER	-	cloning artifact	UNP Q8CGC6
A	111	GLY	-	cloning artifact	UNP Q8CGC6

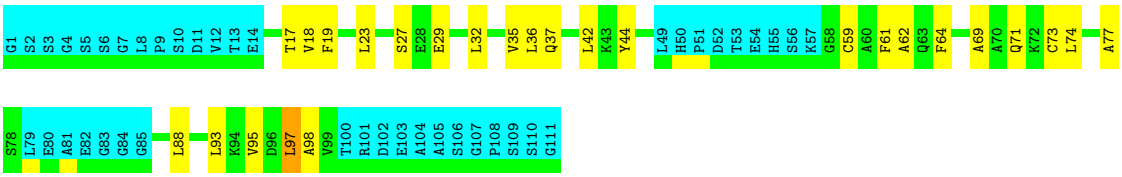
4 Residue-property plots (i)

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: RNA-binding protein 28

Chain A: 39% 23% • 38%



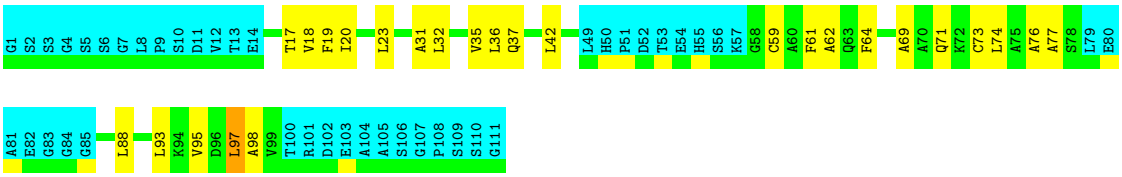
4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

• Molecule 1: RNA-binding protein 28

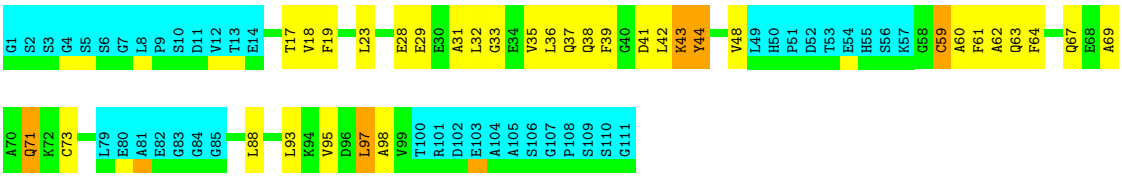
Chain A: 39% 23% • 38%



4.2.2 Score per residue for model 2

• Molecule 1: RNA-binding protein 28

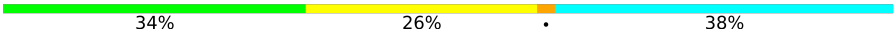
Chain A: 32% 26% 5% 38%

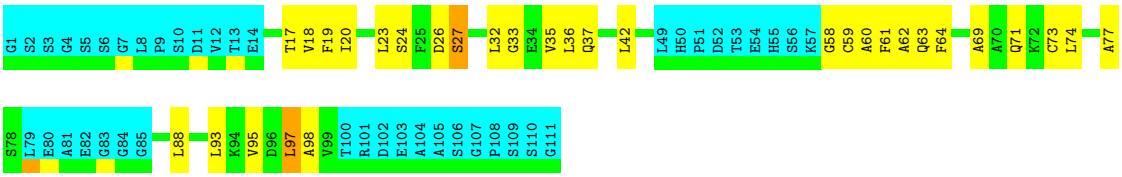


4.2.3 Score per residue for model 3

- Molecule 1: RNA-binding protein 28

Chain A:

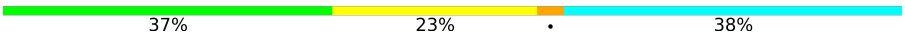


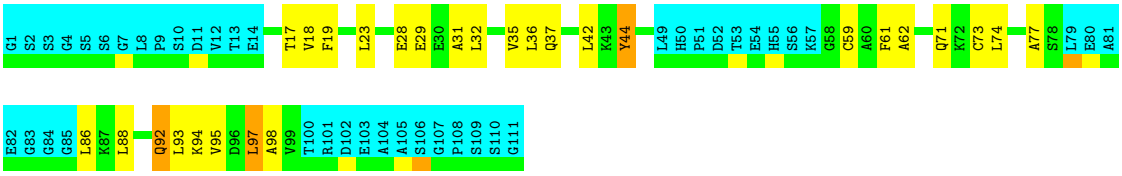


4.2.4 Score per residue for model 4

- Molecule 1: RNA-binding protein 28

Chain A:

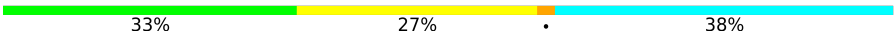


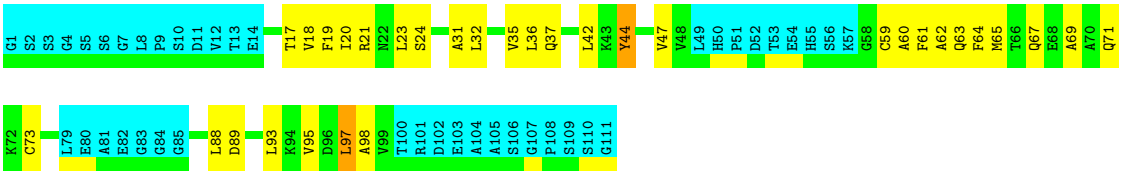


4.2.5 Score per residue for model 5

- Molecule 1: RNA-binding protein 28

Chain A:





4.2.6 Score per residue for model 6

- Molecule 1: RNA-binding protein 28

Chain A: 32% 30% • 38%

G1 S2 S3 G4 S5 S6 G7 L8 P9 S10 D11 V12 T13 E14 T17 V18 F19 I20 L23 D26 S27 E28 E29 E30 A31 L32 V35 L36 Q37 Q38 F39 L42 L49 H50 P51 D52 T53 E54 H55 S56 K57 G58 C59 A60 F61 A62 Q63 F64 A69 A70 Q71 K72 C73

L74 A75 A76 A77 S78 L79 E80 A81 E82 G83 G84 G85 L86 K87 L88 D89 L93 K94 V95 D96 L97 A98 V99 T100 R101 D102 E103 A104 A105 S106 G107 P108 S109 S110 G111

4.2.7 Score per residue for model 7

- Molecule 1: RNA-binding protein 28

Chain A: 36% 23% • 38%

G1 S2 S3 G4 S5 S6 G7 L8 P9 S10 D11 V12 T13 E14 T17 V18 F19 I20 R21 N22 L23 S24 F25 D26 S27 E28 E29 L32 L36 Q37 Q38 F39 L42 K43 Y44 V48 L49 H50 P51 D52 T53 E54 H55 S56 K57 G58 C59 A60 F61 F64 A69 A70 Q71

K72 C73 L79 E80 A81 E82 G83 G84 G85 Q92 V95 D96 L97 A98 V99 T100 R101 D102 E103 A104 A105 S106 G107 P108 S109 S110 G111

4.2.8 Score per residue for model 8

- Molecule 1: RNA-binding protein 28

Chain A: 32% 28% • 38%

G1 S2 S3 G4 S5 S6 G7 L8 P9 S10 D11 V12 T13 E14 T17 V18 F19 I20 R21 N22 L23 E28 E29 L32 V35 L36 Q37 Q38 F39 L42 K43 Y44 V47 V48 L49 H50 P51 D52 T53 E54 H55 S56 K57 G58 C59 A60 F61 A62 Q63 F64 A70 Q71 K72

C73 L74 A75 A76 A77 S78 L79 E80 A81 E82 G83 G84 G85 L86 K87 L88 L93 K94 V95 D96 L97 A98 V99 T100 R101 D102 E103 A104 A105 S106 G107 P108 S109 S110 G111

4.2.9 Score per residue for model 9

- Molecule 1: RNA-binding protein 28

Chain A: 40% 21% • 38%

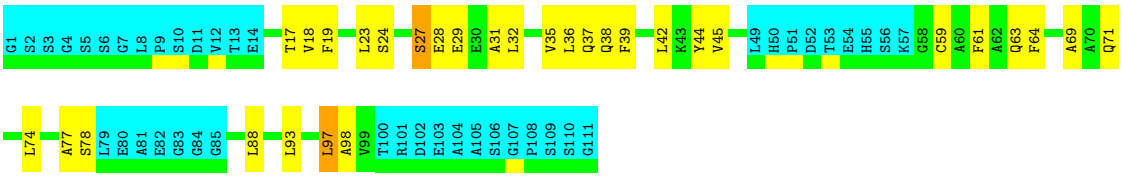
G1 S2 S3 G4 S5 S6 G7 L8 P9 S10 D11 V12 T13 E14 T17 V18 F19 L23 D26 S27 E28 E29 E30 A31 L32 L36 Q37 L42 K43 Y44 L49 H50 P51 D52 T53 E54 H55 S56 K57 G58 C59 A60 F61 A62 Q63 F64 A69 A70 Q71 K72 C73 L74

L79 E80 A81 E82 G83 G84 G85 V95 D96 L97 A98 V99 T100 R101 D102 E103 A104 A105 S106 G107 P108 S109 S110 G111

4.2.10 Score per residue for model 10

- Molecule 1: RNA-binding protein 28

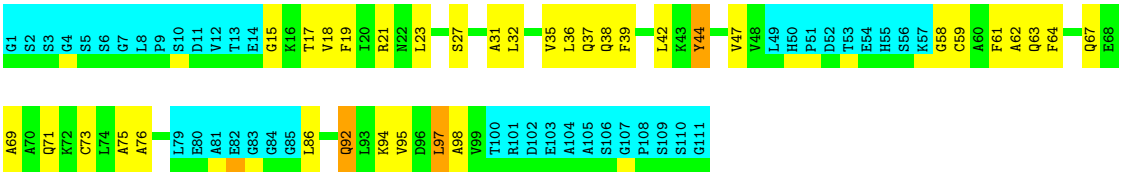
Chain A: 34% 26% • 38%



4.2.11 Score per residue for model 11

- Molecule 1: RNA-binding protein 28

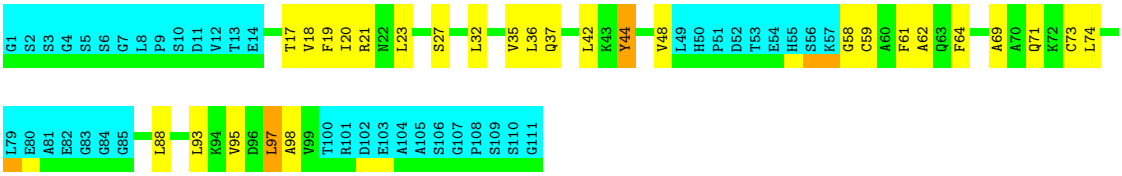
Chain A: 31% 29% • 38%



4.2.12 Score per residue for model 12

- Molecule 1: RNA-binding protein 28

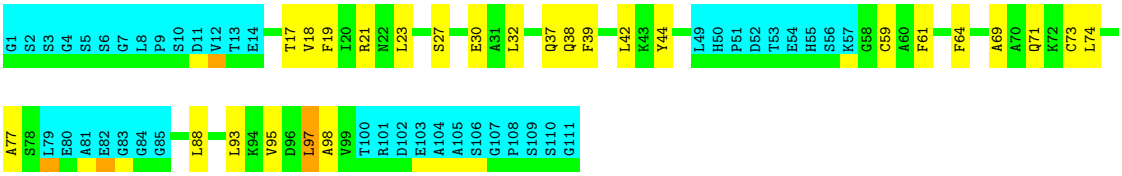
Chain A: 37% 23% • 38%



4.2.13 Score per residue for model 13

- Molecule 1: RNA-binding protein 28

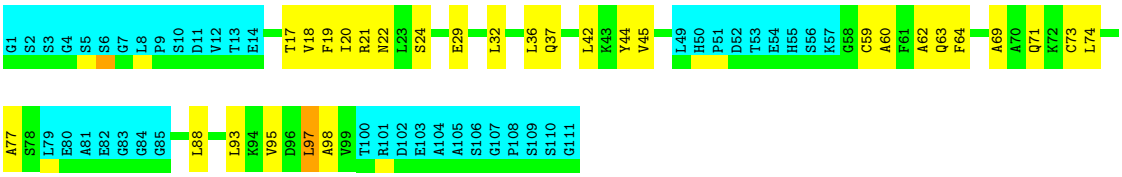
Chain A: 39% 23% • 38%



4.2.14 Score per residue for model 14

- Molecule 1: RNA-binding protein 28

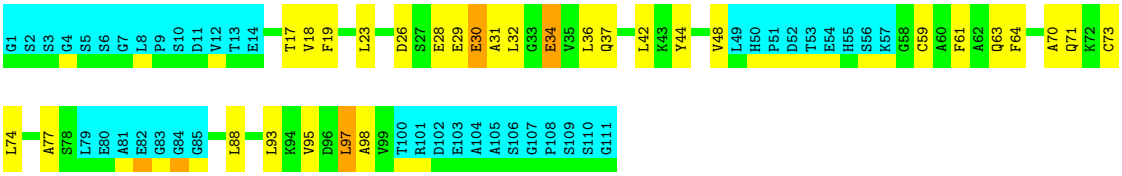
Chain A: 36% 25% • 38%



4.2.15 Score per residue for model 15

- Molecule 1: RNA-binding protein 28

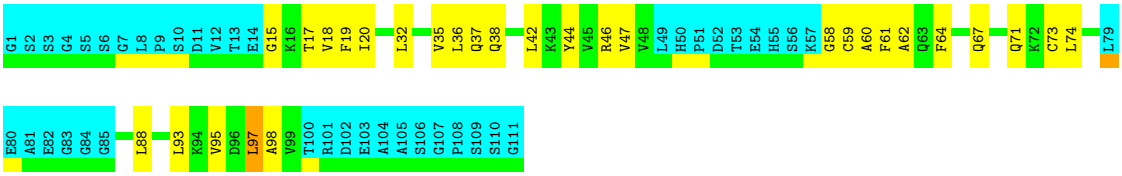
Chain A: 35% 24% • 38%



4.2.16 Score per residue for model 16

- Molecule 1: RNA-binding protein 28

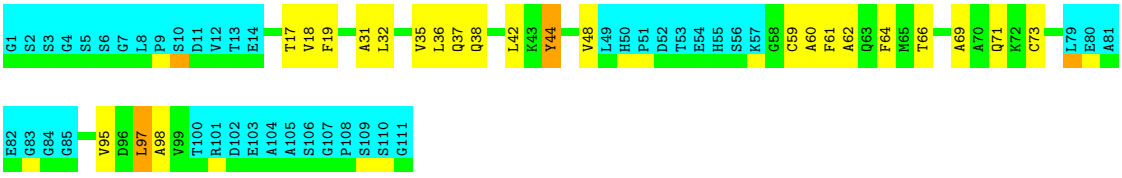
Chain A: 36% 25% • 38%



4.2.17 Score per residue for model 17

- Molecule 1: RNA-binding protein 28

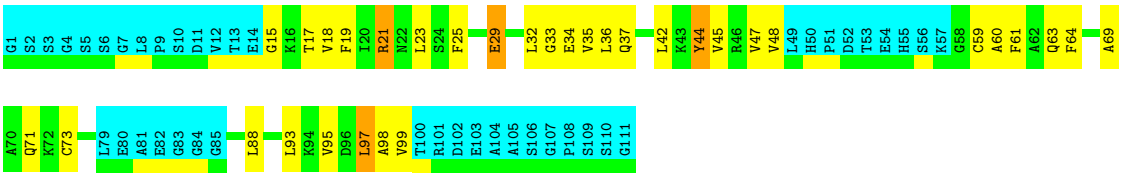
Chain A: 41% 20% • 38%



4.2.18 Score per residue for model 18

- Molecule 1: RNA-binding protein 28

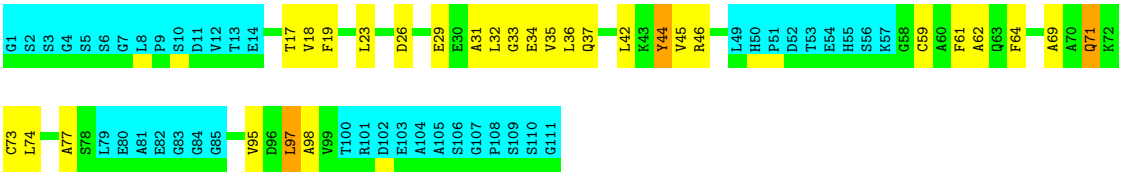
Chain A: 32% 26% • 38%



4.2.19 Score per residue for model 19 (medoid)

- Molecule 1: RNA-binding protein 28

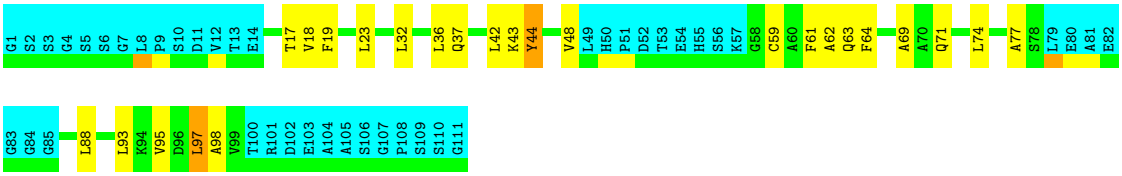
Chain A: 36% 23% • 38%



4.2.20 Score per residue for model 20

- Molecule 1: RNA-binding protein 28

Chain A: 40% 21% • 38%



5 Refinement protocol and experimental data overview (i)

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

Of the 100 calculated structures, 20 were deposited, based on the following criterion: *target function, structures with the lowest energy*.

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

Software name	Classification	Version
CYANA	structure solution	2.0.17
CYANA	refinement	2.0.17

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	530	539	539	35±4
All	All	10600	10780	10780	700

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 33.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:73:CYS:SG	1:A:95:VAL:HG11	0.86	2.10	12	17
1:A:64:PHE:CD2	1:A:69:ALA:HB1	0.86	2.05	3	8
1:A:18:VAL:CG2	1:A:62:ALA:HB3	0.85	2.02	2	15
1:A:64:PHE:CD1	1:A:69:ALA:HB1	0.82	2.08	20	8
1:A:31:ALA:O	1:A:35:VAL:HG23	0.82	1.75	10	9
1:A:19:PHE:CE1	1:A:61:PHE:CZ	0.78	2.70	18	11
1:A:36:LEU:HD22	1:A:73:CYS:SG	0.76	2.20	8	11
1:A:36:LEU:HB2	1:A:42:LEU:HD11	0.75	1.58	18	19
1:A:19:PHE:CD1	1:A:61:PHE:CE2	0.75	2.75	20	19
1:A:27:SER:OG	1:A:88:LEU:HD23	0.74	1.82	13	2
1:A:88:LEU:HB2	1:A:93:LEU:HD11	0.72	1.61	13	14
1:A:37:GLN:CG	1:A:42:LEU:HD12	0.70	2.15	9	16
1:A:19:PHE:CD1	1:A:61:PHE:CD2	0.70	2.79	18	15
1:A:19:PHE:CE1	1:A:61:PHE:CE2	0.69	2.80	18	8

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:32:LEU:C	1:A:32:LEU:HD23	0.68	2.08	11	20
1:A:17:THR:CG2	1:A:98:ALA:HB3	0.68	2.18	17	20
1:A:37:GLN:HG2	1:A:42:LEU:HD12	0.66	1.65	9	5
1:A:23:LEU:HD12	1:A:59:CYS:CA	0.65	2.21	15	14
1:A:39:PHE:CZ	1:A:76:ALA:CB	0.64	2.80	8	2
1:A:71:GLN:HE21	1:A:71:GLN:N	0.64	1.90	11	18
1:A:23:LEU:HD12	1:A:59:CYS:C	0.64	2.13	4	16
1:A:37:GLN:HG3	1:A:42:LEU:HD12	0.63	1.70	1	16
1:A:29:GLU:HG2	1:A:45:VAL:HG22	0.60	1.71	18	1
1:A:17:THR:HG21	1:A:98:ALA:HB3	0.60	1.72	17	17
1:A:35:VAL:HG21	1:A:88:LEU:CD1	0.59	2.27	16	2
1:A:44:TYR:CD1	1:A:44:TYR:C	0.59	2.76	12	13
1:A:48:VAL:HG12	1:A:59:CYS:O	0.59	1.97	18	2
1:A:32:LEU:HD11	1:A:60:ALA:HB3	0.58	1.73	3	3
1:A:64:PHE:CD2	1:A:69:ALA:CB	0.58	2.84	3	8
1:A:97:LEU:C	1:A:97:LEU:CD1	0.57	2.73	1	20
1:A:64:PHE:CD1	1:A:69:ALA:CB	0.57	2.88	18	5
1:A:19:PHE:HB2	1:A:98:ALA:HB2	0.56	1.77	4	12
1:A:32:LEU:HD23	1:A:32:LEU:O	0.56	2.01	14	16
1:A:17:THR:HG22	1:A:18:VAL:N	0.56	2.16	10	19
1:A:32:LEU:C	1:A:32:LEU:CD2	0.54	2.75	3	17
1:A:18:VAL:HG23	1:A:62:ALA:HB3	0.54	1.78	5	6
1:A:42:LEU:HD23	1:A:63:GLN:O	0.54	2.03	18	2
1:A:71:GLN:NE2	1:A:71:GLN:N	0.54	2.56	8	2
1:A:44:TYR:CD1	1:A:44:TYR:O	0.54	2.61	17	5
1:A:18:VAL:O	1:A:18:VAL:HG23	0.53	2.02	14	18
1:A:71:GLN:N	1:A:71:GLN:NE2	0.53	2.56	4	17
1:A:17:THR:CG2	1:A:18:VAL:N	0.53	2.72	16	19
1:A:47:VAL:HG23	1:A:60:ALA:HB2	0.53	1.81	5	3
1:A:71:GLN:N	1:A:71:GLN:HE21	0.51	2.03	8	1
1:A:19:PHE:CE2	1:A:21:ARG:HG3	0.51	2.41	11	6
1:A:20:ILE:HD12	1:A:60:ALA:O	0.51	2.05	14	1
1:A:35:VAL:HG21	1:A:88:LEU:HD13	0.51	1.81	2	2
1:A:19:PHE:CZ	1:A:59:CYS:CB	0.50	2.94	17	2
1:A:74:LEU:CD2	1:A:95:VAL:O	0.50	2.60	19	5
1:A:97:LEU:CD1	1:A:98:ALA:O	0.50	2.60	18	19
1:A:74:LEU:O	1:A:77:ALA:N	0.50	2.45	3	11
1:A:39:PHE:CE1	1:A:76:ALA:CB	0.50	2.95	8	1
1:A:48:VAL:O	1:A:48:VAL:HG13	0.49	2.07	7	3
1:A:19:PHE:CZ	1:A:59:CYS:HB2	0.49	2.42	13	5
1:A:34:GLU:OE1	1:A:34:GLU:N	0.49	2.45	15	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:23:LEU:HD12	1:A:59:CYS:HA	0.49	1.84	7	1
1:A:37:GLN:CD	1:A:37:GLN:C	0.49	2.71	10	1
1:A:15:GLY:O	1:A:67:GLN:NE2	0.49	2.45	16	2
1:A:19:PHE:CZ	1:A:59:CYS:HB3	0.49	2.42	16	5
1:A:44:TYR:CE2	1:A:63:GLN:HB2	0.49	2.43	15	7
1:A:20:ILE:HD13	1:A:32:LEU:HD11	0.49	1.85	12	2
1:A:74:LEU:HD23	1:A:95:VAL:HG12	0.48	1.85	13	2
1:A:19:PHE:CE1	1:A:61:PHE:CE1	0.48	3.01	3	3
1:A:47:VAL:O	1:A:47:VAL:HG13	0.48	2.09	5	4
1:A:38:GLN:HG2	1:A:39:PHE:CD2	0.48	2.43	8	1
1:A:19:PHE:CD1	1:A:19:PHE:C	0.48	2.86	14	1
1:A:86:LEU:O	1:A:92:GLN:NE2	0.48	2.47	4	2
1:A:32:LEU:HD11	1:A:60:ALA:CB	0.47	2.39	3	1
1:A:38:GLN:CG	1:A:39:PHE:N	0.47	2.77	6	4
1:A:18:VAL:O	1:A:18:VAL:CG2	0.47	2.62	4	7
1:A:64:PHE:CD2	1:A:70:ALA:HA	0.47	2.45	15	2
1:A:44:TYR:O	1:A:44:TYR:CG	0.47	2.68	10	2
1:A:32:LEU:CD1	1:A:60:ALA:CB	0.47	2.93	3	1
1:A:18:VAL:CG2	1:A:18:VAL:O	0.46	2.63	12	10
1:A:71:GLN:NE2	1:A:71:GLN:CA	0.46	2.78	2	5
1:A:19:PHE:CD2	1:A:21:ARG:HD2	0.46	2.45	18	1
1:A:33:GLY:O	1:A:35:VAL:N	0.46	2.48	19	3
1:A:35:VAL:CG1	1:A:86:LEU:HD23	0.46	2.41	8	1
1:A:19:PHE:CE1	1:A:59:CYS:HB2	0.46	2.46	20	3
1:A:28:GLU:O	1:A:31:ALA:N	0.46	2.48	15	1
1:A:58:GLY:C	1:A:59:CYS:SG	0.46	2.95	16	2
1:A:20:ILE:HD12	1:A:20:ILE:N	0.45	2.26	1	2
1:A:29:GLU:CD	1:A:45:VAL:O	0.45	2.55	14	3
1:A:18:VAL:HG23	1:A:18:VAL:O	0.45	2.11	5	1
1:A:43:LYS:N	1:A:63:GLN:O	0.45	2.50	2	2
1:A:28:GLU:O	1:A:29:GLU:C	0.45	2.55	2	8
1:A:21:ARG:O	1:A:22:ASN:C	0.45	2.55	14	1
1:A:24:SER:O	1:A:27:SER:N	0.45	2.50	3	2
1:A:29:GLU:OE1	1:A:29:GLU:C	0.45	2.55	18	1
1:A:19:PHE:CD1	1:A:61:PHE:CZ	0.44	3.05	3	2
1:A:88:LEU:HB2	1:A:93:LEU:HD21	0.44	1.89	3	2
1:A:29:GLU:HG3	1:A:45:VAL:HG22	0.44	1.88	14	1
1:A:20:ILE:HD12	1:A:20:ILE:H	0.44	1.72	3	6
1:A:26:ASP:O	1:A:27:SER:C	0.44	2.56	7	2
1:A:17:THR:HG22	1:A:98:ALA:HB3	0.44	1.90	20	2
1:A:17:THR:O	1:A:18:VAL:CG1	0.44	2.66	15	8

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:26:ASP:OD1	1:A:27:SER:N	0.44	2.51	9	1
1:A:33:GLY:C	1:A:35:VAL:N	0.43	2.72	19	4
1:A:23:LEU:CD1	1:A:59:CYS:C	0.43	2.86	15	1
1:A:39:PHE:CE1	1:A:76:ALA:HB2	0.43	2.49	8	1
1:A:35:VAL:O	1:A:38:GLN:NE2	0.43	2.52	17	2
1:A:27:SER:OG	1:A:88:LEU:CD2	0.43	2.67	6	2
1:A:19:PHE:CZ	1:A:61:PHE:CZ	0.42	3.06	18	1
1:A:18:VAL:HG11	1:A:64:PHE:CD2	0.42	2.50	11	1
1:A:30:GLU:O	1:A:34:GLU:CD	0.42	2.57	15	1
1:A:97:LEU:C	1:A:97:LEU:HD13	0.42	2.35	20	3
1:A:26:ASP:CG	1:A:89:ASP:OD1	0.42	2.58	6	1
1:A:66:THR:O	1:A:69:ALA:HB3	0.42	2.15	17	1
1:A:38:GLN:CG	1:A:39:PHE:CD1	0.42	3.02	2	1
1:A:29:GLU:CG	1:A:45:VAL:O	0.42	2.68	19	1
1:A:74:LEU:O	1:A:76:ALA:N	0.42	2.53	1	1
1:A:88:LEU:CB	1:A:93:LEU:HD21	0.41	2.44	20	1
1:A:39:PHE:CZ	1:A:76:ALA:HB1	0.41	2.51	8	1
1:A:29:GLU:HB2	1:A:47:VAL:HG12	0.41	1.92	18	1
1:A:28:GLU:O	1:A:30:GLU:N	0.41	2.53	9	1
1:A:76:ALA:O	1:A:86:LEU:CD1	0.41	2.69	6	1
1:A:66:THR:O	1:A:69:ALA:N	0.41	2.54	17	1
1:A:38:GLN:HG3	1:A:39:PHE:N	0.41	2.30	6	1
1:A:36:LEU:O	1:A:64:PHE:CE1	0.41	2.74	16	1
1:A:32:LEU:CD1	1:A:60:ALA:HB3	0.40	2.46	2	1
1:A:29:GLU:CG	1:A:45:VAL:HG22	0.40	2.46	14	1
1:A:48:VAL:HG13	1:A:48:VAL:O	0.40	2.16	12	1
1:A:74:LEU:C	1:A:76:ALA:N	0.40	2.74	1	1
1:A:37:GLN:O	1:A:38:GLN:C	0.40	2.60	11	1
1:A:23:LEU:HD12	1:A:59:CYS:N	0.40	2.32	15	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	69/111 (62%)	60±2 (86±2%)	9±1 (13±2%)	0±0 (1±1%)	32 76

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	1380/2220 (62%)	1193 (86%)	180 (13%)	7 (1%)	32 76

All 3 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	27	SER	4
1	A	34	GLU	2
1	A	41	ASP	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	55/86 (64%)	52±2 (95±3%)	3±2 (5±3%)	26 75
All	All	1100/1720 (64%)	1041 (95%)	59 (5%)	26 75

All 18 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	97	LEU	20
1	A	44	TYR	12
1	A	92	GLN	3
1	A	26	ASP	3
1	A	59	CYS	2
1	A	67	GLN	2
1	A	71	GLN	2
1	A	94	LYS	2
1	A	24	SER	2
1	A	30	GLU	2
1	A	46	ARG	2
1	A	43	LYS	1
1	A	65	MET	1
1	A	89	ASP	1
1	A	78	SER	1
1	A	34	GLU	1

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Mol	Chain	Res	Type	Models (Total)
1	A	21	ARG	1
1	A	29	GLU	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